SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
l				sequence		
	-	<del> </del>				
4751	35119	Α	4792	3	1426	RRYDELQNSSGRDGKPRAMAV
	1					TRSTSSTSSGSNSNVLVPVSWK
		1				RPQYSQKRAKEKLVHVLSLCG
		1			į.	QEVGLSKNPSVIFSSCGDLDLLE
		1			ł	HQTSLVSSEDGAREQENMDDT
		1			l	NSEQQFRVFRDFDFLDVELEDG
		1				EELQGESMDNFNWGVRRRSLD
		1				SLDKCDMQILEERQLSGSTPSL
				-		NKMHHEDFDESSEEEDLTASQI
						LEHSDLIMTLSPSEETNPMELLT
ŀ		i				TACDSTPPEPHSFNTRMSSFDAS
1		1	1	1		LPDMNNLOISEGSKA\EAVREE
1	l	1				EDTTVHEDDLSSSINELPAAFEC
		1		ŀ		SDSFSLDMTEGEEKGNRALDOF
1			l	l		TLASFGEGDRGVSPPPSPFFSAI
İ				1		LAAFQPAACDDAEEAWRSHIN
		1		1		QLMCDSDGSCAVYTFHVFSSLF
						KNIQKRFCFLTCDAASYLGDNL
					1	
						RGIGSKFVSSSQMLTSCS\LDKL
		1				KFSVLELQEYLDTYNNRKEATL
						SWLANCKATFAGGSRDGVITC
		_				QPGDSEEKVIKAC
4752	35120	С	4793	60	164	
4753	35121	В	4794	44	2547	
4754	35122	Α	4795	401	9546	PRADITTCDRRITPGTCSRPLPV
		1				LPASLYAADMASQQDSGFFEIS
1	1	1				KYLLKSWSNTSPVGNGYIKPPV
		1				PPASGTHREKGPPTMLPINVDP
						DSKPGEYVLKSLFVNFTTQAER
		1				KIRIIMAEPLEKPLTKSLQRGED
	1		İ			PQFDQVISSMSSLSEYCLPSILR1
		1				LFDWYKRQNGIEDESHEYRPRT
	1	1	1			SNKSKSDEQQRDYLMERRDLA
1		1				DFIFSLVLIEVLKQIPLHPVIDSLI
İ		1			1	HDVINLAFKHFKYKEGYLGPNT
		1				GNMHI
4755		1				
4/55	35123	A	4796	2	6107	GERKPKIDLFRTCVAAIPRLLPD
4/55	35123	A	4796	2	6107	GERKPKIDLFRTCVAAIPRLLPD GMSKLELIDLLARLSIHMDDEL
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSIHMDDEL
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNFLLREVNDMHHTLL
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNFLLREVNDMHHTLL DSSLKLLLQLLTQWKLVIQTQG
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNFLLREVNDMHHTLL DSSLKLLLQLLTQWKLVIQTQG KVYEQANKIRNSEARDLELDV
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNFLLREVNDMHTLD DSSLKLLLQLLTQWKLVIQTQG KVYEQANKIRNSEARDLELDV GVDVDVGVDVDADVDVDVDL
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNFLRENVDMHITLL DSSLKLLLQLLTQWKLVIQTQG KVYEQANKIRNSEARDLELDV GVDVDVGVDVDADVDVDL GVDVDVGVDVDADVDVDVD GVDVDVGVDVDADVDVDVD
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNFLLREVNDMHHTLL DSSLKLLLQLLTQWKLVIQTOG KVYEQANKIRNSEARDLELDV GVDVDVGVDVDADVDVDVD GVDVDVGVDVDADVDVDVD MGVDVDVGVDVADVDVDVD MGVDVDVGVDRIYGFGCKCGCDR
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSHMDDEL RHIAONSLQGLLVPSDWRED VLEGFTNFLLREVNDMHHTLL DSSLKLLLQLLTOWKLVIQTOG KVYEQANKIRNSEARDLELDV GVDVDGVDVDADVDVDVDVD GVDVDGVDVDADVDVDVDVD MGVDVDVDRVIGFGCKCGCDR DVDRVVDVDVDIDVDVDVD DVDRVVDVDVDIDVDVDVD
4/55	35123	A	4796	2	6107	GMSKLELIDLLARLSIHMDDEL RHIAQNSLQGLLVDFSDWRED VLFGFTNFLLREVNDMHHTLL DSSLKLLLQLLTQWKLVIQTOG KVYEQANKIRNSEARDLELDV GVDVDVGVDVDADVDVDVD GVDVDVGVDVDADVDVDVD MGVDVDVGVDVADVDVDVD MGVDVDVGVDRIYGFGCKCGCDR

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		03/340,217	sequence	or pepade sequence	Circulati, i pusible acceptance assertion,
4756	35124	Α	4797	3	565	MLPGHLFCLAKAGKEEQEEKG
						QIITRKTITPQNIPGPGAHITATH
1						RGRCTVATKFSGGLCKEPNRLT
						WY/GPPLKGAHGGR/GPSSRVPS
				İ		FPAAGQPPIGGALHGAGSRGLA
						RTRAQLGGPPGGELRGT/SGNG
1						DGQGPDGDSRKSGSPLRPSHL/P
						DPAAVAGAPVSGHLQTPGHHA
						GRRQQAGPRGAGLP
4757	35125	A	4798	1	417	
4758	35126	Α	4799	I	1069	MPRPPVPANALGARGEAVRLQ
	1	1				LQGEELRLQE\ESVRLHQINIYL
			1			SDRISLHRRLPVRWNPLCKEKK
						YDYDNLPRTS\VTKAFYNEAWS
	ļ		1			TLLRTVYSVLETSPDILLEEVIL
1						VDDYSDREHLKERLANELSGLP
	ŀ	ŀ				KVRLIRANKREG\LVRARLLGA
						SAARGDVLTFLDCHCECHEGW
	l .	1				LEPLLQRIHEEESAVVCPVTDVI
	i .	1		l		DWNTFEYLGNSGEPQIGGFDW
	l .					RLVF\RWHTVPERERIRMQSPV
1						DVIRSPTMAGGLFAVSKKYFEY
1			1			LGSYDTGMEVWGGENLEFSFRI
1						WQCGGVLETHPCSHVGHVFPK
	1					QAPYSRNKALANSVRAAEVW
	l					MDEFKELYYHRNPRARLGLAC
		_				DECSIKAGWWL
4759	35127	Α	4800	1	1152	MHNSDGIEVMRQQKAEIGRVG
						GLEGIQLGVTEVIVNGARMLES
						YNCKAELGATGLVNYQISVKC SNOFKLEVYLLNAENKVVDNO
						AGTQGQLKVLGTNLWWPYLM
						HEHPAYLYSWEGRPDGAQAVG
						ALTPGTLAV\EVWLTAQKSLGP/
	1					SDFYTLPVGLRTVAVTESQFLIS
						GKPFYFHGVNKHEDADIQGKG
						FNWPLLVKDFNLLCWLGANTF
1			1			CTSHYPYTEEMLQICYRYGIVVI
		l				DECPAPSGHT\GPSVPSLLARW
1		1				OLFNNVSMHHHMWVVEEPVL
						RDKNHPAMVMWSLAKEPASFL
1		1	1			ESAGYSFKSLTMEQTARVLDLD
				l		TGEAVLOYRSLPRGAHKTLGK
1	1					KRKISSYNVDLTSCOLAKEKCL
1			1			KGPSSFLQSRQERMNSELRDN
4760	35128	A	4801	293	535	I CO. CO. EQUINQUIANISEERDIN
4761	35129	A	4802	94	686	
4762	35130	В	4803	1	2187	
1702	100100	10	1.305	<u></u>	12.0.	L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
4763	35131	Α	4804	596	1789	MFHVIERPYECKECGKNFRSGY
						QLTLHQRFHT\GIHKGGKPYEC
						KECKKTFTLYRNLTRHQNIHTG
						EKLFECKOCGKTYTTGSKLFQH
ŀ	1					OKTHTGEKPYECKECGKAFSL
						YGYLKOHOKIHTGMKHFECKE
		l				CKKTFTLYRNLTRHONIHTGKK
						LFECOECGKAYSTGSNLIQHRK
l		l				THTGEKPYKCKECGKTFSLHG
l						YLNOHOKIHTGVKPYECKKIHT
1	1			i		GGKPYECKECGKAFSRASNLV
1		l				OHERIHTGEKPYVCKOCGKTFR
		1				YGSALKAHQRIHRSIKVNOWL
						DSPRHKSINCDPMSPRTRKTRE
						RSHVSGRSLCQRLLGQGAQLRE
						FKOPPRNRFRRVCGLVARNTFP
						RGLRGRRASRRNAAASRLEDA
		l	ŀ			VAELLKARCSALGGSGLPEGLS
4764	35132	Α	4805	2	489	COGEGAKWEQGMTGRRWVVG
4704	33132	l^	4803	ľ	407	PPASSTPPHS/HFWLLVLSRGLV
					ł	GIGEASYSTIAPTIIGDLFTKNTR
						TLMLSVFYFAIPLGSGLGYITGS
						SVKQAAGDWHCALRESFLQLV
1						RLLKVTHLLQQLQLLYPTNGK
						RODTNHTRSQCAHYLPHLDFQ
			1	ŀ		VALCAYAVLOC
4765	35133	A	4806	l .	327	VALCATAVEQE
4766	35134	A	4807	899	1219	ANRKASTMRWYVRPFCSGLST
1,,00	33134	ľ`	1.007	1077	1217	LSREKLYPLRMLRMRASTGPLS
						GALGMYSTASPRLMFSGCSISS
						AR*LFRSSAVTMPPAAWMSFTI
						WAVRLPL*KAWAPSMASVS
4767	35135	A	4808	2152	2633	SRLDCGQGLVNGSCDYHHGCT
17707	33133	ľ`	1000	12.32	2005	GDTPRRPEWHRSLAHCMSPVD
				i		SLPGCAVSGSSDPWEVSWLWO
			l			O/VDRCDNREE/VMW*QRLGFP
						SPTVSFPORAVSASKPLO*APS
					]	WISLHSTLSQCRASDLRGRHTV
			1		1	PEVVYEWSPCALPTHREHPNAI
						MEGWPPPQAWWA
4768	35136	A	4809	2	387	SNASVILEGEDLRFSCSVRMAG
4708	33130	l^	4009	ľ	301	RLOGRESVIWOLVDRONRRSDI
			l			MWLDR\DGTVOPGSSYWERSSF
						GSVOMEOVOPNSFSLGIFNSRK
			l			
1			1			EDEGQYECHVTEWVRVVDGE
L	L	_	L	L	l	WQIVGERRASTPISIIALGE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4769	35137	Α	4810	46	3753	EIRSWEKRKRLVLCLLEAADM
						KCFFPVLSCLAVLGVVSAQRQV
						TVQEGPLYRTEGSHITIWCNVS
		1				GYQGPSEQNFQWSIYLPSSPER
						EVQIVSTMDSSFPYAIYTQRVR
						GGKIFIERVQGNSTLLHITDLQA
1			İ			RDAGEYECHTPSTDKQYFGSYS
1				1		AKMNLVVIPDSLQTTAMPQTL
l						HRVEQDPLELTCEVASETIQHS
				1		HLSVAWLRQKVGEKPVEVISLS
						RDFMLHSSSEYAQRQSLGEVRL
						DKLGRTTFRLTIFH
4770	35138	Α	4811	1	3728	MKCFFPVLSCLAVLGVVSAQR
						QVTVQEGPLYRTEGSHITIWCN
1	ł					VSGYQGPSEQNFQWSIYLPSSP
	1					EREVQIVSTMDSSFPYAIYTQR
						VRGGKIFIERVQGNSTLLHITDL
l						QARDAGEYECHTPSTDKQYFG
				1		SYSAKMNLVVIPDSLQTTAMPQ
		1				TLHRVEQDPLELTCEVASETIQ
						HSHLSVAWLRQKVGEKPVEVIS
1					ľ	LSRDFMLHSSSEYAQRQSLGEV
						RLDKLGRTTFRLTIFHLQPSDQ
		_				GEFYCEAAEWIQDP
4771	35139	A	4812	897	1217	ANRKASTMRWYVRPFCSGLST
		l		l		LSREKLYPLRMLRMRASTGPLS
1				ŀ		GALGMYSTASPRLMFSGCSISS
1				ľ		AR*LFRSSAVTMPPAAWMSFTI
	l		L	l	l	WAVRLPL*KAWAPSMASVS

553

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequenec ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4772	35140	Α	4813	1	1507	MWNSKINHDHDDQFLKTYYVL
		1				ESSISVGVASNASVILEGDDLRF
	1					SCSVRMAGRPQGRFSVIWQLV
		1				DRONCRSNIMWLDRDGTVOPG
	1	1				SSYWERSSFGSVQMEQVQPNSF
		1				SLGIFNSRKEDEGQYECHVTEW
						VRVVDGEWQIVGERRASTPISII
	1	1				ALEMGFAVTAISRTPGVTYSDS
		l				FDLQCIIKPHYPAQVPVSVTWR
						FQPVGTVEFHDLVTFTRDGGV
		l				OWGDRSSSFRTRTATEKAESSN
		l				NVRLIISRASDTEAGKYQCVAE
						LWWKNYNNTWTQLAERTSNL
		1				LVIRVLOPDRMGVSARALRGEP
		l				SPSOMPOACCHGNTGALVIGIN
l						EPESLPCLQTVTKLQVSKSKRT
						LTLVENKPIQLNCSVKSQTSQN
l						SHFAVLWYVHKPSDANGKLIL
		1				KTTHNSAFEYGTYVEEEGLRAR
						LOFERHVSGDLFSLTVORAEWL
		l				LSPNYAWYKLAEEVSGRTEVT
					1	VKQPGGSLGLGC\SVSGWAAEP
						VCTQGPRPCSWNTPLALTAAC
4773	35141	Α	4814	1	627	
4774	35142	A	4815	166	435	
4775	35143	В	4816	1	240	LILIO LOGO CALLO TOPO DO CALLO DO
4776	35144	A	4817	1	288	VVPASSPGAASEPRRRRRCLQP
ł	1					EKSVSPGSGGGHRDPPKARPPR
ŀ						PPSAPKP*RPRPFS*LARSLCFPA
ŀ						AGCAYGVGVGGAGGGRAGLR
		۱.	1010	201		QPVPAVAE
4777	35145	Α	4818	206	1041	VSVGSAPSDMPAAATRW/CNSR
ŀ	1	l				CQHGQRLSAR/PVAGPGT/RTSS
	1					FPWLAPRNVVVPGSLEMPGTA
l	1					GPQRGSHSSPQGSSALLSFS/CV
		1				HNVESKEPVCLLLPSMASRLLT
1	1					PRGTCRPVPGCLQHPLSLPPVL
l					1	VGTQSPSQAPKSAKRPSPQPQL
l			1		1	GWLQLHPGGSGLCLLPAPAGS
l			1		i	MECAALESVPSQLGIGAPGPCW
l					1	AQAGVQGWSNVATSSPSGPSA
						QGQPRAPPCLVCGPAQCGTSGS
			1			RSRATGLRPSCLECQVWWSPQ
	L	ļ				CGANPGDTTSSQDAGTRCSKV
4778	35146	A	4819	2	487	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
4779	35147	A	4820	152	758	RGARGPEWDGOLDGPGSOMC
						GMASAPRLRRSGVRAAAGHPV
				Ì		QQPRLLDGLSLTDESDSCVSFEP
				l		PSHPSSSSGPVTALSRGWNFLK
				1		AFPLMGETOERER/VLTHFSRR
						YCQCNPD/AQPSEDGIH/TLTCA
						LMLLNTDLHGHVIGEVTGETN
		1				RTDKOONRTEQSKROANADKH
				ŀ		NEHANNEOOHEHDKDNDTRTR
						DTEMRHAKRDNA
4780	35148	A	4821	100	220	
4781	35149	Α	4822	100	1588	CLKISTGYTGSMAEEASGNLTI
						MAEGEGEAGTSTHGQSRRKRE
						KEEVLHPFKQPDLVRSHYRENS
				ŀ		KEEICPHDSVTSCQTPPPTLGITI
1		1				RHEIAASICHVADTAGVAGDA
				i		MMRKTDLIPPFIGLTLQGGRSA
1		l				DMGNQKKWRKGSENLATLVA
1						MASERFHWQYSGNSTIQPKQK
						QHGMITRLVTAPVCPGLVQPSL
	ľ			Ì		CAVGLRNIMSLSSHTCALQNTK
				l .		QAWEGYDDCHSQRVSQPGEN
	ľ	l				MTKLSFLNLLNQMPSWGEGKM
				}		VPADFSGSCWEGTGTGSPAGSQ
	ľ	i				VSFLNRHNDGQLAGDSPGLPPP
	ľ					PCPRGLQGAEQRSALRRHKAD
	ŀ			1		VHRDQWLVISFSKKLRTSARK
	ŀ			ŀ		WYEAGPFSGVPRVLPAAAQGG
				1		TDFPFSPSEEPFQPSPFSMVQAH
	ŀ			l		TVRSKPQFHFPAAGENCLNRSE
						LSRNQGLQARVGPLAIMSSDPS
				ł		GDFVLYTPTILGFVGLEVLVSR
				l		EGTFLWRYSTCP\LNYKLWLPP
						GYLGLLVPKDQKVRAVFLGM
4782	35150	Α	4823	1329	1881	AHLEAAGWSSSVQPGPSPRVLG
	}	l				RAEEHGQQSGRAKEIGHKIPKE
i		1		ŀ		TFDELTAELETISSK\CLYLAKK
						NQVIQQELLSMKEVQQKCKKL
						EEVNKILEQEVVNLKTHEKNM
				1		VEFGDVEECKLQLEERAGQEIE
				1		KLEEINLQRACLSAKKVRAEGE
			1	1		LEPRRHHNHTLGFTEGPWGLM
			1			SVITGAYDLIR
4783	35151	A	4824	176	308	LGNLTSPFFN*KHRSTKGFTTLS
1		1				TVALLLTGHVGIKTSNCHPGY

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide lucation of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
4784	35152	Α	4825	1467	1890	DWFDELTAELETISSK\CLYLAK
						KNQVIQQELLSMKEVQQKCKK
	1	ŀ				LEEVNKILEQEVVNLKTHEKN
					1	MVEFGDVEECKLQLEERAGQE
	1				1	EKLEEINLQRACLSAKKVRAEG
	l					ELEPRRHHNHTLGFTEGPWGL
		<u> </u>				MSVITGAYDLIR
4785	35153	В	4826	I	753	
4786	35154	A	4827	225	410	
4787	35155	A	4828	225	410	
4788	35156	Ā	4829	225	1001	COURCE ON THE LEWIS POLC
4789	35157	Α	4830	141	1001	GGVRGVQQKETCAFKVLESIG
1		ľ				KLG\LALSVAGGAENSALYNVE
						AGHRAVIFDRFRGEQDIVVGEG
						THFLIPWVQK/PPIIFDCRSRPRN
	ļ	ļ.	1			VPVITGSKDLQNVNITLRILF\RF
	ŀ					VASQLPRIFTSIGEDYDERVLPS
		ŀ				TT\ENLKSVVAPFDAGELITQRE
	Į.					LVSRQV\SDDL\TERAATFGLIL
						DDVSLTHLTFGKEFTEAVEAKQ
						VAQQEAQRARFVVEKAEQQKK
						AAIISAEGDSKAAELIANSLATA
						GDGLIELRKLEAAEDIAYQLSR
4790	25150		4831	194	453	SRNITYLPTG\QSVLLQLPQ QPLPEPLELRPKAL*LTPSQIFSA
4/90	35158	Α	4851	194	433	
		ŀ				*RLKTAARLPRKPWAVLPQGFT DTPPHFSQAQISSSSVTYLSIILV
						KTHVLCSPEFHRTGVV
4791	35159	A	4832	1	86	PCESYLEHL*WSCRLLRRLGSV
4/91	33139	^	4032	1'	00	SLOLLS
4792	35160	С	4833	191	263	SEQUES
4793	35161	В	4834	1	741	
4794	35162	A	4835	3	96	
4795	35163	A	4836	li .	301	QEQQKMNTLQGPVSFKDVAVD
4173	33103	ľ`	4050	ľ	501	FTOEEWROLDPDEKITYGDVM
						LENYSHLVSLAYEVATSCTSEIL
						KPSNLPKSFFFSH*QDMISPSQT
						SSLSWSRERSCG
4796	35164	Α	4837	3	273	VLHFISAGNTFAHQQEHSPRKG
	33,04	Γ.	1.03,	ľ	2.3	PNNLSKRKLLPAV\GPRVFHGE
		1	1	I		DRHL/LFSTRKE*ARSLCYVQG
	1		1		I	
	1	1				GVQAPAAAFCSLLSLWGWAGC

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nuclcotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4797	35165	Α	4838	3062	3688	RSVTRAPPRSTFPLAQAPSPRSH
	1				HIREPTPSPHLGPLRGSHRGPPS	
		1		İ		RPLPPALAALSLLETLQPRLLHP
		ł				HLHL\LHDQGRACVRAYAHPS
		1				YLWRCHALGVWVES/ARLRPS
		1				ALPPAHSPPLAAPLLSSSVQPPA
				1		PALEPPPRPPAAGAAARCLAAQ
	1					HHHPSRLGVRQPPLAVGALGST
						WPPQAPAPPPELSALEQDRVGA
		ļ				QPPPPPSQGA
4798	35166	A	4839	1	197	
4799	35167	С	4840	26	358	
4800	35168	Α	4841	84	433	PASAPLGLSATVSACFQEQQKM
	1					NTLQGPVSFKDVAVDFTQEEW
		1			1	RQLDPDEKITYGDVMLENYSH
	1					LVSLAYEVATSCTSEILKPSNLP
l						KSFFFSH*QDMISPSQTSSLSWS
		1				RERSCG
4801	35169	Α	4842	1	372	VQWLFMQICLGGKHQQLRHQG
	1	İ				VQEKMLPLEGS*VIEAGSPTLIG
1	1					ETLSLEIINYIIGAGLESVHTHKS
		1				RQLGGWTRPGSHFQQVLIPAHT
İ		1				PMNLEPSQLSLEPRLVPAQQSL
						PSAPTPSKALSQ
4802	35170	В	4843	7	267	
4803	35171	В	4844	213	3895	
4804	35172	С	4845	141	359	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	:	
4805	35173	Α	4846	831	3017	RRRLHYSGSTRPWRTRAMLPR
						TLSLRPHLSLSLHLPLPCLLLHL
	İ					LPTHLPPGPKHQPTVREL/ARRO
	ļ.	1				RLPRACHPAONLLEQQPLRPSH
	i i					LQRH/LSLLPPLGLSQSGPPG/LA
	1					PQPLL*LQTPDHFAGADPCSIHO
	į.			1		TSH*HOGTSNPSGRDGYQTPSH
				1		ICP\SPAPKOSFLFGTONTSPSSP
				1	i	AAPAASSAPPMFKPIFTAPPKSE
				1		KEGPTPPGPSVTATAPSSSSLPT
1			ĺ	]		TTSTTAPTFQPVFSSMGPPASVF
					Į.	LPAPFFKQTTTPATAPTTTAPLF
			İ	1		TGLASATSAVAPITSASPSTDSA
	1	ĺ	İ	i		SKPAFGFGINSVSSSSVSTTTST
i i						ATAASQPFLFGAPQASAASFTP
1						AMGSIFQFGKPPALPTTTTVTTI
						SOSLHTAVPTATSSSAADFSGF
1						GSTLATSAPATSSOPTLTFSNTS
						TPTFNIPFGSSAKSPLPSYPGAN
						PQPAFGAAEGQPPGAAKPALAI
						SFGSSFTFGNSAAPAPATAPTPA
1						PASTIKIVPAHVPTPIQPTFGGAT
						HSAFGLKATASAFGAPASSOPA
						FGGSTAVFSFGAATSSGFGATT
						OTASSGSSSSVFGSTTPSPFTFG
1						GSAAPAGSGSFGINVATPGSSA
1	1		1			TTGAFSFGAGQSGSTATSTPFT
				1		GGLGQNALGTTGQSTPFAFNV
1		l		1		GSTTESKPVFGGTATPTFGQNT
1						PAPGVGTSGSSLSFGASSAPAQ
		l				GFVGVAPFGNTFAHQQEHSPR
						KGPNNLSKRKLLPAVRAQGPPF
4806	35174	Α	4847	9	935	IPCFGCAMPMYQTRRQENDLR
						TASIAV*RRKQQDDH*KQRRW
1						QNIQRKGPKRYIVIAGNSQSHQ
						PMIFSMLRKLPKVTCRDVLPEIF
1						AICIEEIGCWMQSYSTSFLTDSY
						LKYIGWTLHDKHREVRVKCVK
						ALKGLYGNRDLTARLELFTGRE
						KDWMVSMIMDREYSVAVEAV
1	İ					RLLILILK\NMEGVLMDVDCES
			l		1	VYPI\V*ASN*ALASAVGEFLYW
	1		1			KLFYPECEIRTMGGREQRQSPG
1			1			AQRTFFQLLLSFFVESKSHFVTQ
l				1	1	GGGSGQFSAHRNLCLPGSGNFF
1						VSASRVAGIAGAPPHTWLIYVF
4807	35175	Α	4848	1	1749	
4808	35176	В	4849	282	1227	

SEQ ID	SEO ID NO:	Met	SEQ ID NO	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ		sequence		
4809	35177	A	4850	221	907	   FEDSFNRGVKKKAAKRPLKTTP
4007	33177	ľ.	1.050	1	, · · ·	VAKYPKKGSQAVHRHSRKQSE
						PPANDIFNAAKAAKSDMQHRE
		1		l		VRVKCVKALKGLYGNRDLTAR
			Ì			LELFTGRFKDWM\VSMIMDRE
						YSVAVEAVRLLILILKNMEGVL
				1		MDVDCESVYPIVLFYPECEIRT
				i		MGGREOROSPGAORTFFOLLLS
ł		1				
		1				FFVESKLHDHAAYLVDNLWDC
	1	i		1		AGTQLKDWEGLTSLLLEKDQS
4810	35178	В	485I	I	2361	TCHMEPGPGTFHLLG
48II	35178	B	4852	11	878	
4812	35180	Ā	4853	<del>li</del>	313	MPHTPRCLFRPQASCLVHFLEQ
10.2	33.00	ľ.	1000	ľ	1	QNKLLETKLQFFQNRECCKSNL
				1		EPLFEGY\TLRREAECMEANSG
}	İ			1		RLASELNHVQEVLEGYKKKYE
	1			1		EEVALKATAENEFVALKK
4813	35181	A	4854	188	354	CEVALKATACNET VALKK
4814	35182	A	4855	405	647	LPLISDOVSYSPPLMSKSLASLY
7017	33102		4055	1.00	1	QESY*TILARIPLPLISPFVNSLST
	1			1		DLFILLIGNTSIAIFAEFGVSAISL
				1		PSCNSLE
4815	35183	A	4856	1	585	MSSGEGKRTWLGSLWGGVRVP
1015	155.05		1000	ľ		VPPPICGLRVAVTSAGTSSFSLA
		1		Ì	ľ	PKPTRIRGERGKGQGRG/SSGN
		1				GGRGRAGASAGGSRGEVVSVA
						NDGRWRGRGRGVGCPRSSKRE
						DNRFAKHGRASGKA WEPHPPS
						QALRALFGPIRRGRAAETRIV
		1				YWIKDROLTNRDSTILELOKVL
		1				KTCCAQSMKIFCCLWNFVYKQ
4816	35184	С	4857	12	468	Treeriquiniti sezinii viitq
4817	35185	Α	4858	1	1156	MAFRKKIITAGCIDHVLSVSDS
						QQMQANLTQRTEAEIRKQTQIA
		l				PTFPAHSLPDKYLGFALLNRKII
		ĺ				GTFLVFNMCKRNHEDKNEAFT
		1				VLREKKVFNLEFCTLQNYSSEV
	•	1				KEKERORFSDKOTLREFATRKP
				1		ALKEMLKVLQRYKERKHIRKR
						NVKYSADHTTDHTANQADPNO
						QEPHVPGHAPDNKTIRQKQNQ
	ļ			1		HKDNTTRKHNOMTSDTSRTNT
				İ		KVSGQPRGKQTRRRHERQQKA
	1	l				RERGOHROK/RDAOTREHTOR
		1				QRQARAEE\QVIENKREEKRTS
		1	l	1		ERTNDSTRREGTRRPRRTEKGE
	1	1	l	1		ROEEGDRATATHRKDHDROOP
		l		1		HGAPHCSRSSRHGAPTGPLYCC
1		1		1		SPLPGTPSCTICTVQYGRLWPH
		1		1		MATEQLNMAGPNQDFQDVVW
			L		l	INT LEAFINWARE LACE AND A M.

SEQ ID			SEQ ID NO:		Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4818	35186	Α	4859	1	1580	MAPALLLLLLASGAAACPLPCV
						CQNLSESLSTLCAHRGLLFVPP
	Ì					NVDRRTVELRLADNFIQALGPP
	İ				1	DFRNMTGLVDLTLSRNAITRIG
						ARAFGDLESLRSLHLDGNQAG
	l					GAGHPRALRGPVNLQHLILSGN
	İ				1	QLGRIAPGAFDDFLESLEDLDLS
	ŀ					YNNLRQVPWAGIGAMPALHTL
						NLDHNLIDALPPGA\FAQLGQLS
	ļ				1	RLDLTSNRLATLAPDPLFSRGR
						DAEASPAPLVLSFSGNPLHCNC
						ELLWLRRLARPDDLETCASPPG
	l					LAGRYFWAVPEGEFSCEPPLIA
	l					RHTQRLWVLEGQRATLRCRAL
	l .	1				GDPAPTMHWVGPDDRLVGNSS
	l					RARAFPNGTLEIGVTGAGDAG
				1		GYTCIATNPAGEATARVELRVL
						ALPHGGNSSAEGGRPGPRTSPP
1	l	1				PLALLPRYNSSEDETLIYRIVPA
	l			l		SSHHFLLKHLVPGADYDLCLLA
				ľ		LSPAAGPSDLTATRLLGCAHFS
		l				TLPASPLCHALQAHVLGGTLTV
	İ		İ			AVGGVLVAALLVFTVALLVRG
						RGAGNGRLPLKLSHVQSQTNA
4819	35187	Α	4860	2	403	
4820	35188	Α	4861	87	442	PVFPWHPYSKDQKEESQSVLVI
	į.					WQKTAGGGWSTWWILSFSPET
					1	EKVVKK/AHVDTL*NEMWDVT
	l			İ		K*TAFKIPSCT*HQQHP*SFFRK
	l			1		SESQVIVFAGQGVKIH*YILLHS
						NVIHYMNEI
4821	35189	A	4862	2	651	EFIKQWDADKFEHIQTLEGHHQ
				l		EIWCLAVSPSGDYVVSSSHDKS
				l		LRLWERTREPLILEEEREMERE
	1			l		AEYEESVAKEDQPA\VPGEIQG
						D\SYFT*KKTIETVK\AAERIMEA
	1		l	l		FELYREETAKMKEHKAICKAA
			İ	1		GKEVPLPSNPILMAYGSISPSAY
	1		l	1		VLEIFKGIKSSELEESLLVLPFSY
			l			VPDILKLFNEFIQLGSDVELICR
	1		l	ŀ		CLFFLLRIHFGQITS

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NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1	ĺ	sequence		
4822	35190	A	4863	]1	703	MGLTKQYLRYVASAVFGVIGS
		[				QKGNIVFVTLRGEKGRYVAVP
		1				ACEHVFIWDLRKGEKGLKQEV
						TCLCPSPDGLHLAVGYEDGSIRI
						FSLLSGEGNVTFNGHKAAITTL
						KYDQLGGRLASGSK/RQPGGIV
						FTESILAYSSACQDKQNHYWGS
						SQ*CADFVIQLRQYCCSFSCS*F
		l				H*NMEQVYTAVYSHNDL*ICTL
		1				LILCTW**TGSHRNKAPKTMFP
						RCTEGLDRGNRPATHS
4823	35191	В	4864	I	2616	
4824	35192	A	4865	3	674	PECTGRTLRSASQOHDTFYILA
		1				CELNSLADDAQR\YDVP\NSCL
		1		1		YPPDLPWRPVMQAKKKELARR
		1		1		DDIEDGDSMISSATSDTGSAKR
1	i	1				KSKKNIRKORMKILFNVVLEAR
						EPGSGRRLCDLFMVKPSKKDYP
1		1				DYYIILEPMDLKIIEHNIRNDKY
1		1		1		AGEEGMIEDMKLMFRNARHYN
		1		1		EEGSOVYNDAHILEKLLKEKRK
		1	l			ELGPLPDDDDMASPKLKLSKA
		1			ł	ASHFII
4825	35193	<del> </del>	4866	3	425	ASFILII
4826	35193	A	4867	1	1115	LCSVPTLCLASSHLVSNLSTFKQ
4826	35194	A	4867	'	1113	TSSFIRHVVATLLGLYLALFCF
		1	l			
1						GWYALHFLVQSGISYCIMIIIGV
		l				ENMHNYCFVFALGYLTVCQVT
		1				RVYIFDYGQYSADFSGPMMIIT
1			ł			QKITSLACEIHDGMFRKDEELT
		l				SSQRDLAVRRMPSLLEYLSYNC
						NFMGILAGPLCSYKDYITFIEGR
						SYHITQSGENGKEETQYERTEP
1						SPNTAVVQKLLVCGLALLFHLT
			İ			ICTTLPVEYNIDEHFQATASWPT
				1		KIIYLYISLLAARPKYYFAWTLG
		1				TAPRKWSPCPGPQCIQLRAADP
		ı				SGPEPLLMLSSQERQPKAKPPK
		1	1	1	1	EAHADIAGTPREGEKTRTGGPG
						KAFLRDPGASSSVELSRTQLWV
						LTPPPIAKAPCECLQ
4827	35195	В	4868	218	656	
4828	35196	A	4869	1	180	
4829	35197	A	4870	12	199	GLFPLEPGANGI*GC/SGRIRAQ
1		1		l	l	RWLPGRPKFTGESFIR*PPRVAK
1	1	1		l	l	ESGQLIWFGCVPTQISS
					l	

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NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	delction, \=possible nucleotide insertion)
	l			sequence		
4830	35198	A	4871	1	5058	MKLRGVSLAAGLFLLALSLWG
7030	33120	l^	1071	l'	5050	QPAEAAACYGCSPGSKCDCSGI
	1	ļ.				KGEKGERGFPGLEGHPGLPGFP
1		l			1	GPEGPPGPRGQKGDDGIPGPPG
1		ŀ				PKGIRGPPGLPGFPGTPGLPGMF
ŀ						GHDGAPGPQGIPGCNGTKGER
1		ļ.				GFPGSPGFPGLQGPPGPPGIPGM
		ŀ				KGEPGSIIMSSLPGPKGNPGYPG
						PPGIOGLPGPTGIPGPIGPPGPPG
		ŀ		1	ł	LMGPPGPPGLPGPKGNMGLNF
		ŀ				
		1				QGPKGEKGEQGLQGPPGPPGQI
4831	35199	ļ. —	4872	3	1646	SEQKRPIDVEF
4631	33199	Α	4872	P	1040	EDEGRAKGHHTWQQTRENESQ
		ŀ				AKGETPYKTIRFRETYYHKNSM
1		ľ				GETTPMIQLSPTGSLPQHVGIM
1						GATIQDKIWVTPGLPGFPGTPG
				1		LPVKRGFPGSPGFPGLQGPPVIP
		1		l		GPTGIPGPIGPPGPPGLMVTPGP
1	1					PGLPGPKVNMGLNFQGPKGEK
						VKQGLQGPPGPPGQISEQKRPID
	l			1		VEFQKGDQVIPGDRGPPGPPGI
						RGPPVTPGGEKGEKGEQGEPG
		ŀ				KRVKPGKDGENGQPGIPVMPG
					1	DPGYPGEPGRDG/EKGNAVMG
		1				PPGPPGFPGERGQKGDEGPPGIS
						IPGPPGLDGQPGAPGLPGPPGPA
i i						GPHIPPSNKGDTCFNCIGTGISG
						PPGQPGLPGLPGPPG\IPGAPGA
1	1					PGFPGSKGEPGDILTFPGMKGD
1		ľ				KGELGSPGAPGLPGLPGTPGQD
						GLPGLPGPKGEPVRITFKGERGF
						PGNPGLPGLPGNIGPMGPPGFG
		ļ.			İ	PPGPVGEKGIQGVAGNPGQPGI
		ŀ				PGNKGDPGQTITQPGKPGLPGN
				l		PGRDGDVGLPGIPGLPGQPGLP
1000	0.000	١.	1072	110	244	GIPGSKGEPGIPGIGLPGPPGPK
4832	35200	A	4873	110	256	CSGTYRCYSF/HSRDPYLWSAPS
1		1				DPLE/LVVTGPARQYYTKGNLV
		<u>.                                    </u>			****	RIASGL
4833	35201	A	4874	2	2888	LSDPCSSRWDERSLSQRSRSWS
						YNGYYSDLSTARHSGHHKKRR
						KEKKVKHKKKGKKQKHCRRH
		1				KQTKKRRILIPSDIESSKSSTRR
						MKSSCDRERSSRSSSLSSHHSSK
1		1		I	1	RDWSKSDKDVQSSLTHSSRDSY
1	1	1		l		RSKSHSQSYSRGSSRSRTASKSS
1				l		SHSRSRSKSRSSSKSGHRKRAS
1		1	1	l		KSPRKTASQLSENKPVKTEPLR
1		1	l	I	}	ATMAQNENVVVQPVVAENIPV
1	1	1		l		IPLSDSPPPSRWKPGQKPWKPS
1	I	1	I	1	1	YERIQEMKAKTTHL

NO:	SEQ ID NO: of peptide					Amino acid sequence ( X=Unknown,
		hod	in USSN	Nucleotide location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>		350	986	LWGGGSARLLRLPRGPCLPPAS
4834	35202	A	4875	330	986	
						PSSPSSSSELS*SCSLGPSSSSSSS
						SSSCSLCPSSSSSSSSP*LPPSSSS
						SSSRPLPPPSSSSSSSSSSSSSSSSS
		1				SECLCSPSSRPRTTVAGLGPAPG
						FPSGPVDTCSVWLLRFTSTMIW
						DCSLRL*VPEPPSSSSNSSPPSSL
						HKLAGGPPASSTPPSFSSLKKG
						WAGPMVAGTVPPAVPAPSSTR
						TE
4835	35203	A	4876	1	496	SQSYS\RGSSRSRTASKSSSHSRS
						RSKSRSSSKSAVLASTARCAGS
						RKQCVPLPIRLCQLQSRSLQPS
						MVPWRWGLTGPRGIALPPAAR
		1		į		PGPLHEAPRWGPPPRRAPRPWP
		l				PGARPGRRRRRAAASPAPSSCG
		l				PRASGAAGGGRGAPIGARASA
						GAAVWTPISTT
4836	35204	Α	4877	3	4578	TLAVFVPTLAGFSVALGGPAW
		l				GRRRRSVSGVGVWLQWQCFLF
		l				CSRGPAQAGGQPALAATSVAM
j		l				GAQDRPQCHFDIEINREPVGRI
						MFQLFSDICPKTCKNFLCLCSG
		l				EKGLGKTTGKKLCYKGSTFHR
		l				VVKNFMIQGGDFSEGNGKGGE
						SIYGGYFKDENFILKHDRAFLLS
		1				MANRGKHTNGSQFFITTKPAPH
		l				LDGVHVVFGLVISGFEVIEQIEN
		l				LKTDAASRPYADVRVIDCGVL
			l			ATKSIKDVFEKKRKKPT
4837	35205	Α	4878	I	1689	

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NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	endon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1		l		sequence		
4838	35206	Α	4879	II .	1604	MGISCPGSSKMLNSRALPVLKL
4030	33200	l^	4077	,	1004	TQGALRDCKERANYTNFNIYK
İ		1				AVESQGKFVCVLYNGQQSPEY
		1				VMIPCTSVSPTGQEVPEDRGMR
	1					MVMKNKPNKPSKMOSLKSSKI
						LTNSVIVIAVGIFFSVTLOARDP
						QLDDAIEQLRGVCIRAWEKITS
						GGEQYPSFSAIKQGPKEPYIDFI
						ARLQESLKKMIADSAAQDIVLQ
		l				LLAFDNANPDCQAALRPIRGKA
1						HLVDCIKACDDIGDGSSNGKAS
						YFGSKSKVFQTSYTSAQKAELV
		ŀ				AVIEVLTAFDMPINVISDSSYM
		ŀ				VYSTQLIENAQLRFHTDEQLMT
		ŀ				LFTQLQTAFRSTMHPFYITHIRA
1		ŀ				R\HTPLPGPLTEGNOMADCLVA
1		ŀ				NAISNARHFHNLTHVNASGLK
						HRYSITWKEAKNIIQRCPTCOM
1						VHSSSFRGGVNPRGLEPNSLWC
-						MDVTHIPLEGRLAYVHKRRRIR
	l					GGGGGEGEGEGEGEEEEE
						EEEEEEEEEEEEE
						QEQEEQEQEQEQEERRRKDTE
	l					ELSYSLPLNRTQPCWHPDFGLP
4839	35207	Α	4880	1	1146	
4840	35208	Α	4881	1	1577	MGQVWALVHSTLETFHTDEEE
1	ŀ					GEYNEVTEQVCLPAKAGSAAV
						DLCCTKAVSLLPGESPQKVPTG
						AGGPLPAGMTGLLLGRSSLNIK
						AVQVQTGVTDSDYNGEIQIVTS
		1				TSVPWKAKPGDHIAQLLIVPKK
		l				F\EGLKEPLQVERQSSCQGLGY/
						PFLMAAIVKPPEPIPLKWLTDKF
1						IWTEQWPLSKEKLEALEDLITQ
1						QLKKGHIAPTFSPWNSPVFIIKK
						KSAEQDCEWFVFTILAVNNLQL
		l				KPAKRFHWKVLPQGPNQQPIW
						PSRYLKPYHKPDAKEEIPEGSQ
						GFPVAAMSRLTLRRTPTVTSNT
						HRTQPPTWGQIEKLPQMAEENL
		ŀ		'	1	RKAGQPVTISNWILPRITKFKPI
		1				EGAENVFTDGSSNGKASYSGSK
1		1			1	GPLTEGNQMADRLVAKVISNA
						RHFHNLTHVNASGLKRRYSIT
		1				WKEAKAIIQRCPTCQVMLSAAE
		1				QHLQKSAAKTEAEKLVWWRD
1					1	PITKSREIGKIITWGRGYACVSP
1			l			
						GPNQQPIWIPSKHLKPYHKPDA GEKISGGNCGPHPHPRLQPCPD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide inscrtion)
				sequence		
4841	35209	A	4882	1	420	MTNISTTLKDLKDAGMIDPIKS
						TFNL/PIWIPQKPDGSWKTTANN
						/R/KLNQATISIAAIVLDVASLPG
				1		KARSYHGFSSHAGRVIDSNNOK
		1		1		DIEGCTYILNVAGKNMFGIQLR
		1		ì		RSVIFPCPNLMYTDNCSSHGPR
		1				GPSDYDSDP
4842	35210	A	4883	213	687	PEHILPGAQEGPSC/PLEPELE/V
		1				*NMSSWNTLSESCKMHGDLKY
	1	1				LFVITAKDQQ/VSIAAST/*GFC
		1		1		WNQ*VSASPSQAPGMPLVLGR
		1				RLWOGSRLGGLSISLSDDCHGA
	1	1				HNHSFKRVTTTLQVFSWTVPO
	i	1				AEPAMDCIHTA/DSPRQRLP*QA
		1		1		HESVAEVIIT
4843	35211	A	4884	1	648	MSSWNPLPESFKKIIGYLLYLFV
						ITAKDQQ/VSITASTWGFYWNH
	1	1				SOGKNPEOMEASOKPVAGLWA
						WWLNISLSAASHGAONHPFKR
		1				VTTTLQSQGWNKDLWIMRELL
		1		1		CNNRPEOLLOETATIKAPIAPAD
		1		1		PWSQEVIYNFCKAVSSVSCMPF
		1		1		NIHFNSNIPPESSGDWRMQQPC
		1				KVEQSILGAQRGGGGCRPGSLR
1		1				ELFPCLLAEPNMEEEVAALRA
4844	35212	Α	4885	3	597	GTLEPAAEWSVLLGV\HSQDGP
		1				LDGAHTRAVAAIVVPANYSQV
						ELGADLALLRLASPASLGPAV
						WPVCLPRASHRFVHGTACWAT
						GWGDVQEADPLPLPWVLQEVE
						LRLLGEATCQCLYSQPGPFNLT
						LQILPGMLCAGYPEGRRDTCQP
		1				SPEPGPMCIS/VSHIQRLRDAVS
		1				HTWQRGTEPARLGSWERRQRQ
						QQQGPV
4845	35213	В	4886	387	552	
4846	35214	Α	4887	20	612	
4847	35215	Α	4888	792	959	TGLSSSQNPKATKSIPWHNRLL
						PNVDSQVQQNSQAIIYTN*GNS
						ESQYPFSKMDT
4848	35216	Α	4889	268	500	
4849	35217	Α	4890	1	529	
4850	35218	В	4891	259	1672	
4851	35219	Α	4892	480	657	
4852	35220	Λ	4893	2	377	WCDFSSSLHRSVQALRTFCVTL
		1		1	1	SGAFVRDCTTVLSSTTCEPSTD
	1	1			1	V/CWAMNIVTSVLLLYGSEEEA
		1		1	1	FWLLVALC\ERMLPDYYNTRV
		1		1	1	VVIRTYDQRYEQCVDLYDGLP
				L	L	TTLFTTDDWHVWPDLTGLP

SEQ ID	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	med	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4853	35221	IA	4894	11	251	I TEARKAAAVMPKTAVLAAERP
14033	33221	ľ`	1071	ľ	120.	KKAWGVLIPKKSTKRTPKAFA
1	İ					GGGCW/TKVGWSKVAKKVPKF
		1				EASKPKKAAPKTRRYKSTLKTK
		1				
4854	35222	Α	4895	283	427	PSVSKESPLNSPASQAGSATFAT
		1				TPLTPPK/PAATSSVAAAALLPA
		1				LPR
4855	35223	Α	4896	111	1095	SRGWSRLPVPCCAPALLSPWAV
		1				NGIRRRGAGDGTRRGGSGCAG
						AHSAGLVASGPESWIPGPVPPG
		1				AEPPRRGDSGLARCPAPGHPSR
	İ	1				ASPQRPAEGFDALAAPSRVPGD
		1		1		SRQLSRNNTRSRCEGRGGKTPP
		1				AWAGVHRHGPPPAAPPGRARV
		1			1	HGHRLRGGLGPGGGKRGLPGC
	l	i		1		CPRAADPRGRP/GETSRSGERGP
		1				PGRSAPLSLQPRHRTGLET/RQP
		1				SPLARSRPGLGPRPSARRPSRPA
		1				PPPPPPELHRGAPQRGRVASQT
						RPGARARPAADTHSSLKSPASQ
		1				AGSAAFATAPLTPQKPQLRAP
		1				WQPLHSFRPCRGVTSRLRTAPP
4856	35224	В	4897	243	452	
4857	35225	Α	4898	3	353	RRYLSPKYIKMFVLDEADEMLS
	1					RGFKDQIYDIFQKLNSNTQVVL
	ĺ					LSATMPSDVLEVTKKFMRDPIR
	ł					ILVKKEELTLEGIRQFYINVERE
	į.	ı				EWKLDTLCD\LSAMHGDMDQK
						ERDVIMR
4858	35226	Α	4899	3	410	NLQEWKLDTLCDLYETLTITQA
						VIFINTRRKVDWLTEKMHARDF
	i					TVSAMVCLPAASLLWVCPSEV
						SYLKPGFLEPRCLPGLLHICFLF
	1	1				QHGDMDQKERDVIMREFRSGS
		1				SRVLITTDLLVSRGN**QRQKG
		_				GSKVI
4859	35227	Α	4900	1	235	MLSYVLEVTKKFMRDPIWILVK
		1				KEELILESIHQFCINVEQEKWKL
	1	1				DTLRDLYETLTITQA\VIFTNTR
	L	L		L		RKCCSKVREI
4860	35228	Α	4901	3	48	NSNVEREEWKLDTLCDLYETL
		1				TITQAVIFINTRRKVDWLTEKM
	1	1				HARDFTVSAMHGDMDQKERD
1		1	1		1	VIMREFRSGSSRVLITTDLLVSR
l	1	1	L			GN**QRGTRGVEAGHTM

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4861	35229	A	4902	2	879	AOFPTRLDLKATQALVLAPTRE LAQHIQKVVMALGDVMGASC HACIGGTNVARAEVQKLQMEAP HINGTFGRVFDMLNRRYLSPK YIKMFVLDEADEMLSRGFKDQ YDIFQKLNSNTQVVLLSATMPS DVLEVTKKFMRDPIRLVKKEE LTLEGIRQFVGVENEWKLDT LCDLVETLTITQAVIFINTRRKV DWLTEKMHARDFTVSAMHQD MDQKERDVIMREFRSGSSRVLI TTDLLARGIDVQVSLVINYQL TTDLLARGIDVQQVSLVINYQL
4862	35230	A	4903	1	1764	AINMYTEEDK  MASLEEGIYSLKINSKRSSYNS MNPQFTAGSEQONETEEPNKFC SRKGRPQDSGSLSLSVLQEILG DDIPKVKEEAVISSQSDLGECPY CGERPARNATIFAPQKEKESAP EMSSSCDKRVTVNPPEKFSEGR PKTQNTLICEKCSQPSNFLDDY NPHVIQKRLSNQGRVICEKSSP PLNVPDNYNSHSVIGKHKEKM
						AIERPSSGSDWSDVGGTTVIFSE EKPFSLCLPVSEPPYVATDYT TFPPHYSPWHDYTSSWFSSTKS SCYPSLGSSSNTLQAGKSSCSSS SRSNNNIFQGERSSHOGFLSDYS TSFPVSSENTSRDLKMTEEGRS KNSSLFYYSRNVEAEAKERVY QEETLGHPYGGRASSPPRTIW QPEQPGFIDTHCHLDLLYSRLPF
						KGTFTKFRKIYSNTFPKEFGGCI SCFCNPQNLSDNLWEDQLKDD LVWGVFGCRPHFAHYYNNYQE RSILKALRHPKAVAFGEMGLD YSSKCTTHIPEQQKVFKRLLRL AVSLKIKPMMIHCREADEDLLG ILKKYVPSDHKMYQHCFTGSYF VIKPLLSCFPNLYVGFMAILTYS SAEQARETVKK

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4863	35231	IA.	4904	1125	820	I VLAPNYHITFRNLSSVSSPVTSA
4865	35231	IA.	4904	123	820	
						EPVLQAGQARELSFSSLHPASPL
						LVPSTPALTLHAFNALVLFPSFP
		1			i	LEKAAKRERPKSKIQITARVGK
ŀ		1				MRRTWSPHTTISAGGSVNGAST
						LKNSLVWEAKPADTTNPTPPTT
		1				HPNPGPTPPTNTNRHPPPHHPLT
						NTPAPPHQPPATTP/SPQTQTPN
			1			YCPNTDHTTPTHDTPNPVPPTR
	1		1			RTPPNRTGKRTNTSQNYRLVSP
		<u> </u>				APKIHWEA
4864	35232	A	4905	407	757	OVER THE OWNER OF THE OWNER OWNER OF THE OWNER
4865	35233	A	4906	5	426	GKTSTKSQNASSPPKDHNSSPA
			1			REQN/WIENEFNELTEVGFRRIT
	i		1			SLEKNINDLMELKNTARELREA
	1		1			YTSINSQINQVEERISEIEDQLNE
		1				IKHEDKIREKRMKRNQQSLQEI
						WDYVKRPNLRLIGVPESDIENG
						TKLENTL
4866	35234	A	4907	1	2267	MTGQFQDVVREEARPLPNRIM
			1			RLRFNHFATECSWDHLYVYDG
	1		1			DSIYAPLVAAFRCEVENRYQGN
						PLRGTCYYTLLIDYQFTFSLSQE
			l		-	DDRYYTAINFVATPDEETPPIRG
	1					RQTAHTGELQLTSGGYPSGMK
			İ	]		LPEEGTGERNRITINKKDVHTET
		ı	l			PSKGHQHQRPKVDKSTKIKKN
						QRKKAENSKNKNASSSPEDHN
				l		SSPAREQNWMENEFDELTEVG
		1		ľ		FRRWVITNSSKLKKHVLTQCKE
		1				AKNLEKRLGQLLTRITSLEKNV
		1				KELMELKNKAQELCEAYTSINS
						QIDQAEESISEIEDQLNEIKHED
		1				KIREKR\IKRNKQSLQEIWDYVK
						RPNLRLIGVPESDGENGTKLEN
						TLQDIVQDNFPSLARQANIQIQE
	i	ļ.				ILKTPQRYFSRRATPRNIIITFTK
				•		VEIKGKMLRAVREKDHSAIKLE
						LRIKKLTQNCTTMWKLNNLLL
1	1					NEYWVHNEIKAEINKFFETNEK
1	1	1				KDTTYQDLWDTAKAVFKGKFI
1						ALNAHRRKWERSRIDTLTSQLK
1	1		1			ELEKQEQTNSKASKRQEITKIR
1	1	1				AELKEIETQKTLQKINESRSWFF
1	1					EKINKIDRLLARPIKKKREKNOI
1	1	1				DTIKNDKGDITTEPTEMQTTIRE
1	1	1				YYKHLYANKLENLEEMDKFLD
1						TYTLPRLNQEEVESLNRPTTSSE
		1				IEAIINSLPTKKSPGPDGFTAKL
		1				YQRYKEEVVPLLLKLFQTVGK
						EGPLPNSFYWANIILIPKPGRHT
	1	1	l		1	LOI DI NOI I WANTED KEGKITI

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or peptide sequence	determin, (-pussion macretion)
4867	35235	С	4908	605	760	
4868	35236	Α	4909	94	400	
4869	35237	Α	4910	I	1538	MPIQMQYPQYKLVENKTQPPVI
1				l		YQYWPPADLQYRPPPEVKYRP
	İ			1		QVVCPVPNSTAPYQQPTAVVF
		ŀ				NPTAPPSGQGIIAQNTDLVEWF
		1				FLPHSTIKTFTLYLDQMATLIGQ
						ARLRIIKLCESDSDKIIVPLNKEQ
		1				VRQAFINSGAWQIGLADFVGII
		1				DNHYPKTKIFQFLKLTTWILPKI
						TRHKPLENALTVFTDGSSNGKA
İ						AYTRPKERLIETQYHWAQRAE
						LVAVITVL\QDFNQSINIVSDSA
						YVVQATKDVETALIKYSIDDQL
						NQLFNMLQQTVRKRNFPFYVT
						HIRAHTNLPEPLTKANEQVDLL
			ĺ			VSSAFLEAQELHALTHVNATGL
			į			KNKFDITWKQAKNIVQHYTQC
	1		i			QIPHLPTQEAGVNPREQHFTGK
l						KNSPHEGKLIWWKDKKNKTW
1						EIGKVITWERGFACVSQGENQL
						PGWIPTRNLKFYNEPLGDAKKS
		1				ASAETKNPQLSIIDSPGKAPGCL
				j		MPTTQNWLVEVPTVSATSKFT
						YHMVYPPAPKRQRPARTGHND
						DGSFVKKGDM
4870	35238	A	4911	1	759	FRMVIRCLPQRELDCDRGNWT
						ATSAELTGIKWRRYNFGGHGD
					i	CGPIISVPAQDDPILLSFIRCLQA
						NLLCVWRRDV*PDC*ELWIFW
		1				WGDEPNLVGV\YIMNCRLWKK
	1					DSGKMAFPMNVGRC/FFKAIHN
	ł					LLERCLMDKNFVRIGKWFVRP
	1					YEKDEKPVNKSEHLSCAF\TFFL
		1				\HGESNVCTSVEIAQHQPIYLIN
						EEHIHMAQSSPAPFQVLVSPYG
	1					LNGTLTGQAYKMSDPATRKLIE
						EWQYFYPMVLKKKKK
4871	35239	A	4912	Į I	539	MRHPCDGNSLYFDHISVNMLA
	1	1		1		VMLYYGFGRVSIGKTGLRGVQ
				i		RHLWPLPLDASSTKTVSSSHSD
						KGEIFSPFPCSLINCNNFEMRNT
	1	1	l	1		TKCLMDKNFVRIGKWFVRPYE
			1			KDEKPVNKRVTSQEIWLFDEY\
			l	1		GVSLPCFAVERCALLPLCLLPR
Ι.	1			1		LMISISSTSRQPQYISRRGLKAKI
		L				swvv
4872	35240	A	4913	198	620	

SEQ ID	SEQ ID NO:	Mat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1	1		sequence		
		_		1		
4873	35241	A	4914	63	1267	RNRILRMEFFDWFWAFWSWLL
		1			\	NMIRSQNAKDSSSNSMENTDSP
		ł				WCELFRELCKINALDVPDSLLV
						RGNEFSASVHNTFDHMWRTKE
						RYEAGWLLLSSADRVMKENDE
		1				LRDSVSWLQKQILSLKSAKIAL
						SGSLISYRERAEIVEKQTQTLIM
ì				1		RVADLQQKGYINSPALCHNLIW
				l		RDLDHFSFPYDITLFHYIDDIML
						IGSSEQEVANTLDILKGQRFVLT
1				l		VIDTYSRYWFASPECNASA/KT
i		İ				TIHGFTECIIHYHGIPHSIASYQG
				1		THFMAEEPGW\SKNQGVEVTPF
		ł		1		TITPSDPVATFLLPVPMTLRSAG
		1				LEVLVPEGGTLPPGDTTMIPLN
ŀ						WMLRLPPGHFGLLLPLSQQAK
		1				KGVTVLAVVIDPDYQDEISLLF
		l				HNGAIISDGNGVILIGLLQWFST
4874	35242	Α	4915	2	2210	
4875	35243	Α	4916	1	2036	MDTFLDTYTLPRLNQEEVESLN
		l				RPITGAEIVAIINSLPTKKSPGPD
						GFTAEFYQRYKEELVPFLLQLF
						<b>QSIEKEGILPNSFYEASIILIPKPG</b>
						RETTKKENFRPISLMNIDAKIVN
İ		l				KILAKRIQQHIKKLIHHDQVGFI
		ļ				PGMQGWLNTCKSINVIQHINRA
						KDKNHMIISIDAEKAFDKIOOPF
1		1				MLKTLKKLGTDGTYFKIVRAIY
1	1	1				DKPTANIILNGOKLEAFPLKTGT
1						ROGCPLSPFLFNIVLEVLARAIR
ľ		1				QKEIKGIQLGKEEVILSLFADD
1		1				MIVYLENPIVSAQNLLKLISNFS
		1		1		KVSGYKTNVQKSQAFLYTNNI
						QTGSQIMSDLPFTIASKRIKYLG
				1		IQLTRDMKDLFKNYKPLLTEM/
				1		KTKKWKNIPCS/WELEKTTLKFI
ļ		1		l		/WNRKRARIAKSILSQKNKAGG
				l		ITLPDFKLYYKATVTKTAWYW
						DQNRDIDQWNRTEPSEITPHIY
						NYLIFDKPEKNKOWGKESLFN
						KWCWENWLAICRKLKLDPFLT
						PYTKINSRWIKDLNLRPKTIKTL
			1	1		EENLGITIQDIGMGKDFMSKTP
						KAMATQAKIDKWELIKLKSFCT
		1	1	1		AKETIIRVNRQPTKWEKIFTTYS
	1	l				SDKGLISRIYNELKQIYKKKKQP
		1				HOKDFAYHFTVFVFYFGAFLLE
						AAATSLHDLHCNTTITG/HATPE
			1			
			1			**PV*HKRSSLTITYLCRSG*IIW
4976	26244	-	4017		1250	WCDPHTHS
4876	35244	Α	4917	I	1359	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4877	35245	В	4918	1	948	
4878	35246	Α	4919	1	981	
4879	35247	Α	4920	1	3747	
4880	35248	Α	4921	1	1875	
4881	35249	Α	4922	1	2238	
4882	35250	Α	4923	1	3924	
4883	35251	Α	4924	1	1068	
4884	35252	В	4925	62	389	
4885	35253	В	4926	1	3663	
4886	35254	А	4927	1	1474	MAVSTTVRVDMPCCAVMLYC WGRSGKEQQPDEALKGKGFTV CFEGLRFGQKPGSYFSLDQIGH VEIQMITPPWRGTTLSTKRGGR KRGKTESDREHNLAPPKGRDTP
						IKEGAHVRGGPLSCTPPTEKK GKARSPRYGDTHRGEGLNKTH RAPQNFSESRETTINKIDRPLAR LIKKKREKNQIDTINETPLAR LIKKKREKNQIDTINETPLAN NEETIDKFLDTYTLPRLNQEEV ESLNPPITGSEGEAINSL PHTKKS PGTDGFTAKFYQRYKEELVPFL LKLFQSIEKEGLPNSFYEASILLI AKIVSKILANRIQVHIKKLIHID AKIVSKILANRIQVHIKKLIHID KEIKGIOLGKEFAKLSLFADDTI ECLENPIVSAQNLFKLISNFSKV SYKIHVPKSVSFLYTNNIQAES QIKNAIPFTIASKRIKYJGQLT.
4887	35255	Α	4928	419	1002	CYQRWKVLKKSSGPLARL/IKK REKNQIDAIKNDKGDITIDTEI QTTIREYYKHLYINKLENLEET DKFLDTYTI.PRLNQEEVESLNR PITOSEIEAIINSLQTKKSPGPDG FTAKLYQRYKEELVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RIRIAKSILSQKNKAGGITLPDF KLYYKATVIYTAWYW

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4888	35256	A	4929	11	2502	MFFETNENKDTTYQNLWDTFK
·						AVCRGKFIALNTHKRKQERSKI
ļ						DTLTSQLKEPEKQEQTHSKASR
ŀ			i	1	1	ROEITKIRAELKEIETOKTLOKIL
						<b>QKINESRSWFFEEINKIDRLLAR</b>
1	1		l			LIKKKREKNOIDAIKNDKGDITT
						DRTEIQTTIREYYKHLYANKLE
	İ					NLEEMDKFLDTYNLPRLNQEE
					1	VESL\HRLITGSEIEAIINSLPTKK
İ	1					SPGPDGFTAKFYQRYKEELVPF
	l	l				LLKLFQSIEKEGILPNSFYEANII
		1				LIPKPGTDTTKKENFRPISLMNI
						DVKILNKILANRIQQQIKKLIHH
			ļ			DQVGFIPGMQGWFNIHKSINVI
				l		QHINRTKDKNHMIISIDAEKAF
						DKIQQPFMLKSLNKLVLEVLAR
				l		AIRQEKEMKGIQLGKEEVKLSL
						FADDMIVYLENPIISAQDLLKLI
						SNFSKVSGYEINVQKSQASLYT
						NNRQTESQIMSELPFTIASKRIK
				1		YLGIQLTRDVKDLFKENYKPLL
1					ĺ	NEIKEDTNKWKNIPCSWVGRIN
						IVKMAILPKVIYRFNAILIKLPM
				l		TFFTELEK\TTLKFIRNQKRACIA
					1	KSILSKKE\KAGGIMLPEFKL*Y
1				l		KATVTKTVWYWCQNRYIDQW
					l	NRTEPSEIIPHIYNHLIFDKPDKN
		1		l		KKWGKDSLFNKWCWEHWLAI
						CRKLKLDPFLTPYTKINSRWIK
1				l		DLNVRPKTIKTLAGHLGNTIRD
1					1	GLGKDFMTKTPKAMATKAKID
				l		KWDLIKLKSFCTAKETAIRVNR
4889	35257	Α	4930	1	4187	MGDFNTPLSTLDRSMRQKVNK
				l	1	DSQELNSALHQADLTDICRTLH
1				l	ł	PKSTEYTFFAAPHHTYSKIDHIV
i						GSKALFSKCKRTEIITNCLSDHS
1		1				AIKLELRIKKLTQNRSTTWKLN
1				I		NLLLNDYWVHNEMKAEIKMFF
1	1			1		ETNENKDTTYQNLWDTFKAVY
						RGKFIAFKAVCRGKFIALNAQN
				I		RKQERSKIDTLTSQLKELEKQE
						QTHSKASRRQEITKIRAELKEIE
				1		TQKTLQK\ISESRSWFFEKTNKI
		l		l		DRPLARLIKKKR

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4890	35258	Α	493 I	lı .	1818	MSSRGPCTLETLINPSPSVADDI
						PHLRPKPVYITTTRDNENIYSTK
					1	IPYMAARVVFIKWIVTFFLEKK
						YLTATONTKNGVDVLPKIIOTV
						GGGAVOERAPELDGGGPTEOD
						KSHSNSSTLSDRRLSNSSLCSIE
					l	EEHRMVYEMVORILLSTRGYV
						NFVNEVFHOAFLLPSCEIAVTR
						KVVQVYRKWILQDKPVFMEEP
				•		DRKDVAOEDAEKLGFSETDSK
						EASSESSGHKRSSSWGTH\NSFT
					'	SAMSRGCVTEEG/TIOMLKAGV
		1				OALLOPVLCVFPLIPLPPLCNOA
						ARPAVVSIPLGDLLPWLSVLGG
		1		l		PADQWHLSYLKPEGSSAYACIL
						EALESAGKGLWKVSAVGRKP
						WTRGRSDRKGTVGHQVQFLFF
		1		l		KDEGRVDSRILTLMVAWIRPN\
						LCVYISRELWDDFLGVLS\SLTE
						WEELINEWANIMDSLTAVLAR
						TVYGVEMTNLPLDKLSEQKEK
						KORGKGCVLDPOKGTTVGRSF
				ļ		SLSWRSHPDVTEPMRFRSATTS
				<b>!</b>		GAPGVEKARNIVRQKATAKRS
						QSISNCVHLSEALPATKSVPLLL
				ł		HTLYKNKALKAALGQPVGKAD
				1		QLVVAGSPSVCCVEDQWGRSN
						LEAMVLWLYCIPPDGDVLYL
1891	35259	С	4932	96	278	
4892	35260	Α	4933	1	261	KLRLPPGHFGLLLLLSQQAKKG
				l		VTVLAGVIDPDYHNEISLLLHN
		1		l		GGKKKTRPAEMLAEGKGNTE
						WVGEEVSHQYQL*PHDQLQKR
4893	35261	C	4934	36	385	
4894	35262	Α	4935	1	2349	
4895	35263	Α	4936	207	561	QLAEPPHWIPGTRKDAQCLVGL
			1	Ì		FGFWRQHIPHLGGLLWPIYRVT
	1			1		QKAASFEWGPE*EKALQQIQPS
	1	l		1		VQAALPLGP*DLADPMVLEVS
				1		MADRCAGWSLWQAPIGELQQ
	1	1	1		1	KPLGFWSKALP

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4896	35264	Α	4937	I	1375	MSTTQLDTMGAESLCNMETVQ
						VEDEGIQKLKEIRMVEWITPFRP
						THPSCEGPEDIPLTNALQNTFVR
		ŀ				AAPASLKSPVVALLLSPVGYRT
						HAVVISPVPECRFGIDILSSWQN
		l				PHIGSLAGRAHQKQFVGSWQG
		1				QQYAFTVLPQGHINSLALCHNL
		1				IWRDLDHFLLSQGITLVHYTDD
		ı				IMLIGSNLADPMVLEVSMADRC
	Į.	1				AGWSLWQAPIGELQQKPLGFW
		1				SKALPSSADNYSPFERQFFACY
		l				WALVETECLPTGHQLTMQPEL
ł		l l				PIMNWVLSDPSSHKWVHGQSG
		l				HGGRDSGYSWTQQHGLPLTKG
	ŀ	l				DLSMTTAECQIFQQQRPILSPRY
						GTIPWGDQPATWRQKWQRFVL
i	İ	1				TGIDTYSRYEFAYPACHASTKT
		1				TIHGLMEFLIHHHGIPHSIASDQ
						GTHLMAKEVRQWAHAHGIHW
		ŀ				SYHVPHHPEVAGLIERWNE\GL
						LKSQLQHQLVNRLRRELQCWL
4897	35265	Α	4938	1	324	INCLRNCKTYQA/RKPLWFYNT
						SLKFFLNKP/MLADVVFEIQGTT
				1		VPAHRAILV/ARCEVMAAMFN
				1		AGIFQAMCLLICAE/MYQVSRL
			1	ĺ		QHICELFII/TQLQSMPSRELASM
						NL

SEQ ID	SEQ ID NO:					Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	or peptide sequence	deterion, (-possible fracteoride insertion)
4898	35266	Α	4939	108	2304	VAAAYPPPASPPWSPARSLAGA
	1		1		\	APAPLCVGPAAVEAREGDAAG
	1					DERIAGELAARGPREAVSRCFS
		l				PSRRPALGFEIMSIHIVALGNEG
	l					DTFHQDNRPSGLIRTYLGRSPL
	l					VSGDESSLLLNAASTVARPVFT
		l				EYQASAFGNVKLVVHDCPVW
						DIFDSDWYTSRNLIGGADIIVIK
						YNVNDKFSFHEVKDNYIPVIKR
						ALNSVPVIIAAVGTRQNEELPC
		l				CPLCTSDRGSCVSTTEGIQLAKI
			ŀ			LGATYLELHSLDDFYIGKYFGG
		1				VLEYFMIQALNQKTSEKMKKR
						KMSNSFHGIRPPQLEQPEKMPV
						LKAEASHYNSDLNNLLFCCQC
						VDVVFYNPDLKKVVEAHKIVL
	ļ.					CAVSHVFMLLFNVKSPTDIQDS
						SIIRTTQDLFAINRDTAFPGASH
		İ				ESSGNPPLRVIVKDALFCSCLSD
						ILRFIYSGAFQWEELEEDIRKKL
						KDSGDVSNVIEKVKCILKTPGK
	į.					NCLRNCKTYQARKPLWFYNTS
	l l					LKFFLNKPMLADVVF\EIQGYG
				l		QCPAHRAIL\VAPCEVM\AAMF
	į į					NGNLHGKAKSVLIPVYGVSKET
				1		FLSFLEYLYTDSCCPA\GIFQAM
		İ				CLLICAEMYQVSRLQHICELFII
	1					TQLQSMPSRGTGHPWNLDIS/V
						DLL*KGPSFHHSWIAFSTWAYF
				1		HFHCYLTYLIFQFKRPGIFRDLF
						S/EGRNGSFLFGKRHRWGPSNM
						LLGRQLAGITGKYYFTSPGNVG
4899	35267	В	4940	1	3117	
4900	35268	A	4941	1	1162	MRVCARACVRTRTRMCVYAH
						TCVCVRTYAYVRVRVRVHVRA
	1					RVRVCAYARTRVRNSLSILPFIQ
						LTLATPIHHIHQEEFNIRGIVPVL
	l					RRVKPDLAIGIDITPSCDTPDLH
	1	l				DYSEVRINQGVGITCLNYHGRG
		i			i	TLAGLITPPRLIRMLEQTALEHN
						IPVQREVAPGVITETGYIQLFLP
	1					GWEIGFSPLALLLAFLCSTSPGF
	1			1		GDPDGLGVIAYQDTVRPNAAT
				1		AISELNALAVKGVILTGDNPRA
						AAAIAGELGLEFKAGLLPEDKV
	1			1		KAVTELNQHAPLAMVGDGIND
	1		l			APAMKAAAIGIAMGSGTDVAL
	1					ETADAALTHNHLRGLVQMIEL
	1	1				ARATHANIRQNITIALGLKGIFL
						VTTL\MTGLWLAVLADTGATV

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
4901	35269	Α	4942	1889	3387	QWAIKQFKHAEKENPYLFGGG
		l				HLRAIFR*SGFQ*RQLHTMHWG
	1	l				AS/QQAEHP/LAQPSTRAQLRTPI
	1	l				P/TADS/QRALVGSGMKPRLNG
	ł	l				ERVLICAAGKHPADAFTGLINE
	ì	l				LESAGQTVVLVVRNDDVLGVI
		1				ALQDTLRADAATAISELNALGV
						KGVILTGDNPRAAAAIAGELGL
		l				EFKAGLLPEDKVKAVTELNQH
						APLAMVGDGINDAPAMKAAAI
	1	1				GIAMGSGTDVALETADAALTH
		l		1		NHLRGLVQMIELARATHANIRQ
				ł		NITIALGLKGIFLVTTLLGMTGL
		ı				WLAVLADTGATVLFFPRLFEAR
	1	1		1		NSQVGNGETNQTRFRLCAAPG
	1					GTFIADFTAGTGRRARPRRNRR
		1				RVVVSFDFHQNMRRFLMEIVA
		1				ARFVVSKVAAHFRTFHYGGVIF
		1				ISRENVIWRGFESIFDHLEQRFR
		l	,			LLFTIDNPVGVKNFVAAVLGVR
		l		ł		LGKHIQFDVVRVTTKLCESILQI
		l	1			VNFIFROSOAKTOVSVDORLTA
ĺ			Ì			LPQQINAGNRSRLMVGKQLLCI
4902	35270	В	4943	1	2104	
4903	35271	С	4944	1	1215	
4904	35272	Α	4945	3	268	YEFNRPYPEIQRSGIS\KLLEPLL
l						FAATSDSQLSKTEISSIKINSETV
i						PVYQLRYNGNNALMFATYQD
						KMLVFSSTDMLFKDDQQDTEA
4905	35273	В	4946	1	1725	
4906	35274	Α	4947	1	1437	
4907	35275	Α	4948	2	736	QCPYPYIAATGRILVVTHLICLA
i		1				PQIVENQVTYPLTTTMLSVPGA
		ŀ				KTVRGFSQFGDSYVYVIFEDGT
		1				DPYWARSRVLEYLNQVQGMLP
		1				AGVSAELGPDATGVGWIYEYA
		ŀ				LVDRSGKHDLADLRSLQDWIL
						KYELETIPCVSEVASVGGVVKE
						YQVVIDPQRLAQYGISLAEVKS
						ALDASNQEAGGS\SI\ELAEAEY
	1	1	1	I	l	MGGTCSAHGRALSRGVLWCRF
				1		SAIVRGPPRGMFCGAGAAPNLI
4908	35276	Α	4949	531	632	
4909	35277	Α	4950	532	609	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4910	35278	A	4951		525	LGVEATAUGDFGKWAEKLPVP VELAQACAHAVMKSGIDLAVS YCMQVNHGFAQPLEFLLGGLD KVPVLLVFINGWATPLPGFGRT RMLGEAIGRFTSTPQYAGDTVN DEDISNTIRALFATGNFEDVRVI RDGELRKFPTCESDDNFRPVTF SVNYVIRHDWYGIRRVYPENE
491I	35279	Α	4952	1	2769	
4912	35280	Α	4953	1	681	
4913	35281	Α	4954	1	1230	
4914	35282	Α	4955		774	MLKTSDRPPYOYPKRCIPLSVL EVLRCARRWSLRPYKQLARAY JERYKHDRIDIEREKKGRLNQEI RGLVEOTNASLLNENANKOSK AHERGDIHJYHDLDYSPFPMFN CMLIDLKGMLTQGFKMGNAEI EPPKSISTATAVTAQIGSVHIVO GTTINRIDEVLAPFVTASYNKH RKTAEEWNIPDAAGYANSRTIK ECYDAFQSLEYENVTLHTANV EGLTGDDGJAVEALKKNSQKPR MSASHNCELVSLRGRQYT
4915	35283	Α	4956	1	1278	
4916	35284	A	4957	461	1002	SLSTKGYAAAKWCSTACAGST LLLIVLLWVFIPKGFFPGQDNGI IGGTLQAPQSISFANMAQLORQ VADVILQDPAVQSLTSFVGVDG RVQKVIAKLHTAVDKVPGVDL FLQPTQDLTIDTQGSRTQYQFT LHATSLDALNTWVPQLMEKIQ QLPKLS
4917	35285	A	4958	I	291	MNPVDRPLLDIGLTRLEFLRISG KGLA\GLTIAPALLSLLGCKQED IDSGTVGLINTPKGVLVTQRAR CTGCHRCEISCTNFNDGSVGTF FSRIKPH
4918	35286	A	4959	1	306	MKNFEVLQPLQNSLSGLPLWV SERILQQINQLTHYEPVIGIMGK TGAGKSSLCNALFAGEVSPVSD VAGCTRDPLRFRLQIGEHFMTI VDL\PGVGESGVRD
4919	35287	Α	4960	2666	2775	
4920	35288	A	4961	9	308	GDLDGSRHRAFLCHLPVELKTA LMFPVTLTRALMETAY/ATAVS A/NFRTESRGAH/SRFDFPD/RDD ENWL/CHSLYLPESESMTRRSV NMNPKLRPAFPPKIRT
4921	35289	Α	4962	1	1132	

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nuclcotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
4922	35290	A	4963	1170	1352	RNLPDAAGQSCAGEIRLYRQQ
						QRSRLQRWLHLACFRRCNLHR
						RELDATA*QHVRSCRWR
4923	35291	A	4964	1	312	MRKLTALFVASTLALGAANLA
						HAADTTTAAPADAKPMMHHK
						GKFGPHQDMMFKDLNLTDAQ
						KQQIREIMKG\QRDQMKRPPLE
				,		ERRAMHDIIASDTFDKVKAEA
4924	35292	Α	4965	3	205	KDHIKGVLEAQNSLSTQVSLFF
						*SFFG*NSNMRNLIQIYRSL/CTK
						AI*LMNFKRHKNQLVINYLSRS
4925	35293	Α	4966	1	915	MTGVATARARGLRRPLSVGQV
						PPFARLWKGVQTVERHMLANI
	ı					GTGSQHPGCGFQLINQNSVIVF
						AAGEVNGFTSGDVQCLKMRSC
						DMNDIQRRQRLLPDGNKFGEIQ
	i					TTIREYYKHLYANKLEDLEEM
				1		DKFLDTYTLPRLNQEEVESLNR
						PITGSEIEAVVNSLPTKKSPGPE
						RLTAEFYQRYKEELVPFLLKLF
				l		QTTEKEGLLPNSFYEASVLLIPK
				1		PGKDTTKKENFRPISLMNIDVK
						LNKILANRIQQHIKKLIHHNQV
						GFIIGVQGWFNICKSTNVIYHV
						NRTNDKNH\IISIDTEKAFD
4926	35294	Α	4967	1	1338	

578

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
4927	35295	Α	4968	I	1928	PPLVIHRQTGSGEDLQQTPTDL
						QLRVLTIRRKTNKQKGHPHQNP
1						ISSRRHEITKIRAELKETETQKTL
		1		l		QKKSMNPRSWFF\ERINKIDRLL
		ł	1			ARLIKKKREKNQID\AIKNDK\W
				i		DITHRIPTEIETII\REY\YKHLYT
1						NKL\EN\LEEMDKFLDTYTLP\R
1		ŀ				LN\QEEVESL\HRLITGSEIEAITN
1						SLT\TKKSPGPDGF\T\AEFYQRY
		1				KEELVPFLLKLFOSIEKEGILPNS
						F\YEASIILISKPGRDTTKKENFR
		į.				PISLMNIDAKILNKILANOIOOHI
						KKLIHHHQVGFIPGMQGWFNIL
		ı				KSINVIHHINRTKOKNHMIISIEA
1		1				EKAFDKIQOPFMLKTLNKLGID
		1				GTYLTYLKIIRAVYEKPTANIIL
i						NGQKLEAFPLKTGTRQGCPLSP
1			1			
		ŀ				LLFNVVL\EVLVGAIRQEKEIKG
		1			1	IQLGKEDVKLSLFADDMIVYLE
						NPIVSAQNLLKLISNFSEVSGYK
						INVQKSQAFLYTNNRQTESQIM
						SELPFTIASKRIKYLGIQLTRDV
İ						KDLFKENYKPLLNEIKEDTNK
		1				WKNIPCSWIGRINIVKMAILPKT
		l		l .		LNQKFSYWFRVNKHYIHQRTFP
						LKETEFNTIATLYNGASP/RTAP
		1				KSTGTNGHQASGLPRF*RIAFCS
	l					ALVKSKRKLYQGYLPGQTDRR
	I			1		EEGVSWCPGGP
4928	35296	Α	4969	2	237	QPVEDTWLSTPAAPMVDSLIAR
			1	1		VRVMARGNAITLPVCGRDVK/F
		l				TLEVLRGDSVEKTSRVW\SGIET
		l				YOELVTEDALDDL
4929	35297	Α	4970	1	1752	
4930	35298	Α	4971	I	723	
4931	35299	A	4972	I	1701	
4932	35300	A	4973	1	1446	
4933	35301	Α	4974	T	403	MKLMETLNQCINAGHEMTKAI
		1		1		AIAQFNDDSPEARKITRRWRIG
1		1				EAADLVGVSSQAIRDAEKAGR
		1	1			LPHPDMEIRGRVEQRVGYTIEQI
		1				NHMRDVFGTRLRRAEDVFPPVI
1		l				GVAAHKG\LALKGLRVLLVEV
1		l		1		RHRV
4934	35302	A	4975	1	1374	
1551	1	Ľ.,	1	1	<u> </u>	L

SEQ ID	ISEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
4935	35303	Α	4976	1	2259	MKLMETLNQCINAGHEMTKAI
	1	l .		İ		AIAOFNDDSPEARKITRRWRIG
	1	l				EAADLVGVSSQAIRDAEKAGR
	1					LPHPDMEIRGRVEQRVGYTIEQI
	1					NHMRDVFGTRLRRAEDVFPPVI
	1					GVAAHKGGVYKTSVSVHLAQ
						DLAL/KGLRVLLVEVHKRWS*N
						DEGYRHCTV***\HPEARKITRR
	1	l				WRIGEAADLVGVSSQAIRDAEK
						AGRLPHPDMEIRGRVEOR\LVIO
		1				LNKLIICVMCLVRDCDVLKTYF
	l l	1				HR*SGLLPIKVAFTKP/HVSVHL
		1				AQDLALKGLRVLLVEEPPSAPN
	ł	1				LGIGTINVVCAADVLIVPTPAEL
		1				FDYTSALOFFDMLRDLLKNVD
	l					LKGFEPDVRILLTKYSNSNGSQ
						SPWMEEOIRDAWGSMVLKNV
				l		VRETDEVGKAAPMVDSLIARV
						GVMARGNAITLPVCGRDVKFT
						LEVLRGDSVEKTSRCDNLKTCH
						TSHGSVMAETAVINHKKRKNS
						PRIVOSNOLTEAAYSLSROOKR
						MLYLFVDQIRKSDGTLQEHDGI
	i					CEIHVAKYAEIFGLTSAEASKDI
	1					RQALKSFAGKEVVFYRPEEDA
		1				GDEKGYESFPWFIKRAHSPSRG
						LYSVHINPYLIPFFIGLQNRFTQF
i	1					RLSETKEITNPYAMRLYESLCO
	į.					YHPLTIEKVMKPLITSNTVTDEI
Ì						ERANVFKMNGKWYLFTDSRGS
				İ		KMTIDGINSNDIYMLGYVSNSL
						TGPYKPLNKTGLVLQMGLDPN
4936	35304	В	4977	1	1744	
4937	35305	A	4978	I	2367	
4938	35306	A	4979	1	1215	
4939	35307	A	4980	1	946	MKLMETLNQCINAGHEMTKAI
	1				1	AIAQFNDDSPEARKITRRWRIG
						EAADLVGVSSQAIRDAEKAGR
	1					LPHPDMEIRGRVEQRVGYTIEQI
	1					NHMRDVFGTRLRRAEDVFPPVI
						GVAAHKGGVYKTSVSVHLAQ
	į.					DLALKGLRVLLVEGNDPQGTA
		1		1		SMYHGWVPDLHIHAEDTLLPF
						YLGEKDDVTYAIKPTCWPGLDI
	1	1				IPSCLALHRIETELMGKFDEGKL
						PTDPHLMLRLAIETVAHDYDVI
		[	l			VIDSAPNLGIGTINVVCAADVLI
		1				VPTPAELFDYTSALQFFDMLRD
		1				LLKNVDLKGQAPCMK\LTMRS
						SSSSAPSPWML
4940	35308	Α	4981	I	1572	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
4941	35309	Α	4982	T T	1617	
4942	35310	Α	4983	1	550	
4943	35311	A	4984	1	3818	
4944	35312	A	4985	607	3777	
4945	35313	Α	4986	671	3091	ARCQRVPGRPVPDLLRCLPRAT
						TPAPSPAPGLVVRRLAAPVPAA
			l			APVPAAAPVPAAAPVPAAAPVF
						AAAPVPAAAPVPVAAPVPVAA
						PVPAAAPVPAAAPVPAAAPVPA
						AAPVPAAAPVPVAAPVPAAAP
						VPRFQSPNQTASTSDSPHIGQLP
						HQTVPISDSFHTGQSPHRTDSTP
						DSPHTGQLPHRTVPTPD/ELPHR
						TVPTPDSFHTRQSPHQTASTPDS
						PHIGQLPHQTVPISDSFHTRQSP
						HQTASTQDSPHTGQIPHRTVPT
				l		PDSFHTRQSPYRTASTPDSPHIG
						QLAHRTVPTPDSFHTGQSPHRT
						DSTPDSPHTRQLPHQTVPISDSF
1 1						HTGQSPYRTASTPDSPHTRQLP
					1	HQTASTPDSPHTRQSPHRTVPT
						PDSSPHQTVSTPDSPHTRQLPH
						QTVPTPDSFHTRQSPHQTVPTP
						DSPHTRQLPHQTASTPDSP\TPD
					1	SPHTGQSPHQFPHQTVPTADSP
					1	HTRQLPHQTVPTADSPTPDSFH
			1			TRHSPHQTASTPDSPHIGQLPHR
						TVPTPDSFHTRQSPHQTASTPDT
						PHTRQLPQQTVPTADSPTPDSF
						HTRQSPHQTVPTPDSPHTRQSP
						HRTVPTPDSFHTRQYPQRTVPT\
						QTASTPGSPHTKQSPHQTVPTP
						DCPHTGQSPYQTVSTPDSPHTR
						HSPHQTASTPDSPHIGQLPHQT
			ļ			ASTLDSPHIGRHPRQMAPTPESP
						HARQLPCQMAPTPDSPTLDGPH
	35314	В	4987	I	891	
	35315	Α	4988	157	1990	
	35316	В	4989	I	2157	
4949	35317	Α	4990	1	378	MSIKGTYLKVIKAIYDKPTASSI
				l		LNGENLKAFLLRTGTRQGCPLY
				l		KINVYKSVALLYTTNDQGENQI
				l		NNSTPYTTAPRKIKYIGIYLTKE
				I		VKDLYKENYKTLLKEVIDDT/R
						WKHIPCSWMGRINIV
4950	35318	Α	4991	I	392	

SEQ ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	endnn for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	delction, \-possible nucleotide insertion)
				sequence		
4951	35319	A	4992	3	1570	ETDFAFVGQAGVQWCDLSSPO
4931	33319	^	4992	3	1370	PLPPWVQAILLPQPPRQGCWSG
						IPKWSGISEDVQVWKNCKLDL
						AAATGKNCLGQGEEALLTQMR
			l		ł .	
		l				TGNQREVSDWWEEFVYLRSRN
	1					PLMVNSNYYMMDFLYVTPTPL
		ı	1		ĺ	QAARAGNAVHALLLYRHRLNR
		1				QEIPPVRGPQWVRDGGVVLWP
						LGHVGPGRQLTAHGFLQTLLM
ļ		i			İ	GMRPLCSAQYEKIFNTTRIPGV
					i	QKDYIRHLHDSQHVAVFHRGR
						FFRMGTHSRNSLLSPRALEQQF
				1	i	QRILDDPSPACPHEEHLAALTA
						APRGTWAQVRTSLKTQAAEAL
		ļ	l	ŀ		EAVEGAAFFVSLDAEPA\GLTL
			l			EDPAASLDAYAHALLAGRGHD
	1	l	l			RWF\DK\SFTLIVFSNGKLGLSV
				i		EHSWADCPISGHMWEFTLATE
		l				CFOLGYSTDGHCKGHPDPTLPO
		1				PORLOWALPDHIHSSISLALRG
						AKILSENVDCHVVPFSLFGKSFI
		1				RRCHLSLDSFIQIALQLAHFRDR
		ł		1		GOFCLTYESAMTRLFLEGRTET
				1		VRSCTREACNFVRAMEDKKKT
4952	35320	A	4993	1	1027	MPAKSPGQDVLGTDNIKIDVFK
4932	33320	^	4993	'	1027	QTNQKSHTGEKPYECPECGKAF
					ŀ	SEKSRLRKHORTHTGEKPYKC
						DGCDKAFSAKSGLRIHQRTHTG
1				ì		EKPFECHECGKSFNYKSILIVHQ
1						RTHTGEKPFECNECGKSFSHMS
		1				GLRNHRRTHTGERPYKCDECG
						KAFKLKSGLRKHHRTHTGEKP
		l				YKCNQCGKAFGQKS\QLRGHH
		1				RIHSGEKP\YKCNHCGEAFSQKS
		l				NLRVHHRTHTGEKPYQCEECG
		1				KTFRQKSNLRG\HQRTHSGEKP
		l		İ		YECNECGKAFSEKSVLRKHQR
		l				THT\GEKP\YNCNQCGEAFSQKS
		l		ì	1	NLRVHQRTHTGEKPYKCDKCG
1	l		1	1		RTFSQKSSLREHQKAHPGD
4953	35321	A	4994	154	331	IPAAATCMGSLLGG*ETPGLWA
1						RRSVKSRGLFPGLPSPSRASVRS
1		1	l	I		LLLLPAWAAFLEGIVDTRPTAW
1		1	1	I		RAFPWTLFLSVFCOFLDFPETSL
		1				DSQKLSLDTPSF
L		ــــ	L	L	L	POVINGEDITO

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	delction, \=possible nucleotide inscrtion)
4954	35322	A	4995	657	1455	PEPKPAAVAPPPESPLPAGDSEG
						CLQPGHLL\PASPRLPRPRQAAS
						LAHRPEKSAPGADCPSGRR\GR
				l	1	PWTCGGLSGPAAAPRPCPLAPA
						FAPAFLALGAQR\GPGPEQGGH
				į.		ERQAERPGRRSRRTRAYSARIY
		1		l		LPVAAEWPMGPGPEPGAGGRR
		1				RGEVPGPGAQRSPARRRRGGPA
1						AVSSGGRGVGGLRGAVLFQHP
1						EQQQRPVGLAGLGAQQPAHV
						WRYGPLST/PPALGPPAAARGP\
ļ	i i	1				GRRLFLPFSFSPSAGAPGAASRP
		1				SPRRSP
4955	35323	Α	4996	1	415	
4956	35324	В	4997	8	211	
4957	35325	Α	4998	I	563	MDPNHEEIPDLPEKEFRRVKSK
						NHMTISIDAEKAFDNIQHRFMI
	İ	1				KTLSKIGIQGTHFN\IIKAIYDKP
						TASIILNGENLKAFPLRTGTSIVL
						EVLARAIRREKEIKGIQIGKEEV
		1				KLLLFADDMIVYLENPKDSYRK
						LLEQIKEFSKVSRYKINVQKSIA
	1					LLYANSDQAENQINNPTSFTIA
		_				AKNKIK
4958	35326	Α	4999	667	960	
4959	35327	A	5000	317	1157	EFRMDPAIALVLALSLTVPKLT
						VPDSPLRLYRSFCTSACTSNLV
		ļ				VHFA*KEKWPDV*LYTDSWAV
				1		ANGLAGWSGTWKKHDWKIDD
						NEIWGRGMWIDLSEWSKTVKIF
				l		VSHESAHHIT*KSSAEEDFNNQ
						VDRMIHSVDTTRPLSPATPVITQ
			1	1		WAHEQSGHGDRDGGYAWAQQ
1						HGLPLTKADLAMVTAECPICQQ
1		1		1		QRPTLSP*YGTIPRGDQPATWW
1	1			1		QVDYIGPLSSWKGQRFVLTGID/
				1		TSGYEFAYPARSSANSTIRGLM
	L	_				ECLIHHHGIPHSIASNQLYS
4960	35328	Α	5001	2	15246	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nuclcotide
l	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
4961	35329	A	5002	i	951	MALALNRYL/CLAVLPLITKCA
.,						PLFAG/TEHRAIMVDSMLHTVY
				i		R/LSRGRSLTKAQRDVIED/CLM
						SLC\RLLRRLVFDVPILNEFA/K
Ì						MPLKLLTNHYERCWKY/YCLPT
ŀ						GWANFGVTSEEE/LHLTRKLFW
						GIFDSLAH/KKY/DPELYRMAM
1						PCLCAIAG/ALPPDYVDASYSSK
	}					AE/KKATVDAEGNFDPRPVET/L
ı						NV/IIPEKLDSFINKFAEYT/HEK
						WAFDK/DKEIYRWPIKESLKAM
		1		l	1	I/A WEWTIEKAREDLDPREGYN
						PQPPDLSAV/TLSRELQAMAEQ
1		1				LAENYHN/TWGRKKKQELEAK
1		1				GGGTHPLLVP/YDTLTAKEKAR
		1				DREKAQSY
4962	35330	Α	5003	273	478	
4963	35331	A	5004	2	622	GAPRSESEKERQLMGMINQLSS
		i			1	FREQLLHAHYEQKKLAASQIEK
	1	1				QRQHMKLGKQ\QQEQIARQQQ
1						RLIQQQHKINLLQQQIQQLYAA
		ļ.				QLAAMQVSPGGKLPGIPQGNL
į.					1	GAAVSPTSIHTDKSTNSPPPKSK
		1				TCCLLLWEDEHSASIPEVTNQQI
					1	HLHLASSITDHGGKVIWERCLE
1	1	1				ESGKGVTGFPDWSPRWGRIPPE
	0.000	١.	5005		512	GSKEGFTKE
4964 4965	35332 35333	A	5005	3	642	MHAQTYAHTDTRAQPCTSMEK
4965	33333	I <sup>A</sup>	3006	11	042	QVSLKPTEEAHKKERKPQKPG
	1	1		1	1	KYICQYCSRPC/AKPSVLQKHIR
		1		1	1	SHTGYG\CEMYPHGLEMERIPG
		1			1	EEFEEPTEGESTDSEETSATSG
		1				HPAELSPRPKOPLLSSGLYSSGS
1		1		1		HSSSHERCSLSQSSTAQSLEDPP
		1				PFVEPSSEHPLSHKPEDTHTIKO
		1		1	ì	KLALRLSERKKHQVIDRLGSGI
		1				LAGLSWOLLPOGEAL
4966	35334	A	5007	341	1020	TLNRRQGCCLGSWLTRSNGILL
1	1	1	[ ***	T		FEISRPTYLPILLILFLVKR/HKL
		1				KMSVLNMVVRHDPGSTESAKA
					1	KEELIFRCRSRHFRASPLFSQHA
	1	1		I	1	AADKHKFQRFLTADMALAVTV
		1				YAPTTFPPSSLLLFKOKSNGMH
		İ			·	NLIATGHLLLVDPNRMVIKRVV
1		1				LSDPPFKICTKMAVVCYMFFNR
	1	1		1		EDVOWFKPVELRTKWSRRGHI
		1		İ		QEPSGTHGRMKCSFDRKLKSQ
	1	1				NTELMNLYK
					J	1

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
4967	35335	Α	5008	1	847	EKAQALEDLAGFKDPAPGHTE
		ļ				ESMTHDKTTKIPCKSPPELVDT
						ATSSKKWPRACGOKVEVKEEL
	1					LAVGKLTOTSGETTHTNKEPEC
	l l	l				EGKGMKAFKQPAKQKLDPEN\
		l				TGSRRLPRVPKEKAOPLEDLAS
		l			1	FQELSQTPGHTEELANGADSFT
		ŀ				SAPKOAPDSGKPLKISRRVLOA
						PKVEPVGDLVGTR/D/PVKSOSK
						SNTSLPPLPFKRGCGKDGSVTG
	l .	l				TKRPHCMPAPEEIIEELPASKKO
						R/VVAPRVRGKSPEPLVIMKRSI
						RTSAKRIEPAEDLNSNNMKTNN
4968	35336	A	5009	9	1094	IRHEEESMTDDKTTIIPCKSSPEL
	1					EDTATSSKRRPRTRAOKVEVKE
						ELLAVGKLTQTSGESTHTDKEP
	1	l			l .	VGEGK\GTKAFKQPAKRKLDA
	1					EDVIGSRROPRAPKEKAQPLED
						LASFOELSOTPGHTEELANGAA
		l				DSFTSAPKQTPDSGKPLKISRRV
	L	l				LRAPKVEPVGDVVSTRDPVKS
	ł	İ				OSKSNTSLPPLPFKRGGGKDGS
						VTGT\KRLRCMPAPEEIVEELPT
	ŀ	1				SKKORV\APRARGKSSEPVVIM
	ļ.	l				K\RSL\RTSAKRIEPAEELNSND
		l				MKTNKEEHKLODSVPENKGISL
		l				RSRRONKTEAEQQITEVFVLAE
ì		i				RIEINRNEKKPMKTSPEMDIONE
		İ				DDGARKPIPRDKVTENKRCLRS
	1					ARQNESSQP
4969	35337	A	5010	1	459	MAKPWRALCILLRSLDSFLOLS
				1		ASLTCFGFMHNTYKNRPWGVL
		l				RSSTERSPRKGTAGDMRAGGRI
	i	l				NAPLIGODLLFKEHFASKALDT
						CTNIARSAKTQGGPVAAILLLL
		l				AFGPCIFNLRVKFVSSRIKAIKL
		l		1		QM/RLTIYRGPLDRPAGPSTGL
4970	35338	В	5011	1	687	
4971	35339	С	5012	194	418	
4972	35340	Α	5013	17	396	
4973	35341	A	5014	1	70	

SEQ ID	SEQ ID NO:		SEQ ID NO:		Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		<u> </u>	<u> </u>			
4974	35342	Α	5015	1	994	MGFVKVVKNKAYFKRYQVKF
		1				RRRREGKTDYYARKRLVIQDK
						NKYNTPKYRMIVRVTNRD\IICQ
					İ	IAYARIEGIMIVCAAYAPELPK\
		1				YGVK\VGLTNYAAA\YCTGLLA
						GPAGFFHRFGMDKFYEG\QVEV
						TGDEYNVESIDGQPGCLHPAY
		1				WDARPLPRTSPLAIKVFWLP*R
İ	ì	1				GA\VDGGLVLFPPQYPNRFPWL
						WIPESQGNLNARRYHREGTIHG
	1					PRIVAGLHAPTLMEEDEDA\YK
						KQFVRQYVKNS\VTPD\MMEE
						MYKKAHAAIR\ENPVYEKKPK
	1			l		KEV\KRKRWNR\PKMSLAQKK
						DRVAQKKASPL\RAQERAAEKL
		_				NQTIFYKDFSDIAN
4975	35343	С	5016	27	308	
4976	35344	C	5017	68	307	
4977	35345	A	5018	388	1485	DDD1411 L KMEQEUDEL 4 DVD21
4978	35346	Α	5019	3	1940	RDRMILLKMEQEIIDFIADNNN
		1	İ			HYKKFPQMSSYQRMLVHRVA
						AYFGLDHNVDQTGKSVIINKTS
						STRIPEQRFCEHLKDEKGEESQ
						KRFILKRDNSSIDKEDNQSVCS
						QESLFVENSRLLEDSNICNETYK
						KRQLFRGNRDGSGRTSGSRQSS
						SENELKWSDHQRAWSSTDSDS
						SNRNLKPAMTKTASFGGITVLT RGDSTSSTRSTGKLSKAGSESSS
						SAGSSGSLSRTHPPLQSTPLVAG
						VAAGSPGCVP\YPENGIGGQVA
						PSSTSYILLPLEAATGIPPGSILL NPHTGOPFVNPDGTPAIYNPPTS
						QQPLRSAMVGQSQQQPPQQQP
						SPOPOOOVOPPOPOMAGPLVT
						QSIPAKKELNAFRVRNQEQRDT GTLHEGSGKISRMVLGWEPLSP
		1				
						YAPDRDDVATQFGQMTLSRQS
						SGETPEPPSGPVYPSSLMPQPAQ
						QPSYVIASTGQQLPTGGFSGSGP
					1	PISQQVLQPPPSPQGFVQQPPPA
[		1		1		QMPVYYYPSGQYPTSTTQQYR
				I	1	PMAPVQYNAQRSQQMPQAAQ
		1		1	1	QAVLEVLSPLVSTVMPPKLAVL
					1	VMAGFRLRLELSESVLLQALW
				1	1	WSDHLSSFSELLCRLPDVLPEPS
		1	1		1	LLPLEYDHQKDAQGQDYLTCM
1	1	1	1	1	1	VLVTLLLESPTGIQEDDSNEISVI

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SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence		
4979	35347	Α	5020	3	1353	GDAYALVLRVTLYCGKCH\NE
						VVLAPIFEILSTESIQDQLPYSV
				i		MLMSMLAITEGRRSFSVSVENA
İ						CSNYVTTVQVKEVNQMHISPN
						SCNAIHPRDHILEISGTPTHTLQ
						VEELEDAISQMSQTLLLLIEHDF
l						VSRSPAQLRLDAWLSPHTQNA
						GHPHALSTLDTKDNLEGTLRRC
		1				SLRLSNSISKSPSPSSPKEPLLLS
						RDISCWESLCCSSTYSKQNFRSC
						DLIHGEVLGKGFFGQAIKVTHK
						ATGKVLVMKELMRCDEENQK
						TFLTEVKVTLPSNLLPPGHDLL
						QTGAREQTGILKTGGLSVPGGA
	ľ					GHPAACRAGGVGPHCEHAVRP
						DPRLTPLALAQPPAGGCSTASIA
1				i		PLFSIPAVSRVFRASRGLAACLE
						AEQAGRTILTCEVCKLVVGLSL
				l		DSQQQLSSVLCGWLCLSCPQL
İ						WSLNRHPQHQHHLVEMQNLKS
						HPRPGETESAL
4980	35348	Α	5021	I	588	MEYPDGGSTLDLLEPGPLDETQ
						IITILREILKGLDYLHSEKKIHRG
	1					VKAANVLLSEHCEVKLVDFGM
						AGQLADTQTKRNTFVGTPFWI
						APENNPPTLEENYSKPLKEFVE
						ACLNKELSFRPTAKELLKHKFIL
						RDTKKTSYLTELIDRYKRWRA
						KQSQEDSSSEDSNSETDGQDS\G
						GSDSGDWIFTIQEKDPKNL
4981	35349	Α	5022	<u> </u>	1380	GPRASPPRADRRGPAVPSQEVA
				İ		VLSAMAHSPVQSGLPGMQNLK
						ADPEELFTKLEKIGKGSFGEVF
		1		l		KGIDNRTQKVVAIKIIDLEEAED
		1				EIEDIQQEITVLSQCDSPYVTKY
				l		YGSYLKDTKLWIIMEYLGGGS
						ALDLLEPGPLDETQIATILREILK
						GLDYLHSEKKIHRDIKAANVLL
				1		SEHGEVKLADFGVAGQLTDTQI
						KRNTFVGTPFWMV\PEVIKQAG
					İ	YDSKADIWSLGITAIELARGEPP
į						HSELHPMKVLFLIPKNNPPTLE
						GNYSKPLKEFVEACLNKEPSFIP
		1		1		TAKELLKHKFILRNAK\KTSYLT
						ELIDRYK\RWKAEQSHDDSSSE\
		1		1		DSDAE\TDGQASGGSDSGDWIF
						TIREKDPKNLENGALQPSDLDR
		1	1			NKMKDIPKRPFSQWLSTIISPLF
		1	1	1		AELKEKSQ\ACGGELGGPLKEL
		1	1	l		RGAIYLAEEACPGISDTMVAQL
	1	1	1			VQRLQRYSLSGGGTSSH

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4982	35350	Α	5023	I	346	MAGEKVEKPDTKEKKPEAKKA DAGGKVQEGTGRYSRSAMYSR KAMYKRKYSAAKSKIEKKKEK VLATVTKPVGDKNGGTQVF\ QIITYSSYTQKVQLPKSTLKQRQ GPCPOGAL
4983	35351	Α	5024	67	599	SAAKSEMAGEKVEKPDTKEKK PEAKKVDAGGKVKKONLKAK KPKGKPHCSENPYLVRGIGRY SRSAMYSRKAMYKIRKYSAAK SKVEKKKKEKVLRNLQNOVG GDKINGGTRVGLNFRKMPRIY PTEQDYRKLLSHGQKNPFSQH V/REKLRASITPGTILIILTGRHR GKRVYEIN
4984	35352	Α	5025	101	202	PVPGTSSCTDRYHYKKH**KIN TKLVSKYILNM
4985	35353	Α	5026	2	562	LRTYPDLEGRRFRAMRTGGRF- PELPPDMNSLEQAEDLKAFERR LTEYJHCLQPATGRWRMLLIVV SVCTATGA WNWLIDPETOKVS FFTSLWNHPFFTISCITLIGLFFA GIHKRVVAPSIIAARCRTVLAEY NMSCDDTGKLILKPRPHVQ*OS SLIVMGLRIAFLRISDTAKSHKG FLLRLDM

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NO:   of peptide   sequence   od   n USS)   odos for peptide   sequence   of peptide   sequence   of peptide   of peptide   sequence   of peptide   of peptide   odos for peptide   od	nown,
TRRRATVSTHOEFVVI GLVVSGCLDADTAMP FQWQSQDGQKDIEDEI VDSCIRSLQESGILDPO RVHFIGKTLGLSSEDYY QMVKEVTVTPQVSVL ASALCQEGHDDPLI TGNHYIKDNSLPFWW QSALQNSKPEGSFQV NQTLALGETTESQLPA ATQQSFSQGTTSRAGH APPPPPPPREPFAPSLGI APPAAAAALYYSSSI GGSPLAAPQGGSPTKL PEGATYAAPRGSSPKQ KSYSTSSPINIVVSSAG SSPTVOSTISSSPHQLS ATLSFTKRLVHASEGY LYATATLQRFOSLAAC SQHGHLGPELRAGU YEDRVYQKPMSSLS LPPAHTGTYRTSTARS VPLQRTGSQHGPQNA RASYAAGPASNYADP CSVESPYSKSGPALP SPSIDSIGKDFSKYPIL CALVYPSSERASSL Q*NRLYPKFRVLGSG RRFCASKGIKGRFCGS: EHGGQHPCYPKLVPTI REGNQKNSERV  4987 35355 A 5028 123 3825	mscrtion)
GLVVSGCLDADTAMP   FQWQQDGQKDIEDE    VDSCIRSLQESGILDPQ   RVIHFGKTLGLSSEDY:   QMVKEVTVTPQVXLL   ASALCGQEGHDDPLLI   TGNHYIKDNSLFPWWY   QSALQLNSKPGSFQV   NQTLALGETTFSQLPA   ATGQFSQGTTSLA   APPAAAAAALYYSSST   GGSPLAAPQGGSPTKL   PEGATYAAPGGSFTKL   PEGATYAAPGGSFTKL   PEGATYAAPGGSFTKL   PEGATYAAPGSSPKQ   KSYSTSSPINIVSSAG   SPPTVQSTSSSPHQLS   ATLSPTKRLVHASEQY   LYATATLQRPGSLAA   SQHGHLGPELRALQSP   YEDRVYQKPPMRSLS   LPPAHTGTYRTSTAPS   VPLQRTGSQHGPCVRPMSLS   LPPAHTGTYRTSTAPS   VPLQRTGSQHGPCVRPMSLS   LPPAHTGTYRTSTAPS   VPLQRTGSQHGPCVRPMSLS   CALVYPPSSERASCH   SPSIDSIGKDFSKYPILC   CALVYPPSSERASCH   CALVYPPSSERASCH   GRASKGIKGRFCGS   RFCASKGIKGRFCGS   RFCASKGIKGRFCGS   CHGGQHPCYPKLVPTI   REGNQKNSERV   4987   35355   A 5028   123   3825     4988   35356   A 5029   1 593   MQVCSSGRILRVSGT   EGGRPCLGRQVNLURE   APPTAPSLTALPPDIVD	
PQWQSQDQGKDIEDEI   VDSCIRSLQESGILDPQ    RVIHFGKTLGLSSEDY    QMVKEVTVTPQVSVL    ASALCQEGHDDPLLI   TGNHYIKDNSLFPWVP    QSALQINSKPEGSFQV    QMTLALGETTPSQLPA     ATGQSFSQGTTSRAGH     APPPAAAAALYYSSSI     GGSPLAAPQGGSTFIKLE     EGATYAAPRGSSPKQ     KSYSTSSPINIVVSSAG     SPSTYVGSTISSSPIHQLS     ATLSPTKRLVHASEQY     LYATATLQPRGSLAAC     SQHGHLGPELRAGE     SQHGHLGPELRAGE     VPLQRTGSQHGPQNAR     RASYAAGPASNYADP     CPSVESPYSKSQPALPF     SPSIDSIQKDFSKYPILL     CALVYPPSSERASSL     Q*NRLYPKERVLGSG     RRFCASKGIKGRFGGS     EHGGQHPCYPKLVPTI     REGNQKNSERV     4987   35355   A 5028   123   3825     4988   35356   A 5029   1   593   MQVCSSGRIR.RVSGT     EGGRPCLGRGVNLTRE     APPTAPSLTALPPDIVD     APPTAPSLTALPPDIVD     CROMPANYADP     APPTAPSLTALPPDIVD	VSPFSL
VDSCIRSLQESGILDPQ RVIHFGKTLGSSEDY: QMVKEVTVTPQVSVL ASALCGQEGHDPDLI TGNHYIKDNSLPPWV QSALQLNSKPEGSFQV NQTLALGETTPSQLPA ATQQSPSQGTTSRAGH APPPPPPREPF APSLGST GGSPLAAPQGGSPTKL PEGATYAPRGSSPKQ KSYSTSSPINIVVSSAG SPPTVQSTTSSSPHQLS ATLSPTKRLVHASEQY LYATATLQRGSLAGA SPHORPSSERAGA SQHGHLGPELRALGS YERRAGASSPKQ KSYSTSSPINIVSSAG SPPTVQSTTSSSPHQLS LYATATLQRGSLAGA SQHGHGPERALAGS YERRAGASSPKQ LYATATLQRGSLAGA SQHGHGPERALAGS YERRAGASSPKQ LYATATLQRGSLAGA SQHGHGPERALAGS YERRAGASSPKQPL PESPSSKSQHAP CSVESPYSKSQHAP PSSIDSIGKDFSKYPLC CALVYPSSERAS Q'NRLYPKFRRVLGSG RRFCASKGIKGRFCCSS EHGGQHEVPRLVPTI REGNQKNSERV  4987 35355 A 5028 123 3825    MQVCSSGGRILRVSGT EGGRFCLAGRGYRALGR   EGGRFCLAGRGYRALGR   EGGRFCLAGRGYRALGR   EGGRFCLAGRGYRALGR   EGGRFCLAGRGRAGASR   FEGG	GSAEEQ
RVIHFGKTT.GLSSEDY.	TTGLE
QMVKEVTVTPQVSVL   ASALCQGEGHDDPLI   TGNHYIKDNSLPWW   QSALQNSKPEGSFQV   NQTLALGETTRSQLPA   ATGQSFSQGTTSR AGH   APPPPPPREPF APSLG   APPAAAAALYYSST   GGSPLAAPQGGSPTKL   PEGATYAAPRGSSPKQ   KSYSTSSPINIVVSSAG   SPPTVQSTISSSPIHQLS   ATLSPTKRLWHASEGY   LYATATLQRFOSLAAC   SQHGHLGPELRACH   SQHGHLGPELRA	DYSTGE
ASALCQGGHDDPLLI	SIMEKG
TGNHYIKIDNSLPPWV9   QSALQLNSKPEGSFQV   QSALQLNSKPEGSFQV   QVTLALGETTPSQLPA     ATGQSFSQGTTSRAGH     APPPAPAAAALYYSSTI     GGSPLAAPQGGSPTKL     PEGATYAAPRGSSPKQ     KSYSTSSPINIVSSAG     SPHTVQSTISSSPIHQLS     ATLSPTKRLVHASEQV     LYATATLQRFGSLAK     CSQHGHLGPELRALQSP     YEDRVYQKPPMSLS     LPPAHTGTYRTSSS     VPLQRTGSQHGPQNA     RASYAAGPASNYADP     CPSVESPYSKSGPALP     SPSIDSIGKDPSKYPIL     CALVYPPSSERASL     Q*NRLYPKFRRVLGSG     RRFCASKGIKGRFGGS     EHGGQHPCYPKLVPTI     REGNQKNSERV     4987   35355     A 5028   123   3825     4988   35356   A 5029   I 593     MQVCSSGRILRVSGT     EGGRFCLGRGVRNLRE     APPTAPSLTALPPDIVD     APPTAPSL	KANETI
QSALQLNSKPEGSFQY	TVQMS
NQTLALGETTPSQLPA	WPSLL:
ATGQSFSQGTTSR AGH APPPPPPRPFAPSLG APPPAAAAALYYSST GGSPLAAPQGGSPTKL PGGATYAAPRGSSPKQ KSYSTSSPINIVVSSAG SPPTVQSTISSSPHQLS ATLSPTKRLVHASEQY LYATATLQRFOSLAAQS YEDRVYQKPMSSLS LPPAHTGTYRTSTASS VPLQRTGSQHGPQNA RASYAAGPASNYADP CSVESPYSKSQPALPP SPSIDSIQKDFSKYPILL CALVYPPSSERSASL Q*NRLYPKFRVLGSG RRFCASKGIKGRFCGS: EHGGQHEVPRLVPTI RECONQKNSERV  4987 35355 A 5028 123 3825  4988 35356 A 5029 I 593 MQVCSSGGRILRVSGT EGGRFLCGRGYNLIRE APPTAPSLTALPPDIVD	PASYHS
APPPPPPPREPARSLG: APPAAAAAALYYSST GGSPLAAPQGGSPTKL PEGATYAAPGGSPTKL PEGATYAAPGSSPKG KSYSTSSPINIVSSAG SPPTVQSTISSSPIHQLS ATLSPTKRLVHASEQY LYATATLQRPGSLA QHGHLGPELRALQSP YEDRVYQKPPMRSLS LPPAHTGTYRTSTAPS VPLQRTGSQHGPONA- RASYAGPASNYADP CPSVESPYSKSGPALPF SPSIDSIGKDPSKYPILC CALVYPPSSERASSL Q*NRLYPFRRVLGSG RFCASKGIKGRGS EHGGQHPCYPKLVPTL REGNQKNSERV 4988 35355 A 5028 123 3825  4988 35356 A 5029 1 593 MQVCSSGRILRVSGT EGGRFCLGRGVRNLER APPTAPSLTALPPDIVD	RGTQAF
APPAAAAALYYSSTI   GGSPLAAPQGGSPTKL   PEGATYAAPRGSSPKQ   KSYSTSSPINIVVSSAG   SPPTVOSTISSSPHQLS   ATLSPTKRLVHASEQY   LYATATLQRPGSLAK   CSQHGHLGPELRALQSP   YEDRVYQKPPMRSLSE   LPPAHGTYRTSSS   VPLQRTGSQHGPQNA   RASYAAGPASNYADP   CPSVESPYSKSGPALPF   SPSIDSIQKDPSKYPIL   CALVYPPSSERASL   Q*NRLYPKFRR VLGSG   RFFCASKGIKGRFGGS   EHGGQHPCYPKLVPTI   REGNQKNSERV   4987   35355   A 5028   123   3825     4988   35356   A 5029   I 593   MQVCSSGRILRVSGT   EGGRPCLGRGVRNLRR   APPTAPSLTALPPDIVD	LAGPER
GGSPLAAPQGGSPTKL	SAFHLPI
PEGATYA-APROSSPRQ   KSYSTSSPINIVSSAG    SPPTVQSTISSSPINIVSSAG    SPPTVQSTISSSPINIVSSAG    SPPTVQSTISSSPINIVSSAG    ATLSPTKRLVHASEQY    LYATATLORPOSLA   SQHGHLGPELRALQSP    YEDRVYQKPPMSLS,SE    LPPAHTGTYRTSTAPS    VPLQRTGSQHGPQNA    RASYAGPASNYSO    PSYSTOSHOPONA    RASYAGPASNYSO    PSYSTOSHOPONA    RASYAGPASNYSO    CCLVVYPPSSERASLI   Q*NRLYPEFRRVLGSG    RRFCASKGIKGRFGOS    CRONGNISERV    4987   35355   A 5028   123   3825     4988   35356   A 5029   I 593   MQVCSSGRILRVSGT    EGGRPCLGRGVRNLRE    APPTAPSLTALPPDIVD	LPAPPR
KSYSTSSPINIVVSSAG   SPPTVQSTISSSPIHQLS   ATLSPTKRLVHASEQY   LYATATLQRPGSLAAC   SQHGHLGPELRALQP   YEDRVYQKPMRSLSC   LPPAHTGTYRTSTAPS:   VPPLQRTGSQHHOPQNA.   RASYAAGPASNYADP    CPSVESPYSKSGPALPP   SPSIDSIQKDPSKYPILC   CALVYPPSSERSASL   Q*NRLYPKFRRVLGSG   RRFCASKGIKGRFCGS:   EHGGQHPCYPKLVPTI   RECNQKNSERV   4987   35355   A   5028   123   3825     4988   35356   A   5029   I   593   MQVCSSGGRILRVSGT   EGGRPLCAGROYNRLIRE   APPTAPSLTALPPDIVD	QRGGS/
SPPTVQSTISSSPIHQLS	SPSRLA
ATI.SPTRELVHASEQY   LYATATLQRPGSLAX   SQHGHLGPELRALQSP   YEDRVYQKPPMESLS   LPPAHIGTYRTSSS   VPLQRTGSQHGPQNAX   RASYAAGPASNYADP   CPSVESPYSKSGPALPF   SPSIDSIQKDPSKYPILC   CALVYRPSSERRASL   Q*NRLYPKFRRVLGSG   RRFCASKGIKGRFGGS   EHGGQHPCYPKLVPTI   REGNQKNSERV   4987   35355   A 5028   123   3825     4988   35356   A 5029   I 593   MQVCSSGRILRVSGT   EGGRPCLGRGVRNLRR   APPTAPSLTALPPDIVD	LSPIRVT
LYATATLQROSLAAC   SQHGHLGPELRALQSP   YEDRVYQKPPMRSLSC   LPPAHTGTYRTSTAPS:   VPLQRTGSQHGPQNA.   RASYAAGPASNYADP   CPSVESPYSKSQPALPP   SPSIDISIQKDPSKYPILC   CALVYRPSRERASSL   Q*NRLYPKFRR VLGSG   RFCASKGIKGRGSG   EHGGQHPCYPKLVPTL   REGNQKNSERV   4987   35355   A 5028   123   3825     4988   35356   A 5029   1   593   MQVCSSGGRLRVSGT   EGGRFCLGRGVRNLRI   APPTAPSLTALPPDIVD	STIGTY
SQHCHLGPELRALQSP   YEDRVYQKPPMRSLSC   LPPAHTGTYRTSTAPS: VPLQRTGSQHGPQNAP   VPLQRTGSQHGPQNAP   VPLQRTGSQHGPQNAP   CPSVESPYSKSGPALPF   SPSIDSIQKDPSKYPILC   CALVYPPSSERAFSLU Q*NRLYPFERRVLGSG   RRFCASKGIKGRFGS   EHGGQHPCYPKLVPTL   REGNQKNSERV   VPLQRTGSG   VPLGASKGIKGRFGS   VPLGASKGIKGRFGS   VPLGASKGIKGRFG   VPLGASKGIKG	SKHSQE
VEDRVYQKPPMRSLS(	SRASYS
LPPAHTGTYRTSTAPS:	EHHIDP
VPLQRTGSQHGPQNA.   RASYAAGPASNYADP' CPSVESPYSKSGPALPF   SPSIDSIQKDPSKYPILC   CALVYRPSSERAS, VALSCOPEN, VALSC	SQGDP
RASYAAGPASNYADP   CPSVESPYSKGPALPF	SPGVDS
CP\$VESPY\$KSGPALPE   SP\$IDSIQKDP\$KYPILC   CALVYRP\$SRERASSL   Q*NRL/PPKFRVLIGS   RFPCASKGILGRFGCS   EHGQHPCYPKLVPTL   REGNQKNSERV   4987   35355   A 5028   123   3825     4988   35356   A 5029   I 593   MQVCSGGRILRVSGT   EGGRPCLGRGVRNLRE   APPTAPSLTALPPDIVD	AATFQ
SPSIDSIQKDPSKYPILC   CALVYRPSSRERASSIG   Q^NRLYPKFREV   CALVYRPSSRERASSIG   Q^NRLYPKFREV   CALVYRPSSRERASSIG   RRFCASKGIKGRFCGS: EHGGQHPCYPKLVPTI   REGNQKNSERV   W	/RQLQY
CALVYRPSSRERASSL   Q*NRLYPKERVLGSG   RRFCASKGIKGRECOS   EHGGQHPCYPKLVPTL   REONQKNSERV   4987   35355   A 5028   123   3825	EGTLAF
O+NRLYPKFRRVLGSC   RRFCASKGIKGRFCGS:   EHGGQHPCYPKLVPTI   REGNQKNSERV   123   3825   123   3825   124   124   125   12	DGGNPI
RRFCASKGIKGRFCGS: EHGGQHFCYPKLVPTL	LKSMC
### BHGQHPCYPKLVPTL ### REGNQKNSERV ### 153555 A 5028 123 3825 #### 15029 1 593 MQVCSSGGRILRVSGT ### EGGRPCLGRGVRNLRI #### APPTAPSLTALPPDIVD ### APPTAPSLTALPPDIVD	FEGMQ
REGNOKNSERV	SLEQDC
4987         35355         A         5028         123         3825           4988         35356         A         5029         1         593         MQVCSSGGRILRVSGT           EGGRFCLGRGVRNLRI         APPTAPSLTALPPDIVD         APPTAPSLTALPPDIVD	.WNPHQ
4988 35356 A 5029 I 593 MQVCSSGRILRVSGT EGGRFCLGRGVRLNE APPTAPSLTALPPDIVD	
EGGRFCLGRGVRNLRE APFTAPSLTALPPDIVD	
APFTAPSLTALPPDIVD	
MEDLTEVTTASESHPH	
YSSSKGFLRLCDMRAA	
HSKHPCDDIGPIQIIQGI	
GWMIILPALQSTFRCRI	
RAFLAPRLCDFSTSQPC	
PVMSGLISPWTKPSRSS	VFSM
4989 35357 A 5030 I <b>894</b>	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		_				
4990	35358	Α	5031	1	3115	RQICSMASELGARDDGGCTELA
						KPLYLQYLERALRLDHFLRQTS
		1		l	İ	AIFNRNISSDDSEDGLDDSNPLL
		1		1		PQSGDPLIQVKEEPPNSLLGETS
		1		İ		GAGSSGMLNTYSLNGVLQSES
		1		i	1	KCDKGNLYNFSKLKKSRKWLK
						SILLSDESSEADSQSEDDDEEEL
	Ì	1				NLSREELHNMLRLHKYKKLIIQ
İ		l				NKYSKDKELQQYQYYSAGLLS
		1				TYDPFYEQQRHLLGPKKKKFK
		l				EEKKLKAKLKKVKKKRRRDEE
		_				LSSEESPRRHHHQTKV
4991	35359	Α	5032	l l	1522	MVAQASGQTIREAEVGGSLTA
		l			1	QEVEATSILLSDESSEADSQSED
		1				DDEEELNLSREELHNMLRLHK
		ı				YKKLHQNKYSKDKEWMSQLA
		l				ALNYYLAGGDEQKLLDLSYSPF
		1				QNRQPAMAKAHNNNNNNNN
		l				NNNNHNKNPKRLLDERELLTY
i		1				STATQSFDTRNTRSFDEDAKES
		1				RAAALRAANKSGTGFGESYSL
		1				ANPSIRAGEDIPQPTIFNGKLKG
	1	1		1		YQLKGMNWLANLYEQRLERL
	1	1				RFLQLEQEHTCPQEGRAERLRG
		1				QPLKLWALLHFIMPTLFDSHEE FNEWFSKDIESHAENKSAIDET
					ŀ	
						KLKKVKKKRRRDEELSSEESPR
						RHHHQTKVFAKFSHDAPPPGT KKKHLSIEQLNARRKVWLSIV
					ł	KKELPKKTLYTODAPFHVVITS
						NQLVVQDVKYFQRVKWQYMV
		1				LDEAQALKSSSSLTRSNARYPL
						VSSQRKIHDQQVTTDKSSKMDF
				1		KEEEYIPAKHEMENTKLQFYLS
	1					AIGEKQ\VRWKILLQFQCRNRL
1,00						LLTGTPIQNTMAE
4992	35360	A	5033	1	974	MGFHHVARAGLELLTSGMCCY
4992	33300	^	3033	1'	274	FAQDLRPEQSIKASLQRIILRKY
	1					EKCGHHNLOLKKGYKSVDEYK
		1				VHKGSYNGFNQCLTTTQSKIFQ
1	1				1	CDKYVKDFHKFSNSNRHMTEK
	1	1				NPFKCKECGKSFCVLSHLTQHK
						RIHTTVNSYKLEECGKAFNVSS
	1	1				TLSQHMRIHTGQKHYQCGEM\
		1				GIAFNKSSHLNTHKIIHTGEKSY
	1	1			1	KREECGKAFNISSHLTTHKIIHT
	1	1			1	GENAYKCKECGKAFNQSSTLT
		1		l .		RHKIIHAGEKPYICEHCGRAFN
		1				OSSNLTKHKRIHTGDKPYKCEE
	1		1	Į.		CGKAFNVSSTLTQHKRIQQQQQ
	1	1			l	QTIKQTKNLLNNNNKKLWV
		L	l		l	QTIKQTKIALLIAINIAKKLW V

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
4993	35361	В	5034	22	684	
4994	35362	Α	5035	1	1338	
4995	35363	A	5036	1	596	MGMTDMGKSKKKSQGPPSFPP
						GGAPPPAIGAPAGRERPPGTGD
	1	Į				PFNQRPCDNLKTCHTSHGSVM
		1			1	AETAVINHKKRKNSPRIVQSND
	1					LTEAAYSLSRDQKRMLYLFVD
	i		i			QIRKSDGTLQEHDGICEIHVAK
		1				YAEIFGLTSAEASKDIRQALKSF
		ł				AGKEVVFYRPGEDAGHEKGYE
	1					SFPW/FIKRSPE*RRGKFPFTQM
		1				GQD
4996	35364	Α	5037	787	1692	
4997	35365	Α	5038	289	1338	
4998	35366	Α	5039	982	1347	
4999	35367	Α	5040	1	780	
5000	35368	В	5041	148	334	
5001	35369	Α	5042	2	545	
5002	35370	Α	5043	1	732	
5003	35371	Α	5044	1	1110	
5004	35372	A	5045	1	1170	
5005	35373	Α	5046	1	870	
5006	35374	Α	5047	1	1254	
5007	35375	A	5048	614	1236	TARVAAARRRCQCWGSGACGS
			ļ			ALTLPRTSSLTLTETPIVQQTRM
			1			VVRCPTASLPSQWRSCPSSTWA
						VPKTPPTWTCWRNSAILSL/VVF
						IRDKLMERRNRRTGRTEKARIW
						EVTDRTVRTWIGEAVAAAAAD
		ł				GVTFSVPVTPHTFRHSYAMHM
		l				LYAGIPLKVLQSLMGHKSISSTE
		1				VYTKVFALDVAARHRVQFAMP
****	2.52.7.6	_	50.10		1201	ESDAVAMLKQLS
5008	35376 35377	B	5049	2	1281 893	
5010	35377	A	5051	1	1416	
5011	35378	B	5052	49	768	
5012	35380	A	5052	1	792	
5012	35381	C	5054	1	1461	
5014	35382	Ā	5055	887	1203	RPEKAR/IWGVTDRTVRTWIGR
3014	33302	l^	3033	1007	1203	AVAAAAADGVTFSVPVPPHTF
1	1			l		RHSYAMHMLYAGIPLKVLOSL
	1	1	İ	l		MGHKSISSTEVYTKVFALDVAA
		l		1		RHRVOFAMPESDAVAMLKOLS
	L		L	l	L	KTIKT GEMINESDA VANILKULS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	]			sequence	l	
5015	35383	IA	5056	740	11431	CCQTLPVFHPPHPSHLGPRPCPP
		l'				TH/HLPSEHRSLFLEAACHDSDS
	1	1				LEPLNLSSGSKTKSPSLPPKAKK
	1	1				PKGLEISA/RPAGALRHRHRLHR
1		1				POOPSPPLGIPHPSLL\TAQVFIR
		1				DKLMERRNRRTGRTEKARIWE
		ı				VTDRTVRTWIGEAVAAAAADG
		1				VTFSVPVTPHTFRHSYAMHMI.
		ł				YAGIPLKVLOSLMGHKSISSTE
		1				VYTKVFALDVAARHRVOFAMP
						ESDAVAMLKOLS
5016	35384	A	5057	1040	1477	EDDATAMERQES
5017	35385	A	5058	1	1422	
5018	35386	В	5059	1	1404	
5019	35387	A	5060	353	870	AWSSPRSRCPLHSRTPSLPRVEG
3017	33367	^	3000	333	0,0	QAHIGPGL/HRYQQGHQDLFIL
						RSDLPSQVFIRDKLMERRNRRT
					1	GRTEKARIWEVTDRTVRTWIGE
		l			1	AVAAAAADGVTFSVPVTPHTF
		l				RHSYAMHMLYAGIPLKVLOSL
						MGHKSISSTEVYTKVFALDVAA
		l				RHRVOFAMPESDAVAMLKOLS
5020	35388	В	5061	1	1612	KIIKVQI AMI ESDA VAMEKQES
5020	35389	A	5062	2	429	WGHWASPRLWWAWGSPGPAG
3021	33309	l^	3002	_	727	LKPPGTVAASTGFSOWLLYIETI
						SRTPVELELKNSKVRKDVLS/R
		l				GPHSLYLVQDAQLEHAMEIAK
		l				VSVOALOAYRAPPPRMEOANP
						KTPPDANLYKKGPSPSPRRANT
5022	25200	١.	5062	500	1002	TRLGSRATKTIHPDS
3022	35390	A	5063	508	1007	PPLAQKQAVASQSHSPCGGFHR
		1		Ì		RWFRMRLTGEIMKIITCFKLVP
						EEQDIVVTPEYTLNFDNADAKI
		1	1		1	SQFDLNAIEA\ASQLATDDDEIA
		1	ł		1	ALTVGG\SLLQNSKVRKDVLSR
		ı	i		1	GPHSLYLVQDAQLEHALPLDT
1		1			1	AKALAAAIEKIGFDLLIWTSSRI
1	1	1	ı	ŀ	1	QAVALASPLSNT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5023	35391	A	5064	1	1670	MNIEFFDPPRIVSGLTLNRINIQE
						PFHLTGIRYCIDERQRTVNDVL
1	1				1	QAHAGRVLQQYLPAPATATFR
					ŀ	CQSRNRTENPQFLVCQWAGED
	1					OITOLLOEOWRVLIVMIFRTHN
	1					HMAGPRRWFRMRLTGEIMKIIT
1		1				CFKLVPEEQDIVVTPEYTLNFD
		1				NADAKISOFDLNAIEAASOLAT
						DDDEIAA\LTVGGSLLQNSKVR
	i					
		1			i	KDVLSRGPHSLYLVQDAQLEH
		1				ALPLDTAKALAAALEKIGFDLL
1	1		ļ		1	IFVKGTCLVLLVAFGLVTTHFQ
1		١.				PCLFGVQNGEQETVQILLVGVV
1						GGMERAERIIIPFTLAINNQPTT
	i					RLTKTIAQGMPAIIQRNIPNPRIS
						LQPAPTPRHSANPATMQPHAQ
	ŀ			ı		ATPTPKPHTRTYPTRPPHPQRSA
1						TPGTQRTPTPGPQTARDRAPKP
	1					DHTRPQTAHTAHHTSNDPQQR
						HRTRQRHTNKQHPHPAPPRLPT
				l		LPQNNKRQKPAESDTRKHHTP
						HMRQPTAHAETTARNTQAAQH
					1	CHTQNTPQANRHATGDRPEHH
	l	1				QARDRTRIDPKPNPDPRTITGHT
						KGTTYAHKHTPLATHHMTRPT
						TGHRHGTHH
5024	35392	Α	5065	548	924	GLLRPRFSVNSPHFNTWLLSAN
		1				SINWR*YGFMPSLLILLL*LNPM
	1					GRYSGASLVSRRMASTTLPGHS
		1				IAMRQPVCGIFALTRAIISI/AM
	I					WDFHVEDFMPERMALNLVLNS
						AI*LPKIFPARWMKFS
5025	35393	Λ	5066	33	424	CRFDESFWCDA\HAIFVAPTLY
						AYDFYADKTLVPLTDALANTW
						OKOFPLDYGKGRLWGSVAFVI
	1	1				GSALTGKLVTMFDYRVILALLT
	į.	1		l		LGVASMLLGFLIRPTIQPQGASL
	l l	1				QQESTGWSAWLALVRQNWRF
						LA
5026	35394	В	5067	I	265	
5027	35395	Α	5068	142	609	CLFRQVSAPHITRVCITRSAATI
		1			l	QTIDLNNLDTGD*LQPAFPPVW
l		1		l		LISPGPFHPTPSVTRVPLEKEIRT
1		1		I		FAORLSVLHGINAPEFFDKPLFS
1		1		I		SLVLTLRDEGYISDSGDAEPAE
		1				TMKVYQLQTNIVIIHKCFKAGF
						TLAVGNOFLLINKORASHON
		1			L	TELL GITGI BELINGINGIN

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5028	35396	A	5069	983	1387	LVWKVIPWRPAWKITLCVLNS
						CRRACLFAPAT*TANRLQAVC/
						WLOSANPSINRGTLEKESRTVA
						QRLSVLHGINAPEFFDKAVFSSL
						VLTLRDEGYISDSGDAEPAETM
				1		KVYQLLAELITSDVRLTIESATQ
						GEG
5029	35397	Α	5070	1	1815	
5030	35398	С	5071	1	354	
5031	35399	Α	5072	1	678	MTDKQQGEKQKQKTEDKTKT
ŀ						KQKQRKNKTDKRRKTKTERNT
			l			QRTPERQTNTNQTRTKQ/RRPD
	1					TGVTQADTRQDTSARR\LMRQP
l		1				RSAAAWMAALRGARDPKLITM
		1				VPHSKISRSIVRKGLPMTETQRR
						TETSKNYRPREQQTRNRQQQD
						PROQRTVQTHQQEERRETKDN
		į.				NTHTKPHETLARRHRRHNIHAL
	1					AAADLVIEAASEVWKSKKRSL
						HSWRKFAPTNAIDH
5032	35400	Α	5073	93	729	SADPRNRRDTRAAKFTRDAGK
		İ				TDC*NL*THIETPDPGDRYSRAG
[						SCGPG/PLKRRLNVWKSKKRSL
		l				HSWRKFARHKRY*PLTLRQSLY
	l					TAIAAEIKNPERVAGLHFFNPAP
l		l	Ì			VMKLVEVVSGLATAAEVVEQL
l		1				CELTLSWGKQPVRCHSTPGFIV
	İ	i				NRVARPYYSEAWRALEEQVAA
		1				PEVIDAALRDGAGFPMGPLELT
Į.	l	1				GPDWAGPPFCCHLFGV
5033	35401	Α	5074	145	1038	SILRLROKRKOLTAYDFADNCD
1	1	i i				KALY*RNHRLIREILALVCAHD
1						ROKK/YLPSLAGFL*LKNEINRL
		ļ.				SVRGW/SRRRSFSVR*/PFTNTD
		1				RARSHFYOFVIIDELOSLFOSHA
		l				DRRNONNGFVSTGSTHVGOFL
		1				TGQAVYSQVVRAAMNTDNLTF
		ĺ		l		VNFCTVTEEQLTAILQTEQRER
	1			l		DRFTLTVRDQYAVLTLTHFTRT
	l		1		1	YVVVAEGGVQQTSTGSHGHE
	1				I	LRTEANQTTAWDHVVETYAAF
1			1	l	1	TVWIHVFQVALTFAQRLHYRT
	1		1	l		LMLFFNVQSHVFIRLLFTTVDFT
1	1		l	l		EDNFRTGYROFETFTTH
L	1	1	l	l		EDMEKTOTKOLETETTU

sequence 09:540,217 codon for peptide of peptide sequence deletion, \possible sequence sequence sequence sequence sequence deletion, \possible sequence sequ	ossible nucleotide e nucleotide insertion)
5034 35402 A 5075 39 4329 YAPATFSAA' RNSAMHWO EREQWLAVC PHRAAAGRL RG*PHLCFRP AIMMETTPPG DKGYAPDFF HRPEGGDLA LRVPVANCA LRVPVANCA	
5034 35402 A 5075 39 4329 YAPATFSAA' RNSAMHWQ' EREQWLAVC PHRAAGRL RG*FHLGFR AIIMETTPGC DKGYAFDFH HRPEGDLIA LEVPVANCA	QPTPKKINNPVP
RNSAMHWO EREQWLAVC PPIRAAAGRL RG*PHLCFRP AIIMETTPPG DKGYAFDFFI HRPEGGDLA LRVPVANCA	QPTPKKINNPVP
RNSAMHWO' EREQWLAVC PHRAAAGRL RG*PHLCFRP AIIMETTPPG DKGYAFDFFI HRPEGGDLA (LRVPVANCA	
EREQWLAVG PHRAAAGRL RG*PHLCFRP AIIMETTPPG DKGYAFDFF HRPEGGDLIA LKVPVANCA	TRIQAQANGYWL
PHRAAAGEL RG*FHLCFRP AIIMETTPPG DKGYAFDFF HRPEGGDLIA LRVPVANCA	EQWFWRMEWSO
RG*FHLCFRP AIIMETTPPG DKGYAFDFF HRPEGGDLID LRVPVANCA	CHHHGNDATWH
AIIMETTPPG DKGYAFDFF HRPEGGDLIA LKVPVANCA	CV**RIEQPQEGY
HRPEGGDLIA LRVPVANCA	TGVNFIFVSDPAF
LRVPVANCA	CLEPMSHAPDDH
	LAPGESTTSEMS
AMAIGERAP	VTTASLDSYYGE
	VALLDFAASARL
	ATOIGDIKRIKLS
	HPGEDAGLYEA
5035 35403 A 5076 1 625 MRASGTDEA	VVLVPPIRMTLEC
	VEGAAAAFEALE
	I\RYGEGSP\WFDI
VLPCGGGITI	TLHKLR\SAQPLL
	KPVGLRYDPQAC
	TGWNLNGFEASI
	DGQYYCQGPRT
	GSSDPHDTTDSNN
DRVLGPSRYI	OGQYYCQGPRTL
TIRRTVIMTG	
5036 35404 A 5077 3 516 ATLSCEVVLE	NLAASPVVTTLE
YTLFDGER\V	VHSSAIDHLAIEK
LTSASLAFTV	EQPQQWSAESPY
LYHLVMTLK	DANGNVLEVVPQ
RVGFRDIKVF	RDGLFWINNRYV
MLHGVNRHE	NDHRKRRGVGM
DRVEKDLQL	MKQHNINSVRNA
HYRKRRNKE	VRTKKKIESIEEK
5037 35405 A 5078 3 678 ASYYCTRN/D	LELVAVCDSRLS
QRQALAEKY	GNASVWDDPQA
MLLAVKPDV	VSVCSPNRFHYE
HTLMALEAG	CHVI\QAREM/CD
TARKLGKVL.	AYDFHHRFALDT
QQLREQVTN	GVLGEIYVTTAR
ALRRCGVPG'	WGVFTNKELQGG
GPLIDIGIHMI	.DAA\MYVLGFPR
/SVEDSLCGTI	ELHSGCILWLETS
FALNIREHAI	MNIRFCGDKAGA
SVFPAHIYTA	TQR
5038 35406 A 5079 2 294 YSFMV/PIFGC	GRRWTVFSTAILI/I
PCVWLGIAVO	NPNT/PFGIFIVIA
LLCGFAGAN	FASSMGNISFFFP
KAKQGA\PVF	AF/LGVNGVPQA
DGSVMSLAM	PH
5039 35407 A 5080 I 834	
	VIALLLV\CLAFLY
PAAN\SEIHL\	GVLSIFWGDPDG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5041	35409	ĪA	5082	11	324	MQGGYNIHPLIDALDDAKLAPI
	ł		1			AAKALSHTLLMFDNFYDVEEK
i			1	1		AKRGNEYA\QVMQSWAD/AEW
			İ			FLNRPALAEKLTVTVFKVTGET
					i	NTDDLSPAPDAWSRPDIPLHAL
						GC
5042	35410	A	5083	1	866	MGLAQAKLLIEAPVNGGRNYN
		1				GPKVAKFLVGGASLNDVYLHQ
			1			HDKYRYDRYHLIRNREKTH\IM
		1				PEWVTQNIMNGRGVNRLDDVN
						RPKSPEIKNDIRLFRQELRDAAY
		1				HFQGDADNDQLSVTPLVGLGK
			1			SSLLIK\TIFHRMRWAEQNLSICS
				i		SSFNRPAIFVRNIIQLLREGKKV
						EITVGDKHENDFYIPEDEPFKIIC
		1				ALPYLYEINLRRFLSRLQYYVN
		1			1	TDQLVVRVW\KEDDN\TYHL\K
						GWWGDDKWMVITG\NKLDPR
						AWRLDLENAILIHDPOLELAPO
ř			1			REKELE
5043	35411	Α	5084	1	3483	VMFFFLPGLLMASWATRTPAIR
		1				DILSVSIAEMGGVLFGLSIGSMS
	1					GIL/SLGVVSETLWDT*C/HSWS
						RCPAH*SG**Y*/VLALWLTSPL
	1				l	LFAVGLGVFGASFGSAEVAINV
			1			EGAAGEREMNKTGLPMMHGF
l		1	1			YSLGTLAGAGVGMALTAFGVP
l						ATVHILLAALVAQIAAWYKAL
						QEQIPDFIPRAPQRQMIADVAK
l		1				TLAGEEGRHLAIEAPTGVGKTL
		1	l			SYLIPGIAIAREEQKTLVVSTAN
						VALQDQIYSKDLP
5044	35412	Λ	5085	I	848	MLVGKVVVSEGASFRTHGAVD
		1				TSKAYVSLENSGWTIIADITTTN
						QNTLLNLANLAMSDANVIMME
		1			l	<b>EPVTRSSVTASAENFITLTTNTL</b>
l						SGNGNFYMRTDMANHQSDQL
						NVTGQATAGDSLTLVTTGGGD
		1				AAFTLGNAGRVFDIGTYEYTLL
		1	İ			DNGNHSWSLAENRAQITPSTTD
				1		VLNMAAAQPLVFDAELDTVRE
	1	1	l			RL\GSVKGVSYDTAMWSSAINT
	1	1	1		1	RNNVTTDAGLRAQAIKTVHHR
		1				QNRLIHFSLNGSTFNVYRHFRR
						TKTCPKDAETNGKEQGRCQPE
1						CQT
5045	35413	В	5086	75	1777	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5046	35414	A	5087	1	860	IMKAPGLPADOOFFADLFSCLV LNPQLLGRVWFASQPASLPVGS LCIDFPRLDIVLRGEYGNILEAK QQRLVEGEMLFIPARAANLPVN NRPVMLLSI VPAFTWIGLSFY DSRTTSLLHPARQIOLPSLQRG EGEAMLSALTLFSRSPLEQNIIQ PLVLSLLHLCGSVVNMPPGNSQ PRGDELYHSICTWVQDNYAQP LTRESYAQFFDITPNHLSKLFAQ HGTMRFIEYVRWRMAKARMI LQKYHLSIHEVAQRCGFPDSDY
5047	35415	С	5088	86	601	
5048	35416	Α	5089	1	870	
5049	35417	A	5090	305	625	VAPGDRHAFPLAPSGLSPELTLY QTQCCAQATVQGLEGTRSWSQ SGTSSLSPWSHTSLRRRRKEEG EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
5050	35418	В	5091	1	552	
5051	35419	А	5092	2810	3117	LTLNSHMAPALIPILAMSAPMT PMKN/LSQVHAQGLVIRDLPLIA SNFRNTEDLSSYLKRHNIVAIA DIDTRKHAACAVPNTLVARGL RKHLKRVAAPQHWIAG

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5052	35420	A	5093	2	1902	LKYPMKRVGKRGEGKFERISW
			l			DEALDTISDNLRRILKDYGNEA
		ı				VHVLYGTGVDGGNITNSNVPY
		1		l		RLMNSCGGFLSRYGSYSTAQIS
		1		ŀ		AAMSYMFGANDGNSPDDIANT
						KLVVMFGNNPAETRMSGGGVT
		1				YYVEQARERSNARMIVIDPRYN
						DTAAGREDEWLPIRPGTDGAL
						ACAIAWVLITENMVDQPFLDK
		1		l		YCVGYDEKTLPANAPRNAHYK
						AYILGEGPDGIAKTPEWAAKIT
						SIPAEKIIOLAREIGSAKPAYICO
				1		GWGPORHSNGEOTSRAIAMLS
l						VLTGNVGINGGNSGVREGATG
				1		SAVGEVVFNTSMTGYOEILTD\
						LPI\PSNRYS\SYP\ILAMSAPMTP
		1		l		MKN/LSOVHAOGLVIRDLPLIAS
		l		i		\NFRNTEDLSSYLKRHNIVAIA\
		1		l		DIDTRKLTRLLREKGAQNGCIIA
		1		l		GDNPDAALALEKARAFPGLNG
						MDLAKEVTTAEAYSWTQGSW
				ŀ		TLTGGLPEAKKEDELPFHVVAY
						DFGAKRNILRMLVDRGCRLTIV
						PAQTSAEDVLKMNPDGIFLSNG
		1		l		PGDPAPCDYAITAIQKFLETDVF
		1		l		VFGICLGHQLLALASDVEKNVV
		l				MITAONHGFAVDEATLPANLR
	1	l		l		VTHKS\LFDRYVTGHSSHR*TG\
		l		1		FSFORHPEASPGPHDA\AP\LFD
5053	35421	A	5094	8	456	TST QIGHTENST GITTEN WIT BEE
5054	35422	Ā	5095	377	1228	KQARGRLCPAKPQGWSCPRPW
3034	33422	^	30,5	l'''	1220	OPTFC/GQCDLKVRPGVIGDHF
		l		l		GALKFDCPTGFRTCLGRITPLFL
		l		İ		PSSPIWNGCIFPIPVPGGDCGEG
		1				VOIRSLSCMVHSGSISHAAGRV
	1	l				EDALCGEMPFQDSILKQLCSVP
		l				CPGDCHLTEWSEWSTCELTCID
		1				GRSFETVGROSRSRTFIIOSFEN
		ı				ODSCPOOVLETRPCTGGCSPOA
		I		l		
1		1		l		RPAAIRQCIPACRKPFSYCTQGG
		1				VCGCEKGYTEIMKSNGFLDYC
		1				MKVPGSEDKKADVKNLSGKNR
		ļ	****		410	PVNSKIHDIFKGWSLQPLDP
5055	35423	Α	5096	1	519	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5056	35424	A	5097	I	743	MCPAIDAVLVYVNRKWTNLSD
5050	33.2.	ľ.	3077	1.	1	PMPVGQMGTVKYVLMSAPATT
		1				ASYIQLDFSPVVQQQKGKTIKL
		1				ADAGEALTFP/RGVMPKA/PPOL
						LVPATFLSAELALLOKSFHVNI
		1			[	QDTMIGELPPQTTKTLARFIPEV
		1				AVAYPKSKPLTTOIKIKKPPKV
				l .		AMKTGKSLLHLHSTLEMFAAR
	l					WRRKAPMSLFLLEEHFNLKGO
		1			1	HSLHENQLQMATSLDRRGN/YT
		1				GFITSYLEEAYIPVVNDVLOVG
		1			1	LPLPDFLAMNY
5057	35425	A	5098	2327	3435	KTTTLEDNLGNTIQDIGPGKDF
5057	33423	ľ.	3050	1227	3.55	MMKIPKANATKIKIDEWDLIKL
		ŀ				KSFCTAKATTKRVNKQDESLRS
	İ			ł		HYE*WGMLTDCVVMRDPNTK
		1				RSRGCGFVTYATVEEVDAATN
						ARPHKVDGKVVEPKRTVSRED
						SORPGAHLTVKKIFVGGIKEDT
						EGFAFVTFDDHDSVDKIVIPKY
		1			1	HTVNGHNCEVRKALSKQEMAS
						ASSSORGRSGRGGGGGGNENFO
						CGGNFSGHGGFGGSHDGGGYG
						GSGDGYNGFGNDGGYPGGGPG
	l				1	YSGGSRGYGSGGGGCGNODSG
		ĺ				YGRSGSYDSCNKGGRGGFGSG
						SGSNFGGGGSYNDFGNYNNQY
						SNFGPMKGGNF/GGRRSGP*GD
						GGQYFAKPPNHSGYGGSSSSSS
5058	35426	Α	5099	lı .	636	MRDPNTKRSRGFGFVTCATVE
					1	EVDAAMNARPCKVVGRTVEPK
						RAVSREDSQRPEDTEELHLRDY
						FEQYGKIEVIEIMTDQGSGKKR
i		1				GFAFVTFDNHDSMDKTVIQKY
						HTVNGHNCEARKALSKQEMAR
						ASSSQRGRSGSGNFGGGRGGGF
						GGNDNFGRGGNFSGHGGFGGS
		i				HGGGGYGG/SGDGYNGFGNDG
		1				GGGSYNDFVNYNNQSSHFGPM
5059	35427	Α	5100	1	3622	MTGICYTEDERSYKKNAQPTA
						ASKKQKETQKFCLRVDGQQKV
		1				KLSVLQEKSAQLTVQLKSQKFL
		1				GHPTAGRGRSELCLDLPDPPED
						PVALETRSVGTWVRERDLGMP
	1	1	i			DGEAALAAKVAVLETQLKKAL
	1	1			1	QELQAAQARQADPQPQAWPPP
	l	1				DSPVRVDTVRVVEGPREVEVV
		1	l			ASTAAGAPAQRAQSLEPYGTG
		1	l	1		LRALAMPGRPESPPVFRSQEVV
				1		ETMCPVPAAATSNVHMVKKISI
	1	1	1	1	I	TERSCDGAAEMKWEDQNIGD

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
5060	35428	A	5101	1	782	MRRRLQLDSLLHPPSCFSSTLK
1						CGKAAAAACDSSDQIQERLQT
1		1				GHLPCEASHTICPPNHHSQSTLR
					i	PPLPPP\HNHTLSHHHSSANSLN
1			l			RNSLTNRRSQIHAPAPAPNDLA
	1					TTPESVQLQDSWVLNSNVPLET
1						RFWCCQRFLVFPGLQLQHLTLS
	1				ŀ	LPVWSHGALPVSLCIFTWLSSH
İ						KDTSHFGLRVHLLSLPLEAKYS
						FYPGCPVLEPAPNPLKGPWCLW
						GVGTFRRYCTTFLFNESEPKDL
						VGEKFKSDRLCREAHLQE
5061	35429	A	5102	3	1864	
5062	35430	В	5103	1	525	
5063	35431	Α	5104	2	351	RPAVGAEKSNPSKRHRDRL\NA
				_		E\LDHLASLLPFPPDIISKLDKLS
			İ			VLRLSVSYLRVKSFFQVKRQRR
						EIHGRNCOKKRNONLKDRGWO
						WOMPKMWMTTRANEGPCRSG
	l		ĺ			GPEHWTPRP
5064	35432	A	5105	1	375	RPLOKORPAVGAEKSNPSKRHR
3007	33432	^	3103	ľ		DRLNAELDHL\ASLLPFPPDIISK
1			Ì			LDKLSVLRLSVSYLGVKSFFQG
				1		QGLAVADAEDVDDHTGERRP
						MSFRRPRALDTOALRRTOFGLH
1						LLMVNIAGLIATDRL
5065	35433	A	5106	407	910	NVTPAHYDEQQNFFAQIKGYIR
15005	33433	^	3100	l***/	310	CILFPPDQFECLYPYPVHHPCYR
1						QSQV*LDNPDYERFPNFQNVVG
1				l		YETVVGPGDVLYIPMYWWHHI
			1			ESLLNGGITITVNFWYKGAPTP
						KRIEYPLKAHNKVAIMKNIEKM
						LGEALGNPQEVGPLLNTMIKGP
						IOLACOGSRPPAR
7077	35434	-	5107	237	908	
5066	33434	A	3107	237	908	HEKPGRQRETRSQNHHHHHHH
						HHHHQEKIRIQTFTERP*EDTER
		l				SDCPQAKKRSPRRNQPC*HLDF
						ELPAARAATQPVNSGARAGRA
		1	:			GATVPRHTATLLLLHQRRDYA
1						GGSLCDIDRAPDAKQGGKS*ES
						ETD\$RFWKGTVC*DHTAGWVH
		[		l		GRPTTPHHSSPDSRNGGFQLHQ
1		1		l		QIALAAGWREGASRPKQEPLQP
				l		GPEQGQRRGRREPVQGKAPSG
L		<u>_</u>				HQSWPAE
		_				

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5067	35435	Α	5108	57	873	SGLCTAAFHHQMEVVHT*SVSS
						RS*R\PTTPVIAQWAHEQSGHG
		l	ŀ			GRHGGYAWTQQHGLPLTKAD
						LAMATAECPICQQQKPTLSPRY
						GTIPQGDQPATWWQVDYIGPL
						ASRKGQRYGFAYLARNVSAKT
						TIHGLMECLIHHHGIPHIIASDQ
		1				GTHFVAKEVRQWAHAHGIHW
						FHHVAYHPEAGGLTEWWNGL
		1				LKSQLQRQLGDNTLQDWGKVP
						QKAMYALIQCPIYGIVSPIARIH
						RSRNQGVKVEMAPFTITPSDPL
						AKCLLPVLVTLRSAGL
5068	35436	Α	5109	1	311	QITMQPELPIMNWVLSVPSSHK
						MGHAQQH\QEVAQMPRVSTPA
	1					TLPSLPQPALMAPWTVPYDQL
	1					MEEEKARARYAGTIQKWTAAA
						LQPLSRTSLKDSGEGTSKW
5069	35437	Α	5110	3	591	DPADPMVLEVSEADRDA\VPIS
			ŀ			ESQQRPLGFWSKALPSSANNYS
	1					FFKRQLLACYWVLVEIEHLTM
		l				GHQVTMRPELPIINCVLSDPCSH
					'	KVGHAQQHSIIKWRWYIHDWA
						EGTSKI.HEEVAQIPMVSTPSLP
			l			QPAPMASWEVPYDQLTEEEKT
			l			RAWFTDGSARHAGATQKWTA
						VALQPLSGTSLQDSSEEKSSQW
5070	35438	Α	5111	1	582	
5071	35439	Α	5112	1	635	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5072	35440	A	5113	2	1538	FFPIGFWRQHIPRLSVLLOHIY*
						VT*KAASFEWGPKOEKAL*OV
						QAVVQVALPLGPYDPADPMLL
						EVSVADKDAGCSLWOAPIGES
						QWRSLGFRSKALPSSADNYSSF
						ERQLLACYWALVETECLTLGH
						QVTT*PELPIMNWVLSDPSSHKV
		ı		1		GHEQQHSIIKWRWYICDWAVV
						GRESTTNGLAGWSETWKKHH
						WEMGEKQIWGRSMWMELSEW
		1				SKTVKIFVSYVSAHQCVTSTEE
						DFNNQWDGMTCSVDTTHPLSL
	ì					TTSVIAKWAHEQSDHGGRYGG
						YAGAQQHGLPLTKADLAMTTA
		l		l		ECPICQQQRPSLSPQYGTISQGD
						QPATWWQVDYIGPLPSWKGQR
	1	ŀ		ļ		FVLTVIDTYSGYGFAYPEHNTS
	1	l		İ		AKTTVNGPMECLIHRHGIPHGI
ŀ		1				ASDQGTRFTAKEVWQWAHAH
ł	1					GIHWFYYVPHHPEAAGLIGWW
	l	l		1		NGLLKSQLQCQLGDNTLQGWG
		ł				KVLQKAVCALNQHPIYGTVSP
	ŀ					VARIHGSRNQGVEVEVAPFIITS
						SDRLAKFLLPVSSTSCSAGL
5073	35441	A	5114	488	966	ILVGSKGQSVCPGPSSSGTRGSS
ĺ	ì					SPGVAVSNKAAATVGPQ*VTQ
ĺ		l		İ		QEGGPGSRQRTRAGSPELVPAG
		l			1	PSAVEGEEGSWTPGGPQVPRKR
				l		SAAPSRQR*HWLRCTPA*QRRG
						DWPRAAGRCHAARPPAAGSRA
l	1	1				PTKISARPTRISRLGPRAASKAQ
5074	25112	ļ.	2112	197	421	RLQRL KLKATMNSFHKS*SCALVSTRP
30/4	35442	Α	5115	197	421	
l		1				CSPRGDPRATLTTIPALVEPPCG
1		ı				TQDPKMA AEAPQRPGKRLGRN LLTRRRPT
5075	35443	A	5116	3	5649	LLEKLRQRIHDKAVALERAIDE
13073	33443	l <sup>A</sup>	3110	3	3049	KFSALEEKEKELRQLRLAVRER
l		1				DHDLERLRDVLSSNEATMQSM
		1				ESLLRAKGLEVEQLSTTCQNLQ
		ı				WLKEEMETKFSR WOKEQESIIO
1		1			ŀ	QLQTSLHDRNKEVEDLSATLLC
		1				KLGPGQSEIAEELCQRLQRKER
l		l				MLQDLLSDRNKQVLEHEMEIQ
						GLLQSVSTREQESQAAAEKLVQ
	1	1				ALMERNSELQALRQYLGGRDS
l	1	1				LMSQAPISNQQAEVTPTGRLGK
		l				OTDOGSMOIPSRDDST
5076	35444	A	5117	2	157	YLGRHLCLFSEHEEHSSRKEMV
30/0	33444	^	2117	ľ	l'''	LVEGLCSEQGRRG*TLASSSER
ĺ				1		KPLENER
		<u></u>		L	L	KI LLIVER

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5077	35445	A	5118	248	621	TDEPSLLSHTFCPKGALLSACSG
		l.,		Ī		ACPLSSGTQAGMPPSTEALOPC
				ı		RGLTVPHQ/LG*RPQGMLWWK
				ı		ALAADWSVEWOKGRRGLGKA
ł	1					LSVTSRTGRLLCR*GSAEAAAS
1						PLAASPRRSSRALGAGIP
5078	35446	A	5119	2	157	YLGRHLCLFSEHEEHSSRKEMV
30,0	55.110	Ι.				LVEGLCSEQGRRG*TLASSSER
		1				KPLENER
5079	35447	В	5120	125	994	
5080	35448	Α	5121	1	550	RRYRPRRVQDPGGPAEAERGPP
ŀ	1			ĺ		RRLLNARVHVCRAEASERAPGF
		ŀ		l		CGRVSAHVERARDPRLE*QLED
		l				KAAPRODFTQQLRGPEKQHRM
		1				VWQEKEDMHKQLVEASETLKS
		1	1	i		QAKELKDAHQQQKLALQEFLE
		1		1		LNELMAELYSQKQKVWDKEEE
		1		i		MEVAMOKADMMWQEI*RSKK
						LRKRMLFSQMRWL
5081	35449	Α	5122	135	638	GSFPGPAPLGQTLVTLGLAWQS
		1				SGWILRGWLVPPRAKCSPRGO
	1					ALAICLSLRGLGARSTWAETRP
	1					OGPRGSLASLCPAHMDLSIWKT
						GDGGPRSAFSKVHQGSLNTFG
		ŀ				VDTAARRLSQARTAPSPSV\SAP
		l				SSAAAPASAGPPPAPGAPPTPA
1		1				OALRPAPPSPRPAER
5082	35450	Α	5123	193	610	VGELLPFRFKISLRPFLALCLSSL
		1				GPCRQPHSGSVPA*NPLLGPRA
		1		ŀ		KSSPHSGCGLAPFAIPELLRRLP
		1				LEGSAHCPAPEGAASPPTSWDS
						ADPPCRETSIFAPPRVVLTPGPS
			1		İ	APQASPSQPLLFLTPRWDRLPES
		1	1			VL
5083	35451	Α	5124	2446	2630	VGFFFFFWWGERGTGSYSVTQ
						ARVQ*YDLGSLQLLPPSFKGFS
		1		1		CLSLPGSWYYRHGPPRLG
5084	35452	Α	5125	3	710	EDGDWDQRRGGEAGDQDQRR
						GGEDEDQDQRRGGEDGNRDQ
		1				KRDGENGDWDWKREDENKDQ
1	1	1				DEKREGEDGNQDQRRGGEDGD
1		1			1	QDQRRGGEDGNQDQRRGGKD
1		1			1	GDQDQGRGGEDGDQDQGREG
1		1				EDGDQEQRRRGEDGE*DQRRG
	1	1		I	1	GEDGGODOKRGGEDGNODWS
		1	1		1	REGEDRD*HWRRGGEVGE*DQ
		1			1	RRGGEDGE*GORRGSEDGDWD
		1			1	RSRGGEDGDQDQRSVGHLCHS
1		ŀ	1		1	OGPPASGCVS
				J	L	1400000

SEQ ID NO:	SEQ ID NO: nf peptide scquence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, ^=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5085	35453	Α	5126	506	882	RCSGQGFDGNKGTKALPTISA DTTRCWRTLRVTQMTCRFRRF KAFFIGIMSCGRTGRILFPPCSS MSWIPCRAKNS*GNVISQSPSK NR/WQIMMVIQLLNFYLPGDFV SFRIMLKGNWEVTRTRG
5086	35454	A	5127	107	1327	ERRKRAVGGFDLVLGEQPSDKI FR*VIV*GLALWLPLSKSFVIPP AELAINPSAKCKTDMTVMEDA VEVR*VWLQD*GLDSLEVLLDS FGPVRDCSKDNGGCSKNFRCIS DRKLDSTGCVVGLPCKLVVDS SGCYDRHIGVDCSDGFNGGCE CUCLQQMAPFDDPTLYNILMF CG*VELPARPLDGRSCQLITETC PBGSDCGESRELPMNQTLFGEM FGYNNLSKEVAAGQVLKGT R*TSYT*N*YQQLPDGLVVATV PLENQCLEEISEPTPDPDFLTGE CAFSTLFGYPVLQHWKVRSVM YHIKLINQVAISQGEHCCRLSCD GATSRADFVALLDQFGNHYIQE AIYGFESCSIWYPNKQVQRL WLEYEDISKGEWHACWQILSTF PWIVISLHNCLP
5087	35455	Α	5128	3	23	FYSAFLVADKVIVTSKHNNDTQ HIWESDSNEFSVIADPRGNTLG RGTTIT*VSIPPSL

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SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
i	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
-				sequence		
5088	35456	A	5129	1	2462	MRALWVLGLCCVLLTFGSVRA
3000	33430	^	3129	l'	2402	DDEVDVDGTVEEDLGKSREGS
		ŀ				RTDDEVVQREEEAIQLDGLNAS
						QIRELREKSEKFAFQAEVNRM
		1				MKLIIHSLL*NKGIFLERLISNSS
		ŀ				C\ALDRLSLISLTDENALSVNE*
	ĺ					LTVN\KCDKEKNLLHVOHTGV
		l				
						GMT\REELVKN\LGTIAQIWDQ
		l				ASFLNKMP*SHRKMGPVNLPEL
		l				IGPVWVSGFLFPPSLVADKVIVT
1		l				SKHKQPIPQHIWGVWTPNGIFL
						*LLDPRGKHS*DRGNRQFTLCP
						*KEEASDLPWNLDTIKNLRQKN
1		l				IHSFIKLFLIYVW\SSKTETV*GA
		ı				PWGEEEAAKEEKEESDDEAA\V
1		1				EEEEEEKKPKTKKVEKTVWDW
	İ	1				ELMNDIKPIWQRPSKEVEEDEY
		ı				KAFYKSFSKESDDPMAYIHFTA
						EGEVTFKSILFVPTSAPRGLFDE
İ		1				YGSKKSDYIKLYVRRVFITDDF
		1		1		HDMMPKYLNFVKGVVDSDDL
ŀ		I	-			PLNVSRETLQQHKLLKVIRKKL
ŀ		l				VRKTLDMIKKIADDKYNDTFW
		l				KEFGTNIKLGVIEDHSNRTRLA
ŀ		l				KLLRFQSSHHPTDITSLDQYVE
	1	i				RMKEKQDKIYFMAGSSRKEAE
		l				SSPFVERLLKKGYEVIYLTEPVD
		1				EYCIQALPEFDGKRFQNVAKEG
1		1				VKFDESEKTKESREAVEKEFEP
		1				LLNWMKDKALKDKIEKAVVSQ
		1				RLTESPCALVASQYGWSGNME
		1				RIMKAQAYQTGKDISTNYYAS
5089	35457	Α	5130	45	416	RWGLAMFPSLDNKSETLSQKK
		1				KKKDLCPHISFEMDLTTADAR
1		ı				WVQDAATRLLATTRCPPNSRG
ı						SR**ISWRAGCCPGGWAGPHW
		l				GHDGCL*PSCVSSS
5090	35458	Α	5131	3	477	GRLPRHRGGEPGAAQPAGRQP
		ŀ				RGGAAATAAGAPRAGGGAAA
						GNARRCREAAARDPHHGEGSG
						PEPSQCEGAAHQRAGRAQGD*
		l	1	l		GGSGATGEGGRRGHDSHNPLG
		1		I		RVRGSTLPPS**N*VGL*VPSWP
1	1			I		OCGPAHPPGOHPALOEIHORLP
1	l		l	I		LESGGHRVV
	L	_				DD000int.

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		1				
5091	35459	Α	5132	3	446	RTGSWGWSASQQRHRKDRGL
		1			\	DSAGSGWVSHILPVPAPPPADA
	l	1				RPSASRWRRQGSHPLPGRTECP
	1	1				SVQPLCLPPPAGHHRNHSIASPS
		1				QTPPPRSLPGSQDKSLFLPRDRR
		l			l	TGEGEGHMN*APLSAPGTSCRS
		1				GGSTSWLPEILGPTQ
5092	35460	Α	5133	352	588	DIFKVGGCFLFKRLRCQQRFFL
		1			İ	LIFSSSTQSA*RVSNGPYH*EIK
		1				MAVYYGELRKNGLIQESCDNIQ
		1				PRQGSFNMDSMQ
5093	35461	C	5134	13	144	
5094	35462	Α	5135	587	1078	LSQRFPLSSRIKLQRLSLQNGIP
						QIKELDYLFRTNSNQINFNLLSH
						RVRARPPAPPGRPNPSPGPDRPP
		1				EPPARAGSSRRGPGEPPRRQPQ
		1				RRFRRRGPDRPGRLSRGL*RRR
	1	1				ARPASPQPRQHHSRGPAGRPGV
		1				APRRPAGLAAAAERLTARGAA
						ASPAIPRA
5095	35463	Α	5136	44	455	HLRNRTR/PSQITPHIYNHLIFDK
		l				/PLFNIWWWENWLAICRKLKLD
	1	l				PFLTPYTKINSRWIKD*NIRPKSI
						KNLEENLGNTIQHLG/IGKDFM
		1				TKTPKAMATKAKIDIWDLIKLK
	1	1			i e	SFCTAKETIIRVNRLPT*WEKIF
						AIYP
5096	35464	Α	5137	101	861	LIGYQPKMSRTRRIHSRILPERIK
						YLGSQLIRDVKDLLKENYKPLL
	ļ				İ	NEIKEDTNKWKNIPCSWIGRISI
						VKMAIL/PQAICGKLKLDPFLTP
		l				YTKINSRWIKDLNVGPTTIKTLE
		i			l	ENLGNTIQAIGMGEDFMTKTPK
1		1			ŀ	AMATKAKIDKWDLIKLKSFCT
	1	1		1		AKETTIRVNRQPTEWENIFTIYP
		1			i	SDKGLISRIYKELNQIYKKK\TR
		1				NPIKK*VRDMNRHFSKEDIYAA
1		l	1			HRHMKKCSSLLDIREMQIKTTM
						RYHLTPI
5097	35465	Α	5138	3	314	LKSFCMAKETTIRVNR*PTEWE
		l				NIFAIYPSEKGLIYRIYNEATNK
		1			I	DLVRRSGPLKTPKKKSQLTVLN
	1	1	1		1	LVTFKRTPALSEEKESAQVLWQ
		ĺ				FKKPECVLTSKRVH
				1		

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5098	35466	Α	5139	1	1278	MNIDAKILNKILANRIQQHIKKL
						IHHDOVGFIPEMOGWVNICKSI
						NIIOHINRTKOKNHMIISIDAEK
ļ					į.	AFDKIQQRFMLKTLNKLGIDGT
						YLKIIRAIYDKPTANIILNGOKL
l						EAFPLKTGTRQGCPLSPLLFNIV
						LEVLARAIMOEKEIKGIOLGKE
1						EVKLSLFADDMIVYLENPIVSA
						RNLLKLISNFSKVSGYKINVOK
	į.					SOTFLHTNNRQRESQIMSELPFT
1						IASKRIKYLEIQLTRDVKDLFKE
						NYKPLLN
5099	35467	A	5140	1	430	GGVFFLRTPTDCCGMLQGAAG
	1					STGFYASEARPRGPACSLDRGS
						SSLLSWGLHQDPLFPAAKQHRR
		1				EAGRADONSPRPRLSTG*OTPT
		ı				L*RRPAAATGRRRAQPPRATSV
		l				SAPASPPCPRARPPHHARPPRVL
						ACQP*ATAPGP
5100	35468	Α	5141	1	346	
5101	35469	Α	5142	3	1336	
5102	35470	Α	5143	5	283	
5103	35471	Α	5144	1	1368	
5104	35472	В	5145	1	838	
5105	35473	Α	5146	1	962	
5106	35474	Α	5147	19	87	
5107	35475	A	5148	41	83 I	GLQNPKHQSSQLVDLKMKKSL
	i					LQCMFQYLIVLQ*YLK*YLGTQ
		1		l		LTRDVKDLFKENYKPLLKEIKE
	1	1		l		DTNKWKNIPCSWIGRINIVKMA
	1					ILPKDPTTAQLSPRGSTAQKGH
1		1		l		WRPCPLPPRGVPRSPRGPTSHP
	I			1		HHDPCPGGAPVRNTGSERWQR
	1		1			KLRSGPKSDWAGRAQAPSLGE
1					1	GGAKNGKSHPGSHRAFSLPRAP
1						RRLGPGSQPGRFRGFLKQARGR
l						AGEGHSAILLAPESPNAQVSNV
1	1	1	1		1	TSATYRSNLSGLPRPCSVVLLG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclentide	Nucleotide location of last	Aminn acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletinn, \=possible nucleotide insertion)
				sequence	1	
5108	35476	Ā	5149	li	2233	MKAEIKTFFETNENKDTTYONI
					1	WDAFKAVCRGKFTALNAHKR
					I	KQERSKIDTLTSQLKELEKQEQ
		1				THSKASRRQEITKIRAELKEIET
						OKALOKINESRSWCFEKIHKID
		1				RPLARLIKKKREKNOIDAIKND
						KGDITTOPTEIQTTIREYYKHLY
						ANKLENLEEMDKFLDTYTLPRI
		1				NQEEVESLNRPITGSEIVAIINSL
						PTKNSPGPDGFTAEFYQRYKEE
					1	LRIKYLGIQLTRDVKDL\FKENY
		1				KPLLNEIK\EDTNKWKNIPCSW
						VGRINIVKMAILAQGNL*IYKFI
1						AISIKLPFTFFIGL/EKNLTFKFIW
						\NQKRS\RIAKSILSOKNKAG\GI
	1			-	į.	TLPDFQTITYKATVTKTA\WYW
						YQNRDIDQWNRTEPSEITPHIY
ì		ŀ				ILI\F\DKPEKNKHGGKASL\FIK
						W\CW\ENWLA\ICRKLKLDPFLT
						PYTTINSRWIKDLNLRCQIIKTL
						EENLONTIQDTDIGKDFMTKTP
	1					KAMATKAKIDKWDLIKLKSFC
	1					TAKETTIRVNRQPIEREKIFAIYF
					1	SDKGLISKIYKELKQIYKKKNK
						QPHQKVGEGYEQILLKRRHLCS
l						QQTHESMAHHHWPCREMQINT
	1					TMRYHLTPVRMAIIKKSGNNRO
						WRGCGEIGTLLHCWWDCKLV
						QPLWKSVWRFLRDLELEIPFDP
						AIPLLGIYPNDYKSCCYKDTCT
				1		RMFIAALFTIAKTWNQPKCPTM
						IDWIKKMWHIYTMEYYAAIKIE
5109	35477	Α	5150	1390	3491	DLLTRTACAVPGWGCSSRATC
		1				QARGWRLLSSPPHPSGVQPLLC
		1				HLPYPPSPFSLLSNLTPFLRAFPF
i						SLETS*KWART/WPGAVAHAC
						NPSSLGGRGRWIT*GREFETNL
						TNMEKPCLY
5110	35478	A	5151	310	445	YLTKIWPGAVAHTCNPSTLGGF
						GGWIT*GQEFETSLANMVKPHI
						Υ
5111	35479	A	5152	44	1132	PQVIHPPRAPKLLELQEPPRWIH
		1				DLNQDTPSALCQH*RTC*HRAE
		1	l			GVSWFKSWIHLGGSCNSSSLGA
		_				RGGWIT*GQEFETSLTNMAKPH
5112	35480	C	5153	183	323	
5113	35481	В	5154	504	2474	
5114	35482	С	5155	66	269	
5115	35483	В	5156	2414	3096	L

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
5116	35484	A	5157	9	239	нннүсүннннннннннн
			ŀ			LPAPCRNLRV*PVCFRYKLWFH
	1	1				YGKQHLLFLDFLLSHSEWCEM
						VSHCGFDLHFSDD
5117	35485	A	5158	3	387	TDTKPLSCSSCPPRGKKPVSHR
		ŀ				DQ*RRWGRRCRGEPGTEACWS
		ŀ	l			AGALQF*KPRSRGGRTSKMTSG
		1				PSAEKGGG*AGRKPGRRHFGRR
	İ	l				VLRHSCVLPVARELWGRHGPC
						GWROKNVPWKWSELLPVVAP
5118	35486	A	5159	1	277	MPPPPPPSESPGPGPVGSRLPPG
151.10	55.00	ľ.	,	ľ		PAVTGNEKELRGNP*VGLAPPR
						PRFRASRREGVTGKVHRPNRLO
	1	İ				LRAPPKG*SDORGONVPPSEAK
						SLC
5119	35487	Α	5160	1	3285	SEC
5120	35488	A	5161	3	194	IPLSLQSKEVGQQLQDDLMKVL
3120	33466	^	3101	ľ	174	NELYSVNOMGCLAL*OAEGSSI
İ		1			i	WQLAAIVHQQQN*TPSWGQ
5101	35489	١.	61/0	520	844	VOAPGKCHAOMPAPAAPVPLG
5121	35489	A	5162	520	844	
1		1				RSRNPGRLASAVPVSSLLRFLPF
1		1				LQPIPPSDILPLSFEAVPSSPAAE
					į .	SGLHPCTRRRKRARPSC*VPGL
						LLSPQPHPPPHVWRKGIL
5122	35490	A	5163	1	794	FRGFLDRGDCAALPCTYPHSPC
					1	SH*GGNCLPSLLTRPCVKA*PQ
	1	1				MSGRKSSMRRWRRQSRLTAGT
						SS*TPTSSTMC*ALVGSSTWNC
						MLQAGSTAPGAGTPGSRPTWS
		l				SSSTCSWTAPSGRARCACASSS
1						SCAMSAARRGWTSPACWRRTS
		1				RAWWTTSSPACASSATASVAA
						STASTWPAARTTGGTAESSARP
						ARRASCTGSPARSCWRRRRPPT
						PSPGRPAPPSRRTRRAQAGTSA
						LSPGACFGPRSCC*SSTCSSLSV
						APY
5123	35491	A	5164	3	57	RIGQGVPVVHS*VEGGPNVISIV
1				ľ		LEYLRDTPPVPVVVCDGSGRAS
		1				DILAFGHKYSEEGG*VKVFLWC
1		1			ŀ	THKWKEDPM
5124	35492	A	5165	1	1326	THE WALLSTIN
5125	35492	A	5166	2	337	YSVTMTPGKLRTLCEIDWPALE
13123	55495	l^	3100	<b> </b> *	337	VGWSSEGSLDRSLV*KVLCPEL
1		l	l	1	1	
1		1	l			VPSGGFLVSLTSRMKPQTLTGS
		1	l			VKVLKDGMSGVCSFRCSDVSR
			****	222	440	VSSFWWVRGLAGWSTTLLRKL
5126	35494	С	5167	339	548	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ľ		sequence		
5127	35495	A	5168	3	413	SQAFLPAASRRERPPEPVDPKA
10.21	150,000	Ι.,	15.00	1		TDPRSGTRRLPPRLPCOWTTPE
	1					HSHTSQLNLSRAFPKEPNPAAT
				ł		O*NPSGASPRERPHARAGEDRN
		1				GEC*EGNGSRPDLEEEASTPRA
				1		SPTPSD*PLWLHPPRPLVLETPL
						LOL
5128	35496	IA	5169	3	479	FLHSTHIYWAHSMHELLKTAV
				·		VSISGQCTSLNTESGIWGGVPE
						NAR/CPPAEGTVPASLOPRDPPR
				1		LPGSH/ASLPSASPPSRHVTWPP
	1			1		EP/EAAGPKPS*IRCRWPPAGAT
	1					TKANPKESGRLVESMLPLPKSR
						SAPVTFSAFACSGLPERVHEVF
	1					RVGKLR
5129	35497	Α	5170	81	329	QSVSSPSWFPQFPVQVQKVPCY
						OVYRGDLVV*KHVAPPPSLPSS
	1	1				FSGHVRHDCFPFAFHDDRKFPE
						ASPAMLPVSSLGPHYL
5130	35498	Α	5171	335	467	MPSTPTARKPESPEALARVESIA
						CLPSPAP\PHECSPQASEETG
5131	35499	Α	5172	1	2424	
5132	35500	Α	5173	2	304	CLTKNTSATREKQVTELHRRSK
i				1		LQPEPAKTKALQTVIE*KDITLC
				i .		*VKEHLYIVACWALRLHLVFLP
		1		1		TKAGISPALMKVSYPGKPLTLK
						QLGRLV1LQEQ
5133	35501	Α	5174	44	286	GVQNGVEELILVRRMQKSPGP
		1				GEMESGSLEKEPLGTQTGPVPS
				1		EGTE*TQGPPRTPSLQTQGPQRT
	1	1		1		PSLQTQGPPNTPSL*TQGPLRTL
		1				SLQTQGPPNTPSLQTQGPPRTPS
						LQTQGPQRTPSLQTQGPPNTPS
5134	35502	Α	5175	206	384	KRVFAHQADGRARSGFISSAGP
				1		GSQAGPGQGTG*QREDVEAAG
		_				QPGSTAEGVRT*SDPG
5135	35503	Α	5176	270	818	RNERKPSQRTAVGLGAGQLQP
	į	1		i .		GQPGVQSEEPGPLEAGCAAGV
		1		}		LPGPAEQDREGIYSK*KRVFAH
		ŀ		1		QADGRARSGFISSAGPGSQAGP
	i	ŀ				GQGTG*QREDVEAAGQPGSTA
		ŀ				EGVRT*SDPGSSHPAAAAFYEN
	1	1		1	1	IQDGEALGRCGAKRTATAAP*Q
	1	1		1		RG*EGF*AGPTAAEKNEEGPPP
						VFSLFNSHL
5136	35504	Α	5177	122	436	LTSLFSAISTKAKVSPLCSARAC
		1				SPSPAARAALGSPGFTC*GAGV
1		1			1	APTPVPVAAPAPATAPATAVAA
1	1				I	AATTTVVSAAMFTRRATRAAA
L		L		L	L	ATGA WGF VAGA PWPLQT

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	Incation of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
5137	35505	IA.	5178	20	1341	MRRCVAAPLAHRW*OKLGLPG
3137	33303	^	3176	20	1341	CTPTVCSFLSPOPPPRARSSSAT
					1	
						LSSGAPRRAATPQPQTTPPSSVQ
				1		PCAATPCARGGRPAPAGVTWP
						TTRPSMA*RTS*ASTTAPRMAP
					i	PRSHACARSHRPETARSARTAP
					1	RSAITRRAFTSTRPPPTTRTVAS
		1			1	SGTHTSGLSPTASRLARCRAPG
						RSSTIIT*TCRSPTRLCCPAQRPL
	1	1				PPASSPSSSRTSRSVWTRRCTRL
					l	RWTSSRPPSWMALRTVGTSTGF
						TA*RSLRRCQASTWRSRPSTSA
						PPSWCARWAAT*PLPSACQRK
		1				WSMLWRTGTARVSTSACGAAF
		1			1	STSRSTSRPSTPMLRAPVPAGW
		1				QPPALHPQPPRPSHTRQPWPSA
						RRSCRWRTCTTRPASSTSSPRA
						T*TSHWPPTTRWRMSRCSTPTK
						TNCTCMRGLGTCQAGRLRGCP
						WPPGPSWAPWSRSWPCSLCSA
5138	35506	Α	5179	47	598	ASGPASIVVLRQQFIKFFLDEICS
ľ						LEERVWCRKLCLLYILWKEPR
		1				AVQAKSRCSDIRRELYRPVSLA
	l .					GLSGDFLRAGRYSAHTVNGAW
						SAWTSWSQWA**SRGLLLALH
	1					NMLKIIIAFCSLQVATRIQSTFIS
						SWHLSPSLLGSRSFSLYMSFGS
						VLCPLFISHDTSSYSTKSFQSFSC
						LGVW
5139	35507	Α	5180	236	690	LQNWSYLAEQCWNGGFIYLIM
	i	1			1	LRRFKHKAHSTYNGNSSNSSEP
		1		1		GETPTL*LGDRTAKKGKRTRKF
	1			1		GVISRPPANKAPEESKGSAGCE
	1			1		VSSDPSTELENGPDPELGNGHV
				1		FQLENGPDSLKEVAGPHLERSE
				1		VDRGTEHRIPKTDAPLTTSN
5140	35508	Α	5181	2	480	WPFWAMVQRPSSAILCGPATLP
				ł		PNCRGACCARCRATGALSAYP
				1		AIHRPATRPPAPPAPGPLTSPPPL
					l	SVQNSNPDPLPSARPSPGPAAPR
				1		HARHSPSELPALTLSARGSSAL
	1				i	CTKLKVEAAA*SCSASAWNWR
1						LLPRNHVDSRCQPEPDGARARD
	L	L		1		GRGP
5141	35509	Α	5182	3	153	
5142	35510	Α	5183	3	239	
5143	35511	A	5184	!	394	
5144	35512	A B	5185	84	435 2068	
5145	35513	I <sub>R</sub>	5186	104	12008	I

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5146	35514	A	5187	149	832	DAGLSWREATRPGAPLHRPGC
						QDASTQMTRPGDPGSSALFPLP
						SP*PEREELPMSSRRSPKPELPG
					i	EACSRRPPTRPRPRTATRGPPLN
		ĺ		1	1	GRLPRARLPVSAGAGALGGGR
						CRRRVAPRRVTPRLATRPSGVA
						PRGSG*AATTKLSLAFGVTPLA
		l				LTPWSRTPFRKREERPPF*YPRP
		l				ATPEASPAHVENFRSNQTRYTS
						AE*SGQQLERPSIAEISAQATVE
				Ì		PRSTI
5147	35515	A	5188	45	312	AEAQGGAEAEGHGGGGGPAPS
						QGCPARAAGARGWQPAPSPQK
						P\TPSDTTPPP\RTQPPVTQPCHP
ł						VTQPPVTQPPVTQPRHPMKIPPP
						G
5148	35516	Α	5189	15	549	PRHKEPESQAPGRRAPQAAAY
		l				QQAASPAR*QGGSCSRCPPG*A
l		1				VEAAPAP*GQALGCVSQGPA*V
						GPTRSPHPTAGLSRPHGPPSVRS
		l				TGWSPSSRPLQAQEAPWPVAPT
		l				HIPPPLDPGQPHSCGLGAGCQP
		l				RAPAARAGHP*EGAGPPPPPWP
		1				SASAPPCASAQPVLWLRFPRET
						КТ
5149	35517	Α	5190	1	2445	
5150	35518	Α	5191	ļi	708	FSEGRNRFLNVGPTRFSTSRQTL
		l				MWIPDSFFSSLLSGRISTLRDET
						GAIFIDRDPAAFAPILNFLRTKE
		l				LDLRGVSINVLRHEAEFYGITPL
		1				EKIKMEYCFSVCMYS*QVCFE
		l				MFLVRRLLLCEELERSSCGSVL
		l				FHGYLPPPGIPSRKINNTVRSAD
						SRNGLNSTEGEARGNGTQPVLS
		l				GTGEETVRLANTIDSKYVAND
		l				DWLIFQYVDEEDLMNAIKDFSS
	2.551.0	ļ	4100		220	VTKERTTFTDTHL
5151	35519	A	5192	31	330	YGGTATVQRWAESRHVPFPPS
			l	l		QEQNANKICSVCQEEKDSADSY
				1		GEIPWWQGPERCWPVRLMLAT
		1		1		LGDYKWVLTGIGTDS*LGFTIPT
		<u>L</u> .	L		L	DHANAFSAKEIPQ

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5152	35520	A	5193	1	734	MISEVIVIOMLFLHAFSKVFSAL
						IKNNKKPLODAQIKWKAISGLS
		1				GGMRRSECNRERDOVTRTOCR
		l				DISQK\RGPGD*GMATSKNGAM
		1				A*OLGPGCOGDASTGNAEFGES
		l				AHAWSGGGRVPGVTGPDREEV
		l				GRSWQGTSCGGGTSGCGRLQ*
		1				DGVASRGRW/DPARPREORAG
						VROLAAPLGGP*SRRPWEPPGG
		1				SSCGRYLFAISSWSGVTVAOEG
						ORKRGSGK*RTERSGPGLGRRL
		1				PPLLLTV
5153	35521	A	5194	3	449	EGORSSSPATALSSSGPPSLKM
		1				ATSKNGAMA*OLGPGCOGDAS
	į	1				TGNAEFGESAHAWSGGGRVPG
		1				VTGPDREEVGRSWOGTSCGGG
		1				TSGCGRLQ*DGVASRGRWDRR
		1				DRASSGRESGSWLHHSGARSLG
		1				APGSRPVEAPAAGSEAKTPG
5154	35522	Α	5195	606	841	CTVGFALPVFY*GFSH*CSSGIL
	1	1				V*NSRFLLCLCQALVSG*CWPH
1		1				KMS*GGFPLLLLTGIVSEGMVP
1		1				ASLCISGRIQL
5155	35523	Α	5196	620	930	IPFISFSCLIALARTSNTMLNRSG
		1				ERGHPCLVPVFKGNASSFCPFS
		1				MILAVGLS*IALIILKYVPSIPNL
1		1				LRVFSMKGC*ILSKAFSASIEIIM
		_				WFLSLALFI
5156	35524	С	5197	1	819	
5157	35525 35526	A	5198	591 187	815 387	FFKTICFMRVRVKRPPNRLCVS
5158	35526	I <sup>A</sup>	5199	187	387	NMAVYFTWVQAGLHCESYPEH
		l				L*WSCRLPRRLGGVRL*PLEGE
5159	35527	A	5200	1	1197	L*WSCRLPRRLGGVRL*PLEGE
5160	35528	A	5200	119	375	ILDISPLSDE*IAKIFSHSVGCLFT
3100	33320	<u> </u> ^	3201	117	373	LMVVSLAVOKLFSLIISHLSILA
1		l				FVAIAFGVLDVK/CLVHAYVLN
1		l				GIA*VFF*GFYGFRSNI
5161	35529	В	5202	1	1053	out vii or or or or
5162	35530	Α	5203	2	157	
5163	35531	Α	5204	12	176	
5164	35532	Α	5205	2	223	QTVLEDRSPRARWIF*G**GTIC
						SIPIPSFWWFSSNLSHSFVCRSPP
1	l			l		SSSPGGLPMCTCVSKFPWAVW
						PFSRY
5165	35533	Α	5206	61	308	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5166	35534	A	5207	487	898	DFAEVAYOLGISSGVCRTTDFH
						EPRMLLSDRSSGSFVTII\SVFLS
				ł		FSSLKCL*SPLVHDALHOAFHP
				1		GKSRLRFLGSMACCMSKFTCPF
		1			1	TLSTVPSSTPFSFSCSLIKTRSAT
						LLKLWSISLRFRLHSWSSAFRV
5167	35535	A	5208	9	191	IPOHIYPPKTKPGRI*ISE*TNNR
						L*NCGNDO*LINQKESRTRWIH
		l		1		SRILPKTNREPNHE
5168	35536	A	5209	1	1989	
	35537	В	5210	1	1488	
5170	35538	A	5211	929	1209	IPFISFSCPIALARTSNTMLNRIC
						ERGHPCLVPVFKGNASSFCPFS
		1				MILAVGLS*IALIILRYVPSILNL
						FRVFSMKGC*TLSKAFSVSIEII
5171	35539	A	5212	242	642	FSLKRSFTSLVSWIPRYFILFEAI
		1				VNGSSLMIWLSVCLLLMYRNA
						CDFFPLILYPETLLKLLISSSSLY
1 1						LW*NSAVNLSGPGLFLVGRLLII
		1				ASISEPAIGLFRDSPSSWFSLGR
						VYVSRNLSISSRFSSLFV
	35540	Α	5213	747	885	
5173	35541	В	5214	115	1267	
5174	35542	Α	5215	209	322	
	35543	В	5216	1	3321	
5176	35544	Α	5217	390	655	CLFPVHYPRLHAMMHQMKNP
					ŀ	VLVLGIGGFILGILGVIGGPVSLF
		l				KGS*KLLGLIETGKISLDHPVPG
		l				GTPTKMALYEHFMNTKEFGIE
	35545	Α	5218	3	221	
5178	35546	Α	5219	798	914	FVFLWDRW*YPLYHFLLCLFDS
						SLFFSLLVLLAVYQFC
5179	35547	Α	5220	12	460	YLCMLHEVLVLCFSVPSGHFSF
						SLN*LF*LAVPVTFYQG\LSFLA
		l				QA*ASQVDFRQLCWQQEFQAS
						GS*LAGLHGSGIH*ARPLGSWL
						QLPFQESEWFCLSGVPGATVVS
1			i			CTF**SPF*LV*DGISLWF*FAFL
						*WPVMMSIFFMCLLAA
5180	35548	Α	5221	3	508	AERNGSRQGVGAGAGDHEVLQ
		l		l		LLPDKWKQKILCPVQLLRGAW
		1		1		SNYYSPDANRQP*VQGNAHLF
			l			AECWPHGEDSQPTVPTSQGRM
			İ	ŀ		LAGPARHLPHPHVPSPSGSLRG
			l	1		SDSEDTH*GTVAGSGCLHCLAP
1 1			I	ŀ	1	GHLHPGWPPSRVLPIPDRSVHQ
						GPGRKAPPTPPRVTPLFT

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ŀ	09/540,217	codon for peptide	of peptide sequence	deletion, \sipossible nucleotide insertion)
			l	sequence		
5181	35549	A	5222	584	1052	LRKAAASGSFVFVAPDPNTDTC
15101	33347	ľ	3222	304	1032	SSQCSESESGSRGCSMGHQRSL.
					l	ОННАННИНННОННИННИН
	i i					HLDTGWRGE*SRHSAGLCPPSO
			l			RRLHSCQTSPSCSPPSGHRCI*L1
			İ		1	GIEAA*CHSL*PYOKDACHHFE
					1	EHSPPP*RPPHLPRHHLHPOPSS
5182	35550	A	5223	1614	2308	LRKAAASGSFVFVAPDPNTDTG
3102	33330	ľ	JELJ	1014	2500	SSOCSESESGSRGCSMGHORSL
		1	ŀ			ОННАННИННОНИННИНН
		1				HLDTGWRGE*SRHSAGLCPPSQ
		i				RRLHSCQTSPSCSPPSGHRCI*LT
		1				GIEAA*/WS*PLTLSKRCVSPLR
		1	ŀ			RAQSSSVTSSTSAQASSAPPEKK
					l	*L*PERPYSSPHPASVADLOMC
	1	1				LPLNRITGOTNRPLHRAILLRW
						MRSCNLLTCTVLSNVSFSFSELS
	1					YSRNTMCRG
5183	35551	A	5224	3	407	SVGLILPSSLQHHYHHHHHHHH
1						OHHHHHHHHLHORKLAPPLC*
1		1				ADLPTCAPHQGIRPFGGFPQTS
ł		ŀ				GSPGLPVYAEEQGTERLSLQGT
		ļ.				GCGCQAGLLCWGPPVASTSVG
						FSLESSVSPEQVPLSPGPAGTDA
5184	35552	Α	5225	1	1287	
5185	35553	Α	5226	3	1315	STMALLHSGRVLPGIAAAFHPG
1		ŀ				LAAAASARASSWWTHVEMGPF
		1				DPILGVTEAFKRDTNSKKMNLG
						VGAYRDDNGKPYVLPSVRKAE
						AQIAAKNLDKEYLPIGGLAEFC
1		1				KASAELALGENSEVLKSGRFVT
1		1				VQTISGTGALRIGASFLQRFFKF
		ı				SRDVFLPKPTWGNHTPIFRDAG
						MQLQGYRYYDPKTCGFDFTGA
						VEDISKIPEQSVLLLHACAHNPT
1		1				GVDPRPEQWKEIATVVKKRNL
1		1				FAFFDMAYQGFASGDGDKDA
		1				WAVRHFIEQGINVCLCQSYAK
		ı				NMGLYGERVGAFTMVCKDAD
1	1	1	1			EAKRVESQLKILIRPMYSNPPLN
1	1	1	1	1		GARIAAAILNTPDLRKQWLQEV
1	1		1			KGMADRI\IGHAGLQLVSNLQG
	1	1	1			REG\STH\NWATHSPTKLGMFC
	1		1			FHRG*KLEQVERLIKEFSIYMTK
5106	25551		6007	67	206	DGRISVAGVTSSNVGYLAHAIH
5186	35554 35555	B	5227 5228	1485	386 1883	
5188	35556	В	5229	117	641	
5189	35557	c	5230	1	552	
5190	35558	В	5231	250	378	
E 170	1-2220	12	- 50 .	1=: 1	1	

SEO ID	SEO ID NO-	Met	SEO ID NO:	Nucleatide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5191	35559	A	5232	3	1117	TPDPGQGCSEGGIVHETRPSPQF
19191	33339	A	3232	3	11117	LCQGSCAVGCSPLGLLR*RMM
		1			1	ALGKIPPGHRGPAFLPAVESAH
		1				VVPGLPGLTRETLPAPLGPHRP
	Ì				1	
	į.					QPPQGPLSTAPPAPLVSPLGPHV PGLPGPPPGCPSPLPLRPCPPPS
						WLRPHRPVOPWWGT*GSGWRF
	1			ł		RCRPGAAGRNPGLPRACCRGL
						CRGPH*RPGGPRPGHSGPRTSS
		1				WGRTMGNRPRPSASAG**PRHR
1						R*TSAERPGSPPQQSASRTGGRS
					Ì	PLSHPGSWWGVMGPPGLWAG
					Į.	APSMWG*GPGSRVAGGSGRRP
		1				TSPRPPHYPPHPPGTWPSGAOS
						GRR*QAQTPGAATEG*GGWGL
	1					PPKPWCPQDQFLGVQDWVLPP
		1				NGARVGGTWAWKRESVLVPG
5192	35560	c	5233	229	522	NGARVOGT WAWKRESVL VFO
5192	35561	Ā	5234	1	972	MTAEYYKLKQVVTPIAAAVPD
3193	33301	ΙΛ.	3234	l'	972	VVSLLEQINISLCTWYAVIDLG
1	1	1				NACFYIPVHKAHQKQFAISRHG
	1					OOYTFTVLLO/RRDLDLFSLPO
		1				DITLIVHYVDGIMLIGSSEOEVA
	1	1				STLDLLVRHLHARGWEINLTKI
		1				QGLATSVKFLGVQWYGACRDI
		ı				PSKVKDKLLHLAPPTTKKEAOH
		ı				LAASFEWGPEOKGLOOVOVAV
					l	QAALPLGLYDPADPMVLEVSV
					1	ADRDAVWSLWQAPIGESQWRP
1						LGFONKALPSADNYSPFEROLL
1						ACYWALVETEATPVITORAHE
			ŀ			OSGHGGRDGGYAWAQOHGLP
						LNKADLAVATAKCPISQQQRPI
5194	35562	A	5235	3	246	Si an as Si a a a a a a a a a a a a a a a a a a
5195	35563	A	5236	3	841	
5196	35564	A	5237	1	746	RDLDLFSLPQDITL\VHYVDGIM
1						LIGSSEQEVASTLDLLVRHLHA
						RGWEINLTKIQGLATSVKFLGV
	1					OWYGACRDIPSKVKDKLLHLA
						PPTTKKEAQHLAASFEWGPEQ
						KGLOOVOVAVOAALPLGLYDP
	}			1	1	ADPMVLEVSVADRDAVWSLW
	1	1		1		QAPIGESQWRPLGFQNKALPSA
	1	1		I		DNYSPFERQLLACYWALVETE
			l	1		ATPVITQRAHEQSGHGGRDGG
	İ					YAWAQQHGLPLNKADLAVAT
			Ì	1	I	AKCPISQQQRPILSS
5197	35565	A	5238	i	483	
5198	35566	À	5239	i	1908	
5199	35567	В	5240	i	2718	
	1	17	<u> </u>			L

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide detetion, \=possible nucleotide insertion)
5200	35568	A	5241	522	693	LDFFLVFLQQFLPRPSSSEI*MLP GFPAAAYGPVAAAAVAAARGS GRKVYGTGDSQA
5201	35569	А	5242		225	MGRNQSRKAENSKHESTYSPP KDHSSQAMEQSWTENGFEKL GFRRKEALYYLDLTASCQSQEL FQKWVSLCCPD*S*TYSPPKDH SSSQAMEQSWTENGFEKLGFR RKEALYYLDLTASCQSQELFQK WVSLCCPD
5202	35570	A	5243		1129	PWISAPVPVDVEGAMDSVTV LSFGGLMLYFCAGWPPARRWC FPESISCGSMERDQWWGLQVA KRAGLAGGQSGRTVLRERVRIE LASTHIALAARISDWRCCRNGR YPARGPAALQNFQRYTGIQHV HRIGMAERMWCDNRERHTVS SGGGNRLPNFGPPDRSCDNLKTC HTSHGSVMAETAVINHKKRN SPRIVQSNDLTEAAYSLSROQK RMLYLFVDQIRKSDGTLQEHD GICEIHVAKYAEIFGLTSAEASK DIRQALKSFAGEVVFYRPEED AGDEKGYESPFWFIKRAHSPSR GLYSVHINPYLIPFFIGLQNRFT QFRLSETKEITDPYAMRLYKSL CQYRAFVNGGGEEKARGKPIL CRYGVGM

SEO ID	ISEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5203	35571	A	5244	1	1753	MVDSLIARVGVMARGNAITLP
						VCGRDVKFTLEVLRGDSVEKTS
		l				RVWSGNERDQELLTEDALDDLI
						PSFLLTGQQTPAFGRRVSGVIEI
						ADGSRRRKAAALTESDYRVLV
		l				GELHDEQMAALYRLGNDYRPT
					ŀ	SAYERGQRYASRLQNEFAGNIS
	1					ALADAENISHLHIHAEDTFLPFY
		l				LGKKDDVTYAIKPTCWPGLDII
				ŀ		PSCLALHGIEIELMGKFDEGKLP
						TDPHLMLGLAIETVAHDYDVIV
	1					IDSAPNLGIGTINVVCAADVLIV
					ŀ	PTPAELFDYTSALQFFDMLRDL
						LKNVDIKGFEPDVRILLTKYSNS
		1				NGSQSPWMEEQIRDAWGSMVL
	1				ľ	KNVVRETDEVGKAVINHKKGK
		l			1	NSPRMVQSNDLTKAAYSLSRD
	1	1			ŀ	QKRMLYLFVDQIRKSDGTLQE
		l				HDGICEIHVAKYAEIFGLTSAEA
		l				SKDIRQALKSLAGKEVVFYRPE
						EDAGDEKGYESFPWFIKQSEE/P
		İ				QSGNFYTDTLGMAEFRRGGLR
						ATAGPRLSRTRDCQGTEKVHG
						KTVFDKTVP/WVPKRLKSPSCK
			}	1		NRWP*KMQKLSVCTASSPGQQ
					l	LSTVRVTQREICFPVVRREVLLL
	l					IGTLTQTRKGQISVRA
5204	35572	Α	5245	337	1977	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5205	35573	A	5246	145	1929	VSGVIEIADGSRRRKAAALTES
						DYRVLVGELDDEOMAALSRLG
				İ		NDYRPTSAYERGORYASRLON
				l		EFAGNISALADAECDNLKTCHT
				İ		SHGSVMAETAVINHKKRKNSP
		l				RIVQSNDLTEAAYSLSRDQKRM
						LYLFVDQIRKSDGTLQEHDGIC
						EIHVAKYAEIFGLTSAEASKDIR
				l		QALKSFAGKEVVFYRPEEDAG
						DEKGYESFPWFIK/RPSRGLYSV
						HINPYLIPFFIG\LQNRFTQFRLS
ĺ		ŀ				ETKEITNPYAMRLYESLCQYRK
İ		l				PDGSGIVSLKIDWHERYQLPQS
				ĺ		YQRMPDFRRRFLQGFCRFRNH
		l				HQTGFSPAGANQRGPLAATLSG
1		l				PGGEGQSAVARLTGEKKNHPG
		1				AQYANRLSPRVGRFINAAGTTG
		1				FPTWKAGSERNAINDDVTYAIK
1	1					PŤCWPGLDIIPSCLALHRIETEL
		l				MGKFDEGKLPTDPHLMLRLAIE
	•	l				TVAHDYDVIVIDSAPNLGIGTIN
						VVCAADVLIVPTPAELFDYTSA
1						LQFFDMLRDLLKNVDLKGNSN
						GSQSPWMEEQIRDAWGSMVLK
1						NVVRETDEVGKGQIRMRTVFE
						QAIDQRSSTGAWRNALSIWEPE
						CNEISIGVSLDQDGGSNSVLRK
5206	35574	Α	5247	1	1383	
5207	35575	Α	5248	1	1731	
5208	35576	В	5249	1	1290	
5209	35577	В	5250	1	3345	
5210	35578	Α	5251	1	1959	
5211	35579	Α	5252	3	2356	
5212	35580	В	5253	334	1710	

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SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5213	35581	A	5254	1	1302	MKLMETLNQCINAGHEMTKAI AIAQPNDDSFEARKITRRWRIG EAADL VGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPV WYSKSDTLKINGVEDHKTIED GDGKTYQNVQQFIDEGNYTSG DNHTLRDPHYVEDKGHKYLVF EANTGTENGYGGESLFNKAY YGGGTNFFRKESQKLQGSAKK RVAKFLITSNTCDNLKTCHTSH GSVMAETAVINHKKRNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQFHDGICEH VAKYAKFLGTSAASSLGFHDGICH VAKYAEIFGTSAEASSLGFHDGICH LKSFAGKEVVFYRPEREDAGDE
5014	25500		5255		1460	KGYESFPWFIKRAHSPSRRLYS VHINPYLIPLLYRVPNRVTQFRL SETK/EITHPYAMPLYESLCQYS
5214	35582	В	5255 5256	1	1452 1323	
5215 5216	35583 35584	A	5257	1	1557	
5216	35585	A	5258	1	2259	
5217	35586	A	5259	1	2418	
5219	35587	A	5260		1218	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARLTRRWRIG EAADLVGYSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPYI GVAAHKERNQNISRYISNRLAR RECHDSPEEGTGNTRSVERLOR ELPSRGLTESQEHLLDTRKOFW FEDFKDGLGPILKCDNLKTCHT SHGSVMAETAVISLRSDQKRM LYLFVDQIRKSDGTLQEHDGIC EHVAKYAEIFGLTSAEASKDIR QALKSFAGKEVVFYRFEEDAG DEKGYESFPWEIKRAHSPSRGL SYSHINPYLIPPFIGLQNRFTOFR LSETKEITNPYAMRLYESLSAS NYQRMPDERRRFLQVVCVMEIN KQTSMLESUF
5220	35588	Α	5261	1	2028	
5221	35589	В	5262	I	1653	
5222	35590	A	5263	1	1446	
5223	35591	Α	5264	1	1788	
5224	35592	Α	5265	22	1893	

SEQ ID	SEQ tD NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
5225	35593	A	5266	1	2144	MEKKITGYTTVDISQWHRKEHE
						EAFQSVAQCTYNQTVQLDITAF
		1				LKTVKKNKHKFYPAFIHILARL
						MNAHPEFRMAMKDGFIENMFF
				l		VSANPWVSFTSFDLNVANMDN
						FFAPVFTMGKYYTQGDKVLMP
	ŀ				i	LAIQFFDMLRDLLKNVDLKGFE
		ŀ	1			PDVRILLTKYSNSNGSQSPWME
						EQIRDAWGSMVLKNVVRETDE
				Ì		VGKDTGVRSKISGVIKMPMGV
						AVVNCCTYGSDYRVWLASWM
						MSQWLHYPEWYRKENKHKFY
		1			1	PAFIHILARLMNAHPEFRMAMK
	1					DGELVIWDSVHPCYTVFHEQTE
		ļ		1	1	TFSSLWSEYHDDFRQFLHIYSQ
		1				DVACYGENLAYFPKGFIENMFF
		1				VSANPWVSFTSFDLNVANMDN
	İ	1			Į.	FFAPVFTMGKYYTQGDKVLMP
			ĺ			LAIQFFDMLRDLLKNVDLKGFE
		1		i		PDVRILLTKYSNSNGSQSPWME
				ŀ		EQIRDAWGSMVLKNVVRETDE
	1			l		VGKGQIRMGTELEFFRLSETKE
		1		ŀ		TNPYAMRLYESLCQYRKPDGS
						GIVSLKIDWIIERYQLPQSYQRM
				į .		PDFRRRFLQCDNLKTCHTSHGS
		1		l .		VMAETAVINHMKRKNSPRIVQ
		ı				SNDLTEAAYSLSRDQKRMLYL
		1				FVDQIRKSDGTLQEHDGICEIHV
		1			į.	AKYAEIFGLTSAEASMDIQHAL
		1				KSFSGKEVVFYRPEEDAGDEK/
		1		İ		GYESFPWFIKRAHSPSRGLYSV
		1				HINPYLIPFFIGLQNRFTQFLLSE
5226	35594	A	5267	1	1167	MNMNIKKIVKQATVLTFTTALL
						AGGATQAFAKENNQKAYKETY
		1				GVSHITRHDMLQIPKQQQNEKY
						QVPQFDQSTIKNIESAKGLDVW
		l				DSWPLQNADGTVAEYNGYNV
						VFALAGSPEDADDTSIYMFYQK
						CDNLKTCHTSHGSVMAETAVI
						NHKKRKNSPRIVQSNDLTEAAY
				İ		SLSRDQKRMLYLFVDQIRKSDG
						TLOEHDGICEIHVAKYAEIFGLT
						SAEASKDIROALKSFAGKEVVF
						YRPEEDAGDEKGYESFPWFIKR
		1				AHSPSRGFYSVHINPYLIPFFIGL
					1	ONRFTOFRLSETKEITNPYAMR
					l	LYESLCOYRK\PDGSGIVSLK/ID
				1	1	WIIKRSQLPQSAFYQPFMGLRR
		1		1	1	ESFYFRWERRTLGPLKSFSVKR
				1	1	GTEAGKFRLAALLVRL
5227	35595	A	5268	1	1395	
	1.000	1::-	1			L

SEQ ID			SEQ ID NO:			Amino aeid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequenee		
5228	35596	ĪΑ	5269	li .	1375	MNMNIKKIVKOATVLTFTTALI
				1		AGGATOAFAKENNOKAYKETY
		1				GVSHITRHDMLQIPKQQQNEKY
		1	l			OVPOFDOSTIKNIESAKGLDVW
,			l			DSWPLONADGTVAEYNGYHV
		1				VFALAGSPKDADDTSIYMFYO
		1		1		KIRRKNGPVSATFTSDGKIRLFY
		1				TDYSGKHYGKOSLTTAOCDNL
		1	l			KTCHTSHGSVMAETAVINHKK
		1	1			RKNSPRIVOSNDLTEAAYSLSR
						DOKRMLYLFVDOIRKSDGTLO
			İ			EHDGICEIHVAKYAEIFGLTSAE
		1				ASKDIROALKSFAGKEVVFYRP
l						EEDAGDEKGYESFPWFIKRAHS
						PSRGLYSVHINPYLIPFFIGLQNR
		1				FTQFRLSETKEITNPYAMRLYES
		1	ŀ			LCQYRKPDGSGIVSL/KIDW/IIE/
						RYQLPKVPSPEARKITRRWRI\V
l		1	1			KQRI*LGFLLRLSEMPRKQGDY
		ŀ				RTRIWKFEDGLSNVLVIQLNKLI
5220	25505	_	5250	,	1660	ICVMCLVRDCDVLKTYFHR
5229	35597 35598	B	5270	1458	1668 2675	CDAN AMERICAN A CONTRACTOR
5230	33398	A	132/1	1438	2073	CDNLKTCHTSHGSVMAETAVI
1		1	ŀ			NHKKRKNSPRIVQSNDLTEAAY
1					l	SLSRDQKRMLYLFVDQIRKSDG
1					l	TLQEHDGICEIHVAKYAEIFGLT
İ		1				SAEASKDIRQALKSFAGKEVVF
		1				YRPEEDAGDEKGYESFPWFIKR
1		1				AHSPSRGLYSVHINPYLIPFFIGL
		1				QNRFTQFRLSETKEITNPYAM/R
		1				IPLH*LFR*TLRQTKPDNSAGKC
1		1				VKI**HTQNQRSGRSQNDF*RR
5231	35599	В	5272	1	1317	GI
5232	35600	A	5273	I	987	
5233	35601	A	5274	li .	571	
5234	35602	A	5275	1	4161	
5235	35603	A	5276	1	1228	
5236	35604	A	5277	387	3466	
5237	35605	A	5278	1	6721	
5238	35606	A	5279	1	1651	
5238	35607	A	5280	5082	5879	
5240	35608	A	5281	1	231	NHLAVRRLTELSGGQRQRAFL
240	22000	[^	201	l.		AMVLAONTPVVLLDEPTTYLDI
1		1	1			NHOVDLMRLMGELRTOGKTV
1		1	1			VD*VRDLNQVSRYC
5241	35609	A	5282	1	303	CLRILCPYPYIPLTEKTLA*PAL
3241	33009	^	3202	l'	303	YTLELTADMAETCKOFLPEFSL
		1	l			
1		1	1			TFSFQRGWEKETEYAEVLERNF ERDROLTYTAHGPHKADLRIOE
		1				
			l	1	1	SGVPYNEILVTL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
1				sequence		·
5242	35610	A	5283	1	273	TNSSVGPGDRLL*QTAAPHRGK
						LKVFFGACAGVGKTWAMLAE
						AQRLRAQGLDIVVGVVETHGR
		1				KDTAAMLEGLAVLPLKRQAYR
		1				GRHISEF
5243	35611	A	5284	66	1200	HILPAGHPTLRHSLFPHQQGRSS
			ľ			VQSALGAASGNGLKLVGRFEW
			i		1	GPSRRARSGYPDATGYDQ\PKPI
					i	SAAVKEFFGSSQLSQFMDQNNP
						LSEITHKRRISALGPGGLTRERA
						GFEVRDVHPTHYGRVCPIETPE
1			1			GPNIGLINSLSVYAQTNEYGFLE
			i			TPYRKVTDGVVTDEIHYLSAIE
				1		EGNYVIAQANSNLDEEGHFVE
1					1	DLVTCRSKGESSLFSRDQVDY
						MDVSTQQVVSVGASLIPFLEHD
		1				DANRALMGANMQRQAVPTLR
		ı				ADKPLVGTGMERAVAVDSGVS
	1	i			i	GGVVQYVDASRIGIKVTKTRCI
		1				RVKQVSTSTTLPLFLMESNPLF
	1					WMAVLVSAGILGOWPIGRLAD
1		1				KFGRLLVLRVQVFVVILGSIAM
5244	35612	В	5285	1	862	
5245	35613	A	5286	1	579	DPRD*RLKVAK*MVTLFGPOFV
						RELOGRGFDIFLDLKFHDIPNTA
						AHAVAAAADLGVWMVNVHAS
					l	GGARMMTAAREALVPFRPDAP
		1				LLIAVPV*RSIKASDLVDLGMTL
1		1				SPADYAERLAALTOKCGLDGV
						VCSAQEAVRFKQVFGQEFKLV
						TPGIRPOGSEAGDORRIMTPEQ
		1				ALSAGVEYMENGRPGTOSVK
5246	35614	A	5287	484	978	GIVRIPHRLADIKCWRAVLYNY
		ı		1		THYSYQANLCCANLE*ADLSGS
į.						VLDCANLQGVKMLCSNAEGAS
l		1		1		LKLCNFEDPSGLKANLEGANLK
l .		1				GVDMEGSOMTGINLRVATLKN
l		1				AKLKNCNLRGATLAGTDLENC
l		1				DLSGCDLQEANLRGSNVKGAIF
		1				EEMLTPLHMSQSVR
5247	35615	A	5288	3	504	YRLSOSSSKSLVSRSWLNMRFIS
	1	Γ`	1		[	SVMFMEPTSSSENRFTSPSCSE
1		1			I	MSSSEATLRSFFLGTTSPCRSM
		1				VGLQLVKSSQSSSVSSFSSHVRL
1		1				SQSSSKSKVSRLAGT*EGSEKRS
1		1			1	FREEKVPCLRLGLPESTLYAHC
					1	SV*SRTHVFSGTSHHSSKVAVG
ŀ		1			1	MSIVQMRKL
	1					MISTA ÓMICKE

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5248	35616	A	5289	2	442	HVIWHMPRKTSKCRQLLCSGA SRNADTAARQSTCSSHRPPGKIE SLGPRRVPGCSSVPSSRGEQSTG SPAAPRCGDVTHTEASQEEQP* LRGTHGPASTPEQGTAKAKVR DRRAVVHPGKTGIPSAAG*KGR
5249	35617	A	5290	151	1185	GRPGEPPGAAVQVE  YVDQYTHIESPLPSVSYSFAFG SLISAVDPVATIAIFBALHVEED TEKGHVRLTPASPSTFFFFFSTE EKYAPGSCCRKAAVL*LLHISH QLSLDSPSLTVVIYVLKHIDLRK PSCRHGEIFVODHTAULSVLFS PSLGIMAILFSGIVMSHYTPREA SPYSCCLFTVSSHTVCCHPGLRG AIPYALSLHLDLEPMEKRQLIGT TTIVVLFTILLLGGSTMPLIRLM GLPGGAPRWCQLVAVGPPIP AQGNTVESEHLSELTEEEYEAH YURRQDQLSLFN*N*SCLWPSPC LPPPPTPTHEKHPVASPPFHGPA PDALTAWLCLSTQDLHHGRIQ MKTLT
5250	35618	A	5291	5	198	VCGRQQSLEAGL*GAATPFAVF PRPWSAVRVKEYGYTRLHILN GTHIHIQQVSDDQAFAQCHPP
5251	35619	A	5292	137	308	HLERTGPNLPPGARLATRPTTR LPAASPRGRDT\PLPIPISFYSETE AKGEAPYIEPE
5252	35620	A	5293	612	1078	RPPEKKERGRVRGRRGGGK RRRRKRKKRKGSKGREDAAAA AAAAQSPRTRAPAPD*ERRPQP APSARAPPRPLLPAPRRSRPAQV PPDSASPWAAAAGLALPPPQCP GGGARPLRLLPQPPAPGGTAR WEPRRPRPAAAPGLLQSPGPLP RQS
5253	35621	A	5294	515	817	LALPHLPSNLLLKGWLKLKA*S RPSRTPSFG*LSQWKHALKRLK PVITCLLQHGFLKPINSPYNSLIL PVLKPDKPYKLVQDLRLINQIV LPIHPMVSQA
5254	35622	A	5295	1	951	
5255	35623	A	5296	1	1077	
5256	35624	В	5297	87	1423	
5257	35625	A	5298	29	234	
5258	35626	В	5299	77	327	
5259	35627	В	5300	I	235	
5260	35628	Α	5301	2	2144	
5261	35629	Α	5302	1	855	
5262	35630	Α	5303	845	1057	

SEQ ID NO:	of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
				sequence		
5263	35631	A	5304	1	933	
5264	35632	Α	5305	1	954	
5265	35633	Α	5306	1	1603	MEAEKFHQMPSVSRRTRKASG
					ŀ	VIQSKSENLRTRGANSHALKRL
						KPVITRLLQHGLLKPINSPYNSP.
						LPVLKPDKPYKRFLAFYGWSPR
						SLIVDSCSKLEQHSTLSRVILVIY
						KGFCRFRNHHQTGFSPAGANQ
1					ľ	RGPLAATLSGPGGEGQSAVACL
l					ľ	TGEKKNHPGAQYANRLSPRVG
i					Ì	RFINAAGTTGFPTGKRAVSATQ
1					1	LMDFADFGTTITQDFRLLGQTS
1					1	VDRLLQLSQGQAVKGNQLLPV
1		l				SLVKRKTTLAPNTQTASPRALA
						DSLMQLARQVSRLESGQSSQLS
						SLRLTLPDRLRSPLDHHGRRAS
			i			GNSHSGSPKPPSCLPLISPHLNP
l						QVWDISTPSLATDHMPITIPLKS
1				1		N/TLTPLNLKCQYPIPQHALKRL
1						KPVITRVLQHGVLKPTNSPYNS
l						PILPVLKPDKPYKLVQDLRLINH
1						IVLLPIHPMVPNPYTLLSSIPPSTI
1		ĺ				HYSVLDLKHAFFTIPFHPSSQPL
1		l				LAFTW\TDPDIHQAQQIT\WAVL
ĺ						P\QRFPRTGPHYFNQAQISSSSV
5266	35634	В	5307	1	874	TYLGIILIKTYVLSLPIVSD
5267	35635	A	5308	144	539	
5268	35636	A	5309	1165	1639	PHPAVASRRGRAGPGGLSAPER
3208	33030	^	3309	1163	1039	TPSSELSPLSKGDLRKTHRTFSP
ĺ						O*GDLRKTHRTFSTR*GDLRKT
ĺ						HRTFCTR*GDLRKTHRTFSTR*
ĺ		l				GDLRKTHRTFSTR*GDLRKTHR
ĺ						TFSTR*GDLRKTHRTFSTR*GDL
ĺ			ĺ			RKTHRTFCTR*GDLQKTHRTFS
ĺ						TR*GDLRKTHRTFSTR*GDLRK
ĺ						THRTFSTR*GDLRKTHRTFCTR*
ĺ						GDLRKTHRTFSTR*GDLRKTHR
ĺ		l				TFCTR*GDLRKTHRNFSTR*GD
ĺ						LRKTHRTFSTR*GDLRKTHRTF
ĺ						CTR*GDLQKTHRTFSTR
5269	35637	A	5310	235	453	SHWPWLCSSTSCSSORSIVSSG
1		ľ				MARGPFLRKRDLLFPPPPPGSH
ĺ		ĺ		1		GLELLEIIFHQGISQVHHLLHLQ
ĺ			l	1		VWL*NLNVPDSSLPAENEATGP
ĺ				1		GFVPPPLAPVRGPLFPV\D\ARGP
ĺ			l		1	FLRKRDLLFPPPPPG\AM\FGASR
(	1	ı	J	ı	ı	
ļ	i .		1	l		DYFPPGDFPGPPPAPFASMAFL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5270	35638	A	5311	2	2333	TGRGYCGDHESSFGAMEEPGA TTORYLGLLEELREVVAALPE GMRPDSNLYGFPWELVICAAV OGFFAALFFLWRSFRSVRSRLY VGREKKLALMLSGLIEEKSKLI EKFSLVOKEYEGYEVESSLKDA SFEKEATEAOSLEATCEKLNRS SFELEBELICLEKELKEEKSKHS EQDELMADISKRIQSLEDESKSL KSQVAEAKMTEQIFGMNFERL KIAIKDALNENSQLQESGKYOL QEAEVWKEQVSELNKOKVTFE DSKYHAEQVLNOKESHIKTLTE RLLMKDWAAMLGEDITDDD NLELEMNSESENGAYLDNPPK GALKKLIHAAKLMASLKTLEGE RNQYIQLSEVDKTKEELTFHIK NLQTQASLQSENTHFENENQ KLQQKLKVMTELYGENSKLTLTEE RNQYIQLSEVDKTKEELTFHIK NLQTQASLQSENTHFENENQ KLQQKLKVMTELYGENSKLL HRKLTVEENVRLEKEEKLSKV DKISHATCHENTSCHESTERTHENENGERICHTURENSCHESTERTHENENGERICHTURENSCHESTERTHENENGERICHTURENSCHESTERTHENENGERICHTURENSCHESTERTHENENGERICHTURENGERICHTURENGERICHTURENGERICHTURENGERSCHLTDPHRAPS DTOSLSPPWDODRRMMFPPPG QSYPDSALPPQRODRFCSNSGR MPSEMESSRNDTKDDLGNLDW SSSPPAKKRATOPGVPPDLA SNSSPPAKKRATOPGVPPDLA
						PVRGPLFPVDARGPFLRRGPPFP

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence	İ	u9/340,217	sequence	or peptide sequence	deretion, i-possion nacicolide insertion)
5271	35639	Α	5312	141	2788	GLRVPLSPSSPRSRLRSGPLRLF
						GADSGSGPKAVCSPPFIVAPTG
						RGYCGDHESSFGAMEEPGATP
						QPYLGLLLEELRRVVAALPEG
	ł			l		MRPDSNLYGFPWELVICAAVV
	ı					GFFAVLFFLWRSFRSVRSRLYV
	1					GREKKLALMLSGLIEEKSKLLE
	į	1				KFSLVQKEYEGYEVESSLKDA:
	1					FEKEATEAQSLEATCEKLNRSN
			İ			SELEDEILCLEKELKEEKSKHSI
						ODELMADISKRIOSLEDESKSL
						KSOVAEAKMTFOIFPMNEERLI
	1					IAIKDALNENSOLOESOKOLLO
	1	1				EAEVWKEQVSELNKQKVTFEI
		ļ				SKVHAEQVLNDKESHIKTLTER
						LLKMKDWAAMLGEDITDDDN
	1		l			LELEMNSESENGAYLDNPPKG
	1	1		l		ALKKLIHAAKLNASLKTLEGE
		1				NOIYIOLSEVDKTKEELTEHIKI
						LQTEQASLQSENTHFENENQK
						QOKLKVMTELYQENEMKLHR
				l		KLTVEENYRLEKEEKLSKVDE
	1	1				ISHATEELETYRKRAKDLEEEL
	1	1				ERTIHSYQGQIISHEKKAHDNW
	1			l		LAARNAERNLNDLRKENAHNI
					1	OKLTETELKFELLEKDPYALDV
					1	PNTAFGREHSPYGPSPLGWPSS
		1				ETRAFLSPPTLLEGPLTLSPLLP
					l	GGGGRGSRGPGNPLDHQITNEI
						GESSCDRLTDPHRALSDTGFLS
1	i i					PPWDODRRMMFPPPGOSYPDS
l						ALPPORODRECSNSGRLSGPAE
		<u> </u>				, ,
5272	35640	A	5313	217	447	FQRMSGL*GYSPPLGGQPAL*E
l						CQGAADSAGG\RGLDSERSLGF
						\PAASGPNTALGWQAQPWS*Q
		_				AGPELPRAEFLQA
5273	35641	Α	5314	3	287	TLRNRHRELRTCLSGPGLGLPT
		1		1		QVSVVAGGCCVCPSSSQSPVPF
						PPALSAAPWHSHRAGCPPSGGI
ł						*PQRPLILWNQPLSNTLLEKEL/
						PPPAH
5274	35642	Α	5315	3	468	ALARSPAG*PQSPDGDLCFRHR
	1	1		1		KGERRPAAPAGQCPAGRQRHV
		1		1		PAAGRDGKPGRAPGADR*AGP
				1		LHLYHLPAPCGGGTPGDSNPRI
		1		1		APAQRSE*CTPPPPQ*RNNRKPS
		1		1		TRAGLLLPS*HVQLSGGLTLCP
				1		GDRVS*WPQGVLAAPGPGPCT
		1				HL
5275	35643	В	5316	64	288	
	1200.0	L~		1		

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5276	35644	Α	5317	73	265	NGRTSRCFSPGKH*EYCSGTFH
		ŀ				PLQVVGKIYSNLDKIL*ASRAR
5277	25515		5318	125	461	WGLCSRKPGYWSCTQPPTSS
5278	35645	A	5319	298	593	LGVEVEPVTGGDAVIGASHDAF
32/8	35646	I <sup>A</sup>	3319	298	393	LQVNIESIVPEHSTRCKLLGKFI
	1	ŀ				RIWIKYFRHLVHGGGSAPVSLV
	1	l		l		
	İ					TGPVHGDSLLGPVAPEPPRVVE
	1					PARQVRAHAVVVAGPLRRGRG
	i					LGRHRLRARSG*GMPQSVRGA
1		l				CGAQGHGPAGEDQRLLPRERG
		l				PAGQVQQPGVVPGLQDPEGCL
		1				RVQDQ*PGLREQSPHRARDA*S
						ILSKFE*IFPTTCSGWNVPEQYS
						QCLPGEKHRDWPR*LHHLL*PA
	}	l				QLPPPVTTSTGHPSAIEGLETPL
						RSPLTPGPPGKSIIPHHPQSPDCD
		_				GTDCAAFPENIIRLRSRKICKRG
5279	35647	Α	5320	1124	1835	HSLHFPKFPSFLFLTLITLGLLM
						AVPPGLITTHQQRQAML*YKPL
						ARLLEPLISFPSWKSILKEITSQC
		l				SICYSTTPQRLFRPPPFPTHQTR
		1				GFAPPR/HWQIDITHMPQVRKL
		1				KYLLVLVDTGSKKATVVISSLL
						SDIIPRFGLPTSIQSDNGPAFISQI
		1	į			TQAISLALGIQRTHGLLKTHLT
1	1					NLSHQLKKDWTILLPLSLLRIQ
	1					ACPRNATGLHSDG/VGPKLLPG
	1					SPFQLHHTWDSP
5280	35648	Α	5321	1	1758	
5281	35649	Α	5322	1	1967	
5282	35650	Α	5323	76	1908	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5283	35651	Ā	5324	524	2144	QSDLSASQHGLFPLATEVRSSG
3283	33631	^	3324	324	2144	AASCPDSDSICPAPTIAPGRATP
	İ					PQANCWASEGTLRYQALPGNR
						APVSQVSQAGGANLCVQQPKK
	1					HLTNFKSGKRPLFTLFSNLQGP
					l	RSRPVAFLSKQLDLTVLGWPSC
						LRAAAAAALIVLEALKITNYAQ
		1				LTLYSSHNFQNLFSSSHLTHILF
	ļ.					CSPGSFSCTHSLLSLPQLPIVPGP
	Į.					DFSPASHIILDTTPDPHDCISLIH
	i				l	LTFTPFPHISFFPAPHPDHA*FIN
						GSSTRPNRHTPAKAGYAIVQVT
	1					SPPLKTSHFLSIVEIYPOGNNFS
1						VFHLLFYYSSGIIQAPLLSLHIKL
İ	ŀ	1				RDLPPPRTGKSALLNMPRVRKL
		1				KYLLVLVDTGSKKATVVISSLL
		1				SDIIPREGLPTSIQSDNGPAFISQI
	1				į .	TOAISLALGIORTHGLLKTHLT
	1					NLSHOLKKDWTILLPLSLLRIQ
1	1	1				
1	1	1				ACPRNATGLHSDGEARSSFQAH
ł		1				HFNFITHGTVPDVFVPILQLLNE
	1	1			l .	DFEDPCLGYLPSPEISICLEPTSW
						SKDRSCSSGEEGSAGQTVTGDL
		_				HKAQTPELDQPASLNCPDL
5284	35652	A	5325	1	420	RTRGGEKE*EEKQRSRR*RIK*E
	1	1				EEEK*RRSRGAGDKG*NERRRR
						NRGEPVEKEEDDRRRKRQWRR
	1	1			i	GEEEKRRRGRNCGGGGGEEKE
		1				DGRRRRLPCFLLLPSLLVSLLW
					i	LVSFLPCVFGFFGAPAVVFARF
						RGLRAFCRF
5285	35653	A	5326	2	467	
5286	35654	A	5327	269	777	
5287	35655	A	5328	2443	2627	VGFFFFFWWGERGTGSYSVTQ
						ARVQ*YDLGSLQLLPPSFKGFS
		_				CLSLPGSWYYRHGPPRLG
5288	35656	A	5329	57	394	
5289	35657	Α	5330	33	311	HNTLPKTKPWFQEPGDEEPQQE
1		1			I	EPPTESRDPAPRLPRSP*SADPP
1	1	1			1	WRSQRPQGLTRPPPEPLRPHGS
1		1				PPAHLSLFCQRSCPGPQERPHPS
	1					тм
5290	35658	Α	5331	226	406	
5291	35659	В	5332	51	90	
5292	35660	Α	5333	I	348	PPSQRV*GWHEMRQGGRQHAQ
	1	1	1	1	1	PVLSQQGLTAGHCHHQHCRRP
	1	1		1		LACDVRPVVYEKVSRDHGLVS
1	1	1		1	I	GQHN/PAPESQGQSTSPPRHTGR
1	1	1	1	1	1	KQARAGGEKKVTSDPANTAQH
		1			1	NPNTGSRGRP
5293	35661	A	5334	109	380	
	1	11.7			<u> </u>	

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5294	35662	A	5335	448	724	WPSRSALAAGGRTAPTPRSRAG PPAR*RAGRESARGTS*GIRPRS QPARRPCPPAPVGRGLPPGPAR PPPRAAPREPPRCRAAAHTSRP AGS
5295	35663	В	5336	1	1554	
5296	35664	В	5337	99	366	
5297	35665	A	5338	1	714	
5298	35666	С	5339	391	689	
5299	35667	A	5340	2	614	
5300	35668	A	5341	2	461	
5301	35669	В	5342	45	1148	
5302	35670	A	5343	215	849	IKRLPLMKRMWL*LQPESLEIA GILVQ*ME*CPYKGTNSIPVSK PSPIVYOKPNGOWRQVODLRLI SDAVIPLYPAVSNPYTLLSQILE EAEWFTVLDLKDAFFCIPLRSD SOFLLAFEDITDHTSQLTWTTY TQGFMDTPHEGGGLAQDLGH FSSPGTLVLQYVDDLLLAKQQA TLLINFLANGGTKLSKLKAQ LCELLVFSSCARMHS
5303	35671	A	5344	I	1035	MGQWWALVRSTLELFHTDDEE GEGYDEVTEEVTEGVVLPAKA KVAQEEEVHPYPSAPPHYYFEE KEWPDPPDLSFLEGTGREVVAP TYEQHLERLLSVLFRQEFSRLD ERDDAVEQLRGVCIRAWEKITS GEQYPSFSAVKQGPKELYADF IAWNLLRGESLKKVISDSAAQD IVLQLLAFGRVNLDCQAALRPI FTGGSAHLDVIKACDGIGAKQD SERFAFTIPVVNNLQPAKHFHY FTDGSSNGKASYSGSKGQNQQ PIWLSRHLKPYHEPDAKEEIPG GCPRTWLQPCRD*C*GGP*P VTSNTR*T*GPTWGQIKKLSPM VEENLRKAGQLVTMTVVWN
5304	35672	A	5345	1566	1767	KGGWSQRHSQGACYTCRKSGH WAKECPQPGIPPKPRPICVGPH* KSDCSTHLAANPRAPGTLAQGS L
5305	35673	В	5346		3429	
5306	35674	Ā	5347	1	1776	
5307	35675	Ā	5348	i	933	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=1)nknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5308	35676	_	5349	I	1743	I MGKVWAVVRSTLELFHTDDEE
5508	33070	A	3349	1	1743	
	1	ŀ		l		EGEYNEVTEEITEQVYLPAKAK
	1					AVKEREQRGNITATFEPFPFKLI
				I		KEFKQAINQYGPGSHFVMGLL
				I		KNVAVSSQMIPTDWDALTQAC
				l		LTPAQFLQFKTWWAHEASIQA
				l		ACNAQAQPQINITTGQLLGVGG
				i		WAGLDAQVVMQDDAIEQLRG
		l				VCIRAWEKIPLCGEQYASFSAIK
			1			QGPKEPYVDFIAWLQESLKKVI
						ADSAAQDIVLQLSAFDNANPDO
						OAAL*PIRGNAHLVDYIKACDG
		1				IRGNMHKATLLVQAMAGLRVI
	1					KGNPLLPGACFNCGKHGHTKO
						ERRKKSVSQAARWGKRKTADE
						EICPKCKKGKYWANQCHSKFD
	l					KDGTLISGNAMRAEQDCEWFT
						FTIPAVNNLQPAKHFHRFTDVS
					1	SNGKASYSGSKGGQARVQLFE
						NASVRATNSDLPQSSLWCRRKT
						SVSVAVLVSATIPISRVQGPSQV
						LGQGEKQTNQNVVPNPYTLLS
						QIPEEAKWFTALDLKDAFFCIPL
	ļ.					HSDSQFLFAFEDLTDHTSQLTW
						TILPQGFRDSPHLFGQALAQDL
					1	GHFSSPGTLVLQYVDDLLLATS
						SEASCQQATLDFLSFLAN
5309	35677	Α	5350	1	1085	
5310	35678	Α	5351	I	3105	
5311	35679	A	5352	1	5172	
5312	35680	Α	5353	41	324	
5313	35681	Α	5354	18	270	KLSQVCIDLL*IREGERDMYPG
				1		WAKFPSPYSLKGT*PIAQGVLW
				1		SFGDFFYC/IPSTLPTPKSWRLFE
	1		-		i .	SPFPESLTPVSLVWWPC
5314	35682	Α	5355	80	384	SNNRTEGAWGKCQLMSS/PLTE
		1		1	I	PQVTLTIDSQEIDFLLDTGAAFS
	1	1		1	1	VLISCPEQLSSRSVTI*GILGQPV
ŀ					i	TRYFSHLLSCNWETLLFSHAFL
					1	VMPESPTPLLGR
5315	35683	С	5356	99	317	
5316	35684	Α	5357	388	476	KVCPRPCRTSM/LPIRII*KLPQV
1		1		1		CLDLL*HEGEGDMYPG*AKFPS
ı	i	l	1	1	I	PYCLKGT*PGTIAGSWARGVSA
l						

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nuclcotide insertion)
5317	35685	A	5358	254	849	LQPESLEIAGILVQ*MIE*OPKK
3317	33003	,	3330	1	0.5	GTNSIPVSKPSP/GVOKPNGOW
			ŀ			ROVODLRLISDAVIPLYPAVSNP
						YTLLSQILEEAEWFTVLDLKDA
				l		FFCIPLRSDSOFLLAFEDPTDHT
ĺ						SQLTWTVFTQGFMDTPHLFGO
				1		SLAQDLGHFSSPGTLVLQYVDD
						LLLAKQQATLDLLNFLANOGY
			1	1		KLSKLKAQLCELLVFSSCARMH
5318	35686	Α	5359	1	909	
5319	35687	A	5360	153	436	CFCCCVEGNKPRNLORTTKTPR
					1	LSVMSPSSCRGRGIWPNPGTC/R
l				l		PSPSLi*SRSRQTWRITTPCOOG
						NKTGORMNLTN*QEQASEGG*
				1		*OTPLS
5320	35688	A	5361	1	1632	
5321	35689	С	5362	1	675	
5322	35690	Ā	5363	604	1047	SNNRTDNPTSVAYLSKETDVV
				1		AKGWPHCLWVVVAVAILVLEA
						IKIIQGKDFTVWTSHDVNGILG
						AKGNSWLSDKRLLRYQALLLE
			Î	l		GPVLQIHTCVALNPAIFLPEDGE
						PIKHDYQQIVAQTYVT*EDLLE
l				1		VPLANPDLNLYTNGSSFV
5323	35691	Α	5364	749	1002	QLKKGTNSLLVSKPSPVWIPTG
		ĺ	1			TLTQIMGTGVANIC*PVF*KD*G
			1	1		ELGKMNYAMMSTITQGKEENP
				1		AFLKWLWEALRKYTPLSP
5324	35692	В	5365	114	2309	
5325	35693	Α	5366	413	1157	
5326	35694	Α	5367	105	478	YGHCCYDHRICCFFPATEQKVC
						PCAAQG*PL*LRGDDPEMSVYI
						*QLPLYYSSDLLSAANEVQILAF
			l			FQGDVSFFPVATTTDTLSVTFN
			İ			FPFNYQGVNDFDFDFKQFLHSS
				-		FDFCFGRVFSNFE
5327	35695	Α	5368	531	1087	RLQPPGAPVEDITRPVSAKPRD
			1			ADRNSTGCYLV*LQHQRQTES
						GRQLSGL*GPGCNGVH/ASLYR
				İ		TSAMFAERFGSYSRRSTTAGIPS
1	1			Ī		LLRLKSTIRRSDRSRRKAQRKR
l			1			CGQVMPQHRRSIRPLLQPITPSL
		1	1			NRNLHRSPHRSRNRWSRLNRR
						LKHHLRRSQNRSRSWKKKLHR
			L			RVKPMLCNWVR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6220	35696	-	5369	544	1381	VNPALOVLVVAITPPPSLPSPSCI
5328	33696	A	3369	344	1381	RVLTRVSNAIAAKPLCLAVCAV
						VEGGRIRALVAVAAWGAGVTG
						GPAGLIACGPVSPSVIRGQFRHA
			İ			GISFFLYAIGGEMVPAVRRQNH
						TPA*HKRFAKAFQLAHPNAVN
			l			AEHFAGGDRHLFSHLNQGCVV
		_				KHHVRRDITFIGYRFTQFA
5329	35697	Α	5370	81	863	AYGNPVEIAGGARQAGVNFTG
ŀ			l	9.		VFRPRFSRRWRRISGETCKLWW
					!	RRWRSAWASINQTFASWSTLIF
						RAISNPIIRKPDAPGVMACPRKR
			l		1	CCFTIRLIWRGCAVVWKRSR/E
					1	GQLQDIERHKLNAMGAFAEAQ
					i	TCRRLVLLNYF/GRRASGAVRE
1						LRYLPRSAETVRRFNRCSDCPF
ļ						HHWSCESAVWDGLCGGSDSCC
						GVSRARLFASPVNLPITGEIPER
						GFHPFCGRTTENGKNHPRNLFI
						WRSNCSVLPVKVMSLCSSTPCP
5330	35698	В	5371	12	273	
5331	35699	A	5373	145	336	SEEEEEDEEEEEEEEEE
						E*EEGESAIICAKVCISVFPRRK
		l				NELNMAITPNTIPKLNHW
5332	35700	A	5374	294	657	VAPGDRHAFHGGGSGLSPELTL
			l			PQTQCCAQATVQGLEGTRSWS
						QSGTSSLSPWSHTSLACPQKEE
ļ					i	GEEEEEEEEEEEEE
						EEEEEEEEEEEEAKTQ*KSG
						QKI*TDSPQKK
5333	35701	A	5375	2	588	SRPGITGSTISYGDPGHGAGPPG
						ADLGPARSLKPERAAGAQLAA
		l				GEARQSGDPGLPGGPGHSLGTA
					l	PC*VDKGWGHPVSTVHHQRQP
1		l				QPGGLRAPGTALLAGTQPSHPA
						AGPWEPQPQRGVRVLGGRRDS
						*VGGG*GQHNKALWGPR*PHT
						EQKPDRKLSRIPLRAAGGEKRG
ĺ						CGCDRAGCLVLGPPQLPAQGL
5334	35702	Α	5376	1	445	SLSHRAGGGGGVGGGAVCLFS
				l		PPRTKRESAPESPSRVLGHSPVP
			l	l		S*GAPSTRGSVSRILTSGGTHER
1			l			SNGLTCHRNQAGTGPSALRSGR
l			l	l		P*CLSRANPPGSKRSAGPVHEE
			1	l		RT*PCRLSGSAGITQ*DGN*KAG
1	1		l			PRVPEAPERGCATC
L		Ц			_	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
ĺ				sequence	9.7	
5335	35703	ĪA	5377	3	313	QNDEVAFRKLKLIJEDVQGKSY
						LTNFHGMNLTHDKMCSMVKK
ĺ	1	l				WOTVIEAHVDVKTTNGYLLCL
ĺ		l				FCVGFTKKCNNQIWKTSLF*00
ĺ		1				SNMEDFFVLTTGIISHLHEPFLV
ĺ		1			1	VTDYDQ
5336	35704	Λ	5378	45	764	TSFLTTGGKKGS\KKKVVDPFS
		l				KKD/WL*YVKHRAMFNIRNIGK
		1		ŀ	i	DVGSPRTOGTKIAS\DGLKG\RV
1		l		•		FE\VSLADLQNDEVAFRKFKLIT
1		l		1		\EDVQGK\NC\LTNFHGMDLTP*
		1				QKCCSMVKKM/WQTMI*SSPL
ĺ				l		MVKTT\DGLLASVCSCVGFTKK
				i		\RNNQIRKTSYAQHQQVRQIRK
				1		KMMEIMTREVOTNOLKEVVNK
				I		LIPDSIGKDIEKACQSIYPLHDVF
		l		1		VRKVKMLKKPKFELGKLMELH
		l				GEGS
5337	35705	Α	5379	3	501	SSARFVSSSSSGGYGGGYGGVL
ĺ		l				TASDGLLAGNEKLTMQNLNDR
		l	ľ			LASYLDKVRALEAAKILSDMRS
		l	ŀ			QYEVMAEQNRKDAEAWFTSRT
		ļ				EELNREVAGHTEQLQMSRSEV
		1				TDLRRTLQGLEIELQSQLSMKA
		l				ALEDTLAET/EGDVRADSERQN
		ı				QEYQRLMDIKSRLEQE
5338	35706	Α	5380	1	716	AQLKVKFWYWPEAGAGGLRR
		ĺ				FKHY\YTPFKDCRDKILGATIKN
	1	l				SRIVLQIDNAGLAADDFRTKFE
		l				TEQALRMSV*ADITGLRRVLDE
	1	1				LTLARTDLEMQIEGLKEELAYL
		l				KKNHEEEISTLRGQVGGQVSVE
	İ	1				VDSAPGTDLAKILSDMRSQYEV
	1		1		1	MAEQNRKDAEAWFTSRTEELT
1	1				l .	REVAGHTEQLQMSRSEVTDLR
	1					RTLQGLEIELQSQLSRLWGFCC
		1	l			PLEGVFWVEGWEGRDPYPRLF
5339	35707	Α	5381	3	832	
5340	35708	В	5382	141	1067	

SEQ ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
5341	35709	A	5383	13	1316	GVAPSVLRLAMTSYSYROSSAT
2241	33707	ľ^	3363	ľ	1.5.0	SSFGGLGGGSVRFGPGVAFRAP
						SIHGGSGGRGVSVSSARFVSSSS
		ŀ				SGAYGGGYGGVLTASDGLLAG
		ŀ				NEKLTMQNLNDRLASYLDKVR
		1				ALEAANGELEVKIRDWYOKOG
		1				PGPSRDYSHYYTTIQ\ELRDKIL
		1				GATIENSRIVLQIDNARLAADDE
ł		1				RTKFETEQALRMSVEADINGFR
	į	1				RVLE*S*TLAQEPNLEDARIEG
	ļ	ı				LKEE/LAYLKKNHEEEISTLKGP
		1			ŀ	KCEAQV\SVEVD\SA\PGTRSSPK
l l		1				
		1				ILSDMRS\QYEVMAEQ\NRKD\A
		1				EA\WFT\SR\TERIETREVAWPHR SSFOMSOAPRLLDLAAATPOGS
		1				*DLSCQSQLEPLKAALGKTPLA
		1			1	ENRKA\RFGNPQLAPYPQALDS
		1				
		1				AVI*KPQLG/DIVAKLDSSTGRI QEYQ\RL\MDIKFARLEQEIAHP
		1				NRSLA/LEGOEDHYNN\LFASK
5342	35710	A	5384	23	279	GCLRGSLERCGTLCKI\SLHEISG
3342	35/10	A	3384	23	2/9	PESRVO\QPLSSREEEEEEEEE
						EEEEEEEEEEEEEEEEEEKK
						ECSKAQCKHFPLSEVL
5343	35711	A	5385	1	507	MEKNEKEQEEEEKKEKNSKKK
3343	33711	^	3363	['	307	EEEEEEGGGEEEEEGEGGEE
						EEBEEEEEEEEEEEEEEE
	ł					EEE/EEEEEEEEEEEEEEE
						EEEEEEEEEEEEEEKKKKKK
						KKKKKKKKKKKKKKKKK
1						RKKKKKEEEEKVVEEEDEFIWF
	1					LGNSLYFPSFSHFAWSOIPSRED
1		1			ĺ	EGERRLRVNSMIMDFTSNTNH
5344	35712	A	5386	3	259	
5345	35713	Α	5387	53	387	LEEEKEEEKEEEKEEEKE
	İ	1				KE/DEEGEEGEGEGEEGE
		1				EEEEEEEEEEEEEEE
						EEEEEEEEEEEEEEE
	1	1				EEEEEEEEEEEEEEEE
						EEEEEEEEMIVLKIIVAKQLF
5346	35714	В	5388	I	1446	
5347	35715	Α	5389	3	122	
5348	35716	Α	5390	239	432	CLWLFQEEEEEEEEEED*EEE
		1				EEE/EEEEEEEEEEEEEE
	1	1	ĺ			EGEEGEGEGEGEGEKI
			l			FLGHRVGI
5349	35717	В	539I	I	1269	
5350	35718	В	5392	44	244	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5351	35719	ĪA.	5393	1	626	EEGEVEEEGEEEEEEGEGEE
555.	155715	1	3373	l'	020	EEEEGEGEGEGEGEEEEE
	1	1				EEEEEEEEEEEEEEE
	1					EEEEEEEEQEEEEEEEEE
						EE\EEAAAAAAAASRDSHTSLEL
						TYWPPCPALRDTLVSNCSLSSI.
						CTSGDSFHW*ETTIPAMSSCSH
						QHSLHQLGIIPRQILMRMASLM
		1				RRIC\EDHPATAEQ**HV*GPPD
5352	35720	Α	5394	2	506	
5353	35721	Α	5395	1	480	
5354	35722	A	5396	1	492	
5355	35723	Α	5397	1	870	
5356	35724	A	5398	111	407	
5357	35725	Α	5399	1	651	
5358	35726	В	5400	1	2427	
5359	35727	Α	5401	571	966	SPFTNSRLTIFISFSECGQIAEIYI
		1				LSQPFMVRIMATEPPIINLQPGN
	ı	1				FTLDIVSRDHTTAL*PGRQEQNS
	1	1				VSKKKEEEEEEEEEEEEEE
		1				EEEEEEEEEEEEE
		1				EEEEEEEEEEEEEEE
		1				EEEEEEEEEEEEEEKKKK
5360	35728	Α	5402	1	1674	
5361	35729	Α	5403	1	306	
5362	35730	A	5404	2	431	
5363	35731	Α	5405	1	585	
5364	35732	Α	5406	1	708	
5365	35733	A	5407	3	595	
5366	35734	Α	5408	287	659	
5367	35735	A	5409	1	633	
5368	35736	Α	5411	3	634	
5369	35737	A	5412	344	481	
5370	35738	Α	5413	1	525	
5371	35739	A	5414	1	501	
5372	35740	Α	5415	12	461	a GGI BIOGEDVENICO GGOVENI
5373	35741	Α	5416	302	567	MLCCLEISSTRYPKSSLSSSKFH
		1	İ			KSLGQGQNAASLFAKT*RESPL
	l	1				LQFPASSSSPSETTSAWTLLFISL
		١.			0.11	SAFLTKAFNKSLGGSKLSH
5374	35742	A	5417	251	844	NLGRGSQTSILDFCAPAGLIPCG
		1				SCQGLGLPHSEATARAVYWPL
		1				SAMAGVAGTQGTKSLDSSLFA
						KT*QESPLLRFPTSSSSPSETTSA
		1				FILLFISLSEFLSKPFNKSLGGSK
						LSHIFVSSSEPSKLSQPLHMPIQ
	1	1				ARISSFTSGHTDDSTVLFSVLLK
						LPLPVPSQAFSLKPGSIVMLLSS
	I	١.		ļ.———		WSDNFNIPSISDSDA
5375	35743	A	5418	1	I113	
5376	35744	A	5421	1	337	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5377	35745	Α	5422	2	680	
5378	35746	Α	5423	144	373	
5379	35747	A	5424	1	597	
5380	35748	A	5425	3	3319	
5381	35749	A	5426	I	612	
5382	35750	С	5427	46	168	
5383	35751	Α	5428	1	663	
5384	35752	A	5429	10	417	IAIMNOTVAIRTREFMTNRLLE RKQMVIDVLHPGKATVPKTEIL EKLAQMYKTTPDVIFVFGFRTH CGGGKTTGFGMIYDSLDYAEK NEPKHRLARHGLYEKKKTS*K QRQERTNRMKKVRGTAKANV VAG*KPNE
5385	35753	A	5430	67	263	GKTTG\FGMIY\DCLDYAKKNE PKHRRARHGLYEKKKTSRKQR KERKNRMKKVRGTAKANVGA GKK
5386	35754	A	5431	2	537	TPOSITITIK PPTASTSEDRSPIM NOITVTIPH*EKFMTQPTYFRGN QMVIDVLSPPGKGDQCPKHRK FGKKLAQNVPRPTPDVIFVFWI VOFFIGGERTTG-FIGMIYGFPGI YAKEKMNPDHRLCKDMGLVL RKEKGPSRKANGKGTARNRIG RKVPGGTGKGPNVGCWAKRR NEVSSS

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SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			Ì	sequence		
5387	35755	A	5432	1	2195	ARGLSMGH*FP/PHFQCALA*M
						PAPGRGPPPPLPP/CPDAPPACA
	l					ATMERPEAGLRVAPRSPVOPG6
				ŀ		TSVLPVAKRFNARILWLKRPOF
		1				QLWSLWRAQATVSLGGFHVM
						LSLQVHRINARVKEAWQLPPRI
			l			QMMYQKAWVLRQKPAAAVEI
	1			ŀ		SQRNSPRAMLGGNVGLEPPPRV
				ľ		STRALPSGAVGRGLPPSRPKND
-	1					TATGSLHPELGKAADIQFHPVR
			i			AATGASPCKSIGTELPKALGAH
	1		l	1		VLLQCALDVGHGVEGELWSFK
						TRQPSDFSIFSPPFPPFYSTKPPL
				ŀ		SWPIPNEPLGTPPRRGRGGAEG
				I		LLTSQCSHILNGLCFTGGINSNE
		İ		l		CENVSRKKKMSEEFEANTMDS
	1					LVDMPFATVDIQDDCGIFFDVV
		1				KLRVNCQEILANRHPGRAMRK
						VVLTKTSWEGESLAVGKLPLK
				į.		RLVSLDCQLRCLQCECGILIRQ
l						HVVWLERTTGHWHPRSSQSCR
				l .		LNTTSTALEHCNAFIYNTVCSH
		i		l .		KLKDHSHDNGKSSGFLNPVAA
						PHSCIVMGHLTLLITTSYYTPLT
	İ			1		KPDTDPTLKKEGLISQDSSSLEV
						LLHTDPLGKRGTPDPRVDDDSI
				1		GKFPVTNSQARKRILEPDDFLD
		1				DLDDEYCEDAPKHRGKGCGSA
	Ì		l			HKELDASNLEDQDKPYACDIC
	Į.	1		l		GKRYKNRPGLSYHYAHSHLAE
l		i		l .		EGEDKEDSQPPTPVSQRSEEQK
		1				SKKGPDGFALPNNYCNFCLGN:
5388	35756	A	5433	1	580	FSPLIHLILSGHSTCFREHRVGG
						KVTDQQDPKAEEFFLVQNKMK
l		İ				SLPCLLLSTQTRQPSDFSIFSPPF
						PPFYSTKPPLSSWPVLNELLGTF
		İ				PRRGGGRAEG/PPHFPVG\GPGR
	İ					GAPSPPRRGGWPGGGLTPQPPS
				Į.		RTGRLAGRGADPPTSLPDGAA
						GRAGG*PHHLPPGRGGWPGRG
				1		APHFPVGVAGQRRLFIC
5389	35757	Α	5434	405	685	KVSHVYFYPHRPRNHPISQFFPH
						PSRLSIPQNRHCHHGPS/RNEPL
				1		GTPPR/PGSWPGRGAPHFPETFN
1	1	1	1			HGRRWKGSRHVFTWPEQERE
		L	L			WGSATHF
5390	35758	A	5435	1	654	
5391	35759	Α	5436	1	426	
5392	35760	Α	5437	1	548	
5393	35761	A	5438	1	459	
5394	35762	Α	5439	11	346	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
5395	35763	A	5440	i	1248	
5396	35764	A	5441	I	1257	
5397	35765	Α	5442	I	1659	MGDFNTPLSTLDRSTRQKVNK
		1				DTOELNSALHOADLIDIYRSLH
		l	1		[	AKSTEYTFFSAPHHTYSKIDHIL
		l				GSKALLSKCKRTEIITNYLSDHS
		l			ļ	AIKLELRIKNLTQNRSTTWKLN
		1			i	NLLLNDYWIHDEMKAEIKMFF
		l				ETNENKDTTYQNLWDAFKATA
		l				SKTNKEKEKNQIDTIKNDKGDI
		l			1	TTDPTEIQTTIREYYKHLYANK
	1	l			ł	LENLEEMDKFLDTYTLPRLNQE
		ı				EVESLNRPITGAEIVAIINSLPTK
	1	1			i	KSPGPDGFTAEFYQRYKEELHI
		1			ŀ	NRAKDKNHMIISIDAEKAFDKI
	1	1			ł	QQPFMLKTLNKLGIDGTYFKIIR
		1				AIYDKPTANIILNGQKLEAFPLK
	1	1			į .	TGTRQGCPLSPLLFNIVLEVLAR
						AIRQEKEIKGIQLGKEEVKLSI.F
						ADDMTVYLENPIVSAQNLLKLI
		l				SNFSKVSGYKINVQKSQAFLYT
		ŀ				NNRQTESQIMSELPFTIASKRIK
						YLGIQLTRDVKDLFKENYKPLL
		l				KEIKEDTNKWKNIPCSWVGRIN
		1				IMKMAILPKVIYRFNAIPIKLPM
	l					TFFTELEKTTLKFIWNQK\RARI
		1				AKAILSQKNEAGGITLP
5398	35766	Α	5443	1007	1719	TEPKTKTT*LSQ*MQKKPLTKF
		l				NNPSC*KLSIN/IVLEVLARAIRQ
		l				EKEIKGIQLGKEEVKLSLFADD
						MIVYLENPIVSAQNLLKLLSNFS
		l				KVSGYKINVQKSQAFLYTNNR
	ı					QTESQIMSELPFTIASKRIKYLGI
						QLTRDVKHLFKENYKPLLKEIK
			ĺ			EDTNKWKNIPCSWV\GRINIVK
						MAILPKVIYRFNAVPIKLPMTFF
					i	TELEKTTLKFIWNQKRACIAKSI
			l			LSQKNKAGGITLP
5399	35767	В	5444	1	1020	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
5400	35768	A	5445	1	1576	MDKFLDTYTLPRLNOEEVESLN
15.00	33700	ľ.		ľ		RPITGAEIVAIINSLPTKKSPGPD
		1				GFTAEFYORLISNFSKVSGYRIN
		1				VOES\OAFLYTINROTESOIMSA
		1				LPLTIASKRIKYLGIOLTROVKD
	ŀ		ì			LFKENYKPLLNEIKEDTNKWK
		1				NIPCSWVGRINIVKMAILP/KEL
	l .					EETTLKFIWNQKRARIAKSILSO
			ŀ			KNKAGGITLPDFKLYYKATVT
	İ					KTAWYWYONRDRDOWNRTEP
						SEIMPHIYNYLIFDKPEKNKQW
1	1					GKDSLFNKWCWENWLAICRKL
						KLDPFLTPYTRINSRWIKDLHV
ł	ŀ	1				RRKTIKTLEENLGNTIQDIGMG
						KDFMSKTPKAMATKAKIDKW
		l		l		DLIKLKSFCTAKETTIRVNRQPT
	İ			i	•	KWEKIFATYSSDKGLISRIYNEL
1	i					KQIYKKKTNNPIKKWAKDMNR
						HFSKEDIYAAKKHMKKCSSSLA
						IREMQIKTTMRYHLTPVRMAII
						KKSGNN/R/CAPGTPERQNHSLS
	i	1				WKGS*SQEPSGLAQWIPLPWSP
		Į.				AS*DPLA*NSCCQHSCLKSTWD
						AQACARKLRTLIKGYRNCQLE
5401	35769	Α	5446	1	984	
5402	35770	A	5447	1	1563	
5403	3577I	Α	5448	1	1449	
5404	35772	В	5449	1	1605	
5405	35773	В	5450	1	1569	
5406	35774	Α	5451	1	690	MSELPFTIASKRIKYLGIQLTRD
						VKDLFKENYNPLLNEIKEDTNE
						WKNIPCSWVGRINIVKMAILPK
						ATVTKIAWYWYQNRDIDQWN
		1				RTERSEIMPHIYNYLIFKKPEKN
		1				KQWGKDSLFDKWCSENWLAIC
		1				RKLKLDPFLTPYTKINSRWIKD
		l				LNVRPKTIKTLEENLGITIQDIGI
		1	l			GKDFMSKTPKAMATKAKIDK
		1				WDLIKLK\FCTAKETTIRVNRQS
	2.000	١.	5.152	l	1010	TKWEIISSLD
5407	35775	A	5452	1	1919	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		sequence		
5408	35776	-	5453	,	1416	MIILIDAEKAFDKIQQPFMLKTL
3408	33776	Α	3433	I	1410	SKLGTDGTYLKIIRAIYDKPTAN
						IILNGOKLEAFPLKTGTROGCPL
		ŀ	ŀ			
						SPLLFNIGLEDLARAIRQEKEIK
		1	1			GIQLGKEEVKLSLFADDMIVYL
						ENPIVSAQNLLKLISNFSKVSGY
						KINVQKSQAFLYTNNRQTESQI
						MSELPFTIASKRIKYLGIQLTRD
						VKDLFKENYKPLLKEIKEDTNK
						WKNIPCSWVGRINIVKMA1LP\R
						DIDQW/NRTEPSEIMPHTYNYLI
						FDKPEKNKQWGKDSLFHKWC
						WENWLAVCRKLKLDPFLTPYT
						KINSRWIKDLNIRPKTIKTLEEN
						LGITIQDIGVGKDFMSKAPKAM
		ĺ				ATKAKIDKWDLIKLKSFCTAKE
		l				TTIRVNRQPTTWEKIFATYSSD
		l				KGLISGIYNELKQIYKKKTNNPI
			ŀ			KKWAKDMNRHFSKEDIHAAK
						KHMKKCSSSLAIREMDIKTTMR
						YHLTPVRMAIIKKSGNNRCWR
						GCGEIGTL
5409	35777	В	5454	1	810	
5410	35778	В	5455	1	1277	
5411	35779	В	5456	130	1701	
5412	35780	Α	5457	1	1395	
5413	35781	Α	5458	3	1646	
5414	35782	A	5459	1	759	
5415	35783	A	5460	2821	5781	
5416	35784	В	5461	1	2025	
5417	35785	Α	5462	1	3663	
5418	35786	В	5463	1	2265	1
5419	35787	Α	5464	1	2241	
5420	35788	Α	5465	1	2478	
5421	35789	A	5466	1	2067	
5422	35790	A	5467	1	2988	
5423	35791	В	5468	1	2061	
5424	35792	Α	5469	1	2141	
5425	35793	Α	5470	1	400	
5426	35794	A_	5471	2	2507	
5427	35795	Α	5472	1	768	
5428	35796	Α	5473	1	1527	
5429	35797	Α	5474	1	1293 •	
5430	35798	Α	5475	1	1038	
5431	35799	Α	5476	1	1572	
5432	35800	Α	5477	1	1290	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stup codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5433	35801	A	5478	1	524	MSELPFRIASKRIKYLGIOLTRD
13433	33601	Ι^	3478	'	324	VKDLFKENYKPLLNEIKEDTNK
						WKNISCSWVGRINIVKMAILPK/
					i e	VKHR/FSACLQSLGRSGTTGLE
						ALAM*PIWPQEVE*VKFPALPS
						GASSTKGGCVP*QIQVEERLLS
			1			WKL*QA*TSW\YQRQRRSDSSL
		_				RERK*PKSIQRNVRRLSYYTP
5434	35802	A	5479	2	1547	
5435 5436	35803 35804	A	5480	1	2376 1824	
5437		A	5481	1	1071	
5438	35805 35806	A B	5482	1	1839	
5439	35807	В	5484	1	1368	
5440	35807	A	5485	1	1884	ļ
5441	35809	A	5486	1	1053	
5442	35810	В	5487	1	2532	
	35811	A	5488	1	2373	
5444	35812	A	5489	1	2361	
5445	35813	A	5490	1	2274	
5446	35814	A	5491	1	1686	MASPGPAPTASPKIHSELLTATR
3440	33014	n	5471	ļ <b>.</b>	1000	EAQRHHPVPRGQDLVTSESFSL
						SFCFSAAIFIFELLGSNSEGVTDL
					ł	RLWLCOPAPRCGEWTYNPLEO
	1					CCDDGVILDLNQTRLCGSSCTF
						WPCFOHCCLESLGSONOTVVRF
						KVPGMKPDCKSSPITRICAQAG
						VQISNFSKVSGYKINVQKSQAF
	- 6					LYTNNRQTESQIMSELPFTIASQ
						RIKYLGIQLTRDVKDLFKENYK
						PLLKEIKEDTNKWKNIPCSWVG
						RINIVKMAILPKVIYRFNAIPIKL
						PMTFFTELEKTTLKFIWNQKRA
						LIAKSILSQKNKAGGITLPDFKL
						YYKATVTKTAWYWYQNRDID
			i			QWNRTEPSEITPHIYNYLIFDKP
						EKNKQWGKDSLFNKWCWENW
						LAICRKLKLDPFLTPYTKINSRW
						IKDLNVRPKTIKTLEENLGITIQ
						DIGMSKDFMSKTPKAMATKDK
						IDKWDLIKLKSFCTAKETTIRV\
		1				NRQPTKWEKIFATYSSDKGLIS
						RIYNELKQIYKKKTNNPIKKWA
		1				KDMNRHFSKEDIYAAKKHMK
						KCSLSLAIREMQIKTTNQNH\M
L		L				RYHLTPGHG
5447	35815	Α	5492	1	1872	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5448	35816	A	5493	195		PPGOHLORRCLLEVSGFSENAK KGMLEVLARAINGCKKIKGG GKEEVKLSLFADDMIVYLENPI VSAQNLLKLISNFSKALGYKISG QKSQAFLYTNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNK WKNI PCSWIGRINIVKMAILPKYIYGF NAIPIKLPMTFFTELEKTILKFI WNQKRARIAKSILSQKDKAGGI TLPDFKLYYKATVTKTACNSN GSQSPWMEEQIRDA WGSMYLK NVVRETDEVGKGQIRMRTYFE QAIDQRSSTIDTSLSTPAAPMVD SLIARVGYMARGNAITLPVCGR DVKFTLEVLRODSVEKTSRVW SGNERDQELLTEDALDDLIPSFL LTGQQTPAFGRRVSGVIEIADG SRRRKAAALTESDYRVLGGEL DDEOMAALSKLIGDP
5449	35817	Α	5494	1	1845	
5450	35818	Α	5495	1	2109	

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SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217		of peptide sequence	deletion, \-possible nucleotide insertion)
ł				sequence		
5451	35819	A	5496	I	2535	MKSGHPEKEQDNSDVQETREIT
i			İ			IRGLLCTALMRHSTGAIAYLGV
						LSGSASLKLAGVPLRCCEGDKD
						AGHPLETQTALCERGRGARSLV
						GNTIMTSQPVPNETIIVLPSNVIN
						FSQAEKPEPTNQGQDSLKKHLH
			1			AEIKVIGVNLIQNVLERGWGKC
						QEMIYVLGLDICRPFFVSRVSEE
						GRMGQRGEEDANSLDFPPASLL
						CLICQEQGVNGESCSPVGMYH
i						REIVPVYEVLSVITGLQIQVFSG
						KEADSVIKRSIGWGPFFKPRTK
1						DKNHMIISIDAEKAFDKIQQHF
						MLKTLSKLGIDGTYLKIIRAIYD
1		1				KPTANIILNGQKLEAFPLKTGTR
		ı				QGCPLSPLLFNIVLEVLARAIRQ
		ł				EKEIKGIQLGKEEVKLSLFADD
		l				MIVYLENPIVSDQNLLKLISNFS
		l				KVSGYKINVQKSQAFLYTNNR
		l				QTESQIMSELPFTIASKRIKYLGI
		1				QLTRDVKDLFKENYKPLLNEIK
		l		İ		EDTNKWKNIPCSWVGRINIVK
1						MAILPKVIYRFNAIPIKLPMTFF
		l				TELEKTTLKFIWYQKRARITKSI
		l				LSQRNKAGDITLPDFKLYYKAT
		l				VNKTAWYWHQNRHIDQWNRT
		l				KPSEITLHIYNYLFFDNPDKNKK
		l				WGKDSLFNKWCWENWLAICR
		l				KLKLDPFLTPYTKINSRWIKDL
		1				NIRPKTIKTLEENLGITIQDIGMG
		l				KYFMTKTPKAMATKAKIDKW
		_				DLIKLKSFCTGKETTIRVNRQPT
5452	35820	A	5497	3	2284	
5453 5454	35821	A	5498 5499	I	1245	
5455	35822	A	5500	383	1185	
5456	35824	A	5501	1	3159	MLEVLAWAVROEKEIKGIOLG
3430	33024	^	3301	'	3137	KEEVKLSLFADNMTVYLENPIV
		l				SAONLLKLISNFSKVSGYKVSG
		ł				QKSQALLYTNNRQTESQIMSEL
						PFTIASKRIKYLGIHLTRDVKDL
		1	1			FKENYKPLLKEIKKDTNKWKNI
		1				PCSWVGRINIVKMAILPKDIIOE
		l				,
		1	l			NFPNLARQANIQIQEIRKTPQRY
		1				SSRRATPRHIIVRFTKVEMKEK
		l	1			MLRAAREKASHHTYSKIDPILG SKPLLSKCKRTEIITNYLSDHSAI
			L	L		KLEFRIKNL

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	nf peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5457	35825	IA	5502	583	2515	MQKKPLTKFNNPSC*KLSIN*LI
						SNFSEVSGYKISVQKSQAFLYT
		1				NNR/OESOIMSELPFTIASKRIKY
						LGIQLTRDVKDLFKENYKPLLK
		1				EIKEDTNKWKNIPCSWVGRINI
l						VKMAILPKAIYRFNAIPIKLPMT
l	ľ				i	FFTELEKTTLKFIWNQKRARIA
						KSILSQKNKAGGITLPDFKLYY
						KATVTKTAWYWYONRDIDOW
						NRTEPSEITPHIYNYLIFDKPEK
ļ.		1				NKOWGKDSLFNKWCWENWLA
l		1				ICRKLKLDPFLTPYTKINSRWIK
		1				DLNVGPNTIKTLEENLGITIQDI
						GTGKDFMSKTPKAMATKAKID
1	l	1				KRDLIKLNSFCTAKETTIRVNR
1						OPTKWEKIFTTYSSDKGLISRIY
				1		NELKQIYKKKTNNPIKKWAKD
						MNRHFSKEHIYAAKKHMKKCS
		1				PSLAIREMQIKTTMRYHLTPVR
						MAIIKKSENNSLLAAGGGNRRT
				ł		ANVVAHGFANLLTLDKKTLQEI
						LVHYPDSERILMKKARVLLKQ
						KAKTAEATPPRKDLALLFPPKE
						ETPKLFKTLLGGTGKASLARLL
	1					KLKREQAAQKKENSEGGEEEG
		1				KENEDKQKENEDKQKENEDKG
	1	1				KENEDKDKGREPEEKPLDRPEC
		1				TASPIAVEEEPHSVRRTVLPRGT
		1				SRQSLIISMAPSAEGGEEVLTIE
5458	35826	Α	5503	1	2463	
5459	35827	В	5504	1	1221	
5460	35828	A	5505	1	4494	
5461	35829	A	5506	1	2825	MARTSYGQHFFPTLISMNIDSG
1		ı				RQNNGIPKLSTSYSLKPMNTLC
		l				YLVKRDLEGVLKLRILTWESSL
1						DYPGGPSVITKVLIRQKEGQSQ
					1	RTRYDNGSRGWSDAIAVKRPQ
1						AKECGWPLEAGKGKEWILRKE
		1	1			CIPANTLMLAQCPPTLRVGGSV
		1				CSAWRMIQNSDGERRKRNRIQL
		1	l			QAVRLSKVIHDTFRNFPRFVHS
		1				RELSKGAEKSSSLKKGLEQVII
		1	1			WTKCRQCGESRCTKKVEERKV
		L.				LHNTFISTSTTITTLG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, ≔possible nucleotide insertion)
				sequence		
5462	35830	Α	5508	1184	4791	TSMQKSSIKYWQTESSSTSKSLS
						TMIKWASSLGCKAGSVYANO*
1						M*SSI*TEPKTKTI*LSO*MOKK
l		l				PL/YKIQQPFMLKTLNKLAQNL
						LKLISNFSKVSGYKINVOKSOA
1	1					FLYTNNRQTESQIMSELPFTIAS
		1				KRIKYLGIOLTROVKOLFKENY
l						KPLLKEIKEDTNKWKNIPCSWV
1						GRINIVKMAILPQVIYRFNAIPIK
						LPMTFFTELEKTTFKFIWNQKR
						ARIAKSILSQKNKAGGITLPDFK
			Ì		i	LYYKATVT
5463	35831	Α	5509	516	2233	
5464	35832	В	5510	286	4131	
5465	35833	В	5511	1	4911	
5466	35834	Α	5512	1080	3119	SSGLHPWDARLVQYTQINKCN
						PAYKQSQRQKPHDYLNRCRKK
						AFDKIQQPFMLQTLNKLGIDGT
						YFKIIRAIYDKPTANIILNGQKLE
						AFPLKTGTRQGCPLSLLLFNIVL
						EVLARAIRQEKEIKGIQLGKEEV
						KLSLFADDMIVYLENPIISAQNL
	1				İ	LKLISNFSKVSGYKINVQKSQTF
						LYNNNRQTESQIMSELPFTIALK
						RIKYLGIQLTRDVKDLFKENYK
						PLLKEIKEDTNKWKNIPCSWVG
				ł		RINIVKMAILPKVIYRFNAIPIKL
						PMTFFTELEKTTLKFIWNQKRA
						RIAKSILSQKNKAGGITLPDFKL
			ŀ			YYKATVTKTAWYWYQNRDID
						QWNRTEPSEIMPHIYNYLIFDKP
		1				EKNKQWGKDSLFNKWCWENW
		l				LAICRKLKLDPFLTRYTKINSR
						WIKDLNVRPKTIKTLEENLGITI
						QDIGVGKDFMSKTPKAMAAKA
						KIDKWDLIKLKSFCTAKETTIRV
						NRQPTTWEKIFATYSSDKGLISR
						IYNELQQIYKKKTNNPIKKWAK
						DMNRHFSKEDIYAAKKHMKK\
						CSSSLAIR\EMQIKTTMRYHLTP
1	1					VRMAIIKKSGNNRIRRHFQPRS
	1					AMFFCCCPGGEGSGLQWELLL
	1					AAWTVLPYPCPAATVGRFLKQ
1		l				AQTADHSFLGHVWRVPSSRSW
						TDKEILSLVVNRQNQEVVQLIG
		<u> </u>	l			GLCGTHTISPTQHPATG

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	noa	09/540.217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	Jacque Lance	1	05/010,217	sequence		
	<u> </u>		}			
5467	35835	Α	5513	2494	4549	LQTILQGYSNSKQHGTGTKTA
						WYWYQNRDIDQWNRTEPSEIT
						PHIYNYLIFDKPDKNKKWGKDS
ŀ						LFNKWCWENWLVICIKLKLDP
					ł	FLTPYTKINSRWIKDLNVRPKTI
ŀ						KTIEENLGNTIQDIGMGKDFMS
l						ETLKARATKAKIDKWDLIKLKS
İ						FCTAKETTIRVNRQPTKWEKIF
						AIYSSDKGLIPRIYKELKQIYKK
						KTNSPIKKWVKDMNRHFSKEDI
						YAAKKHMKKCSSSLAIREMQI
					1	KTAMRYHLTPVRMAI
5468	35836	Α	5514	1	5582	MGDFNTPLSTLDRSTRQKVNK
1						DTQELNSALHQADLIDIYQTLH
1				1	ŀ	PKSTEYTFFSAPHHTYSKIDHIL
						GSKALLSKCKRTQIITNYLSDHS
		l				AIKLELRIKNLTQNHSTTWKLN
						NLLLNDYWVYNEMKAEIKMFF
						ETNENEDTTYQNLWDAFKAVC
				1		RGKFIALNAHKRKQERSKIDTL
						TSQLKELEKQEQTHSKASRRQE
		l				ITKIRAELKEIETQKTLQKINESR
		l				SWFFERINKIDRPLARLIKKKRE
	i					KNQIDTIKNDK
5469	35837	Α	5515	3371	5375	TDTSQKKTFMQPKKHMKKCSP
						SLAIREMQIKTTMRYHLTPVRM
		1				AIIKKSGNNRSWYFEKINKIDRL
	1		ŀ			LARLIKKKREKNQIDAIKNDKG
						DITTDPTEIQTTTREYYKHLYA
						NKLENLEEMDKFLDTYNLPRL
						KQEEVESLNRPIRGSEIVAIINSL
						PTKKSPGPDGFTAEFYHRYKEE
						LVPLLLKLFQSIEKEVILPNSFYE
		1		1		ASIILIPKPDRDTAKKENFRPISL
	1		1	l		MNIDAKILNKILANRIQQHIKKL
		l				IHHDQVG

O: of p		tod	SEQ 1D NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
358	/ /	A	5516	314	2695	GSACRDPDPDPLRLVGGGAAA PPCSSVSPSAWRQSR PREYYEG GGGLHAPDRETALGLGJATSER MLGIGGGRKFLAASLSILCIPA ITWIYLFSGSFEDGKPVSLSPLE SQAHSPRYTASSQRERESLEVR MREVEEENRALRRQLSLAQGR AFSHRRGNHSKTYSMEEGTGD SENLRAGIVAGNSSECGQQPVV EKCRRNPLHFRILDSIAGQILA LTEQTWWYPAVRVDFYYADEL KSEVSWIPNKHYSGIYGL MKLU LTKTLPANLERVIVLIDTDIFFAT DIAELWAVFHKFKGQQVLGLV ENQSDWYLGNLEWKNHRPWPA LGRGYNTGVILLLDKLKRMK WEQMWRLTAERELMGMLSTS LADQDIFNAVIKQNPFLVYD LKVIHWNSPKLRVNKHYPU FRRNLYLTELYDGNLLRRELF GCPSEADVNSENLCKQLSELDE DDLCYEFRREFTVHRTHLYFL LSDAEAQGFRYAQGSELDE DDLCYEFRREFTVHRTHLYFL LSDAEAQGFRYAQGSEVALL KLSDAEAQGFRYAQGSEVALL KLSDAEAQGFRYAQGSEVALL KLSDAEAQGFRYAQGSEVALL KLSDAEAQGFRYAGGSEVALL KLSDAEAQGFRYAQGSEVALL KLSDAEAQGFRYAQGSEVALL KLSDAEAQGFRYAGGSEVALL KLSDAEAQGFRYAGGSEVALL KLSDAEAQGFRYAGGSEVALL KLSMLDMKHISTPYMFLSDIDFLP MYGLYSPLKSVIQLDLANTK KAMIVPAEETLRYRLSFPKSKA

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5471	35839		5517	l3	2079	GKPVSLSPLESQAHSPRYTASS
54 / 1	33839	Α	3317	P	2079	ORERESLEVRMREVEEENRALI
						ROLSLAOGRAPSHRRGNHSKT
		1				YSMEEGTGDSENLRAGIVAGN
						SECGOOPVVEKCARRNPLHFHL
		1				ADSIAEQILATLFQTWMVPAVI
						VDFYNADELKSEVSWIPNKHY
		l				GIYGLMKLVLTKTLPANLERV
		1				VLDTDITFATDIAELWAVFHKE
		l			ŀ	KGOOVLGLVENOSDWYLGNL
		l				WKNHRPWPALGRGYNTGVILI
		l		1		LLDKLRKMKWEQMWRLTAE
	1	1				ELMGMLSTSLADODIFNAVIKO
	1	1				NPFLVYQLPCFWNVQLSDHTR
		1				EOCYRDVSDLKVIHWNSPKKL
	i	1				RVKNKHVEFFRNLYLTFLEYD
		l				GNLLRRELFGCPSEADVNSENI
	1					QKQLSELDEDDLCYEFRRERFT
				1		VHRTHLYFLHYEYEPAADSTD
		l			1	VTLVAQLSMDRLQMLEAICKE
	1	1		1	ŀ	WEGPISLALYLSDAEAQQFLRY
İ					1	AQGSEVLMSRHNVGYHIVYKI
		l				GQFYPVNLLRNVAMKHISTPY
		1				MFLSDIDFLPMYGLYEYLRKS'
		ļ			i	IQLDLANTKKAMIVPAFETLRY
		1				RLSFPKSKAELLSMLDMGTLF
		1				FRYHVWTKGHAPTNFAKWRT
		1				ATTPYRVEWEADFEPYVVVRF
						DCPEYDRRFVGFGWNKVAHIN
		1			1	ELDVQEYEFIVLPNAYMIHMPI
		1				APSFDITKFR\$NKQYRICLKTLI
						EEFQQDMSRRYGFAALKYLTA
5472	35840	Α	5518	403	2757	
5473	35841	В	5519	128	353	
5474	35842	A	5520	2	333	
5475	35843	В	5521	25	1359	
5476	35844	В	5522	1	1113	
5477	35845	A	5523	1	2526	
5478	35846	Α	5524	3	555	L

649

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5479	35847	Α	5525	1	1710	MSQGTTPWGPTPAGTTPESEVE
	l					RPFPFPVPVPVPETSERSFPVRG
l	l					VCGQAKSGLRRGAARLAPAAY
	İ	1				LFTRQQTRELIHSACVSISVNTN
	ŀ	l				HGLSVAINSRRCTYYRKYVIDF
	l	i				SKSEIIGIPISKNIDLTVGTTVTQ
						LQNLNTVGIIGSRGGRGQVAAL
	ĺ					NCDRQGHLWLFTRVTVHWRM
		l				GNDRTFWGLLDTVSELMFIPGN
						PKHHCGPPVKVGAYGVTFLGV
						HWCGACQDTPCKMKDKLLHL
				-		APPTTKKKAQYVVGLLGFWRP
		ŀ				YRVTQKAASFEWGPEQDKALP
ŀ						QVQAAVQPALLFGPYDSADPM
						VLEASVADRDAVWSLWQAP/IS
		l			ĺ	HKMGHAQQHSIIKWK*YICDW
		l				ARAGPKGTT\APMASWGVLYD
	ì	1			ĺ	QLTEEEKTRAWFTDGSARYAG
1		l			1	TTQKWTAAALQPLSRTSLKGS
		ı				GEGKSSQWAELQAVHLVVHFS
	İ	1				WKDKWPDVRLYIDSWAVANG
	1	1				LAGWSGTWKKHDWKIGDKEI
	l .	1				WGRGMWMDLSEWPKPVKIFG
		l				SHVSAHQWVISAEEDFNNQVD
		ı				KMTCSVDITQPLSPATPVITQW
		1				AHKQSGHGGRDGGYTWAQQH
						GLPLTKTGLAMATAECPI
5480	35848	Α	5526	!	438	
5481	35849	Λ	5527	1	612	EKOAMTAI COKI ICOOKATEAK
5482	35850	Α	5528	2	736	EKCAMTALSSKLISQQKAFFAK MVVDAVMMLDDLLQLKMIGI
		l				KKVQGGALEDSQLVAGVAFKK
	ŀ	l				
	l	l				TFSYAGFEMQPKKYHNPKIALL
		l			l	NVELELKAEKDNAEIRVHTVEC
		l				YQAIVDAEWNILYD\KLEKIHH
		l				SGAKVVLSKLPIGDVATQYF\A
		l				DRDMFCAGRVPEEDLKRTMM
	1	l				ACGGSIQTSVNALSADVLGRCQ
		l				VFEETQIGGERYNFFTGCPKAK TCTFILRGGAEQFMEETERSLH
						DAIMIVRRA
5483	35851	A	5529	3	474	D. III. HUM
5484	35852	Α	5530	374	968	
5485	35853	Α	5531	1	568	
5486	35854	Α	5532	1	2136	
5487	35855	Α	5533	I	240	
5488	35856	Α	5534	248	1034	
5489	35857	Α	5535	I	1602	
5490	35858	Α	5536	120	340	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	ł	
5491	25050	<u> </u>	5537	2	1408	DEDDDDDDEEDDDEDDDDDD
3491	35859	Α	3337	12	408	
				l		DDEEAEEKAPVKKSIRDTPA\K
				1	l	NAQKSNQNGRDSKP\SSTPRSK
l	İ					GQESFKKQEKTPKTPK\GPSSVE
	1			1	l	DIKAKMQASIEKGGSLPKVEAK
1						FINYVKDCF\RMTDQEAI\QDLW
				L		QWRKSL
5492	35860	Α	5538	194	1027	WSFISIHLLSYLSACHHLMEDS/
				1		MDMGMRPLRPQNYLFSCELKA
						NKDYHFK VDNNENEHQLPLTTI
						NLGAGAMDELDIVEAEAMNYE
1						GSPIKVILATLKMSVQPTVSLG
1						G\FEITPPVV\LRLKCGSGPVHIS
	1				ı	GOHLVAVEEDAESEDEEEEDV
	1	1				KLLSISGKRSAPGGGSKVPOKK
İ	1					VKLAADEDDDDDDEEDDDED
						DDDDDFDDEEAEEKAPVKKSIR
	1					
	1					DTPAKNAQKSNQNGKDSKPSS
						TPRSKGQESFKKQQKTPKTPKG
		_		<u></u>		PSSVEDIKAKMQASIEKAH
5493	35861	C	5539	212	367	
5494	35862	Α	5540	14	1515	
5495	35863	Α	5541	1	540	
5496	35864	Α	5542	1	1881	MDAALDDLIDTLGGPEETEEEN
	1					TTYTGPEVSDPMSSTYIEELGK
ł	1	1	,			REVTIPPKYRELLAKPIGPDDAI
1						DALSSDFTCGSP*LYPSQVFHLL
	1					DLLPFSPGYQPRLLQHHLA/AVP
						FKVAGSGGADCILHMEVRDTA
1						SDTGAGAAALDSSVFSVGLDGF
						SLHSDRSKSSESSSMSSDSLRGL
						GFSSGSGNSGFPSLSVAGFNLYS
1						DGIVSSSSPHFSSFSSLAFASSTS
1	1					LIERRSSSGSACRVPSEADRASS
5497	35865	Α	5543	1	930	
5498	35866	Α	5544	1	183	
5499	35867	A	5545	i i	555	
5500	35868	A	5546	162	499	FPGSGNMAKDAGLIEANGELK
1	1	1		1	1	VFIDQNLSPGKGVVSLVAVHPS
				1	I	TVNPLGKOLLPKTFGOSNVNIA
					1	QQVVIGTPQRPAASNTL/VWVG
1	1		1		i	SPHTPSTHFASQ\NQPSDSSPW\S
		1	1	1	İ	
	05050	<del> </del>	55.47	-	461	AGKR
550I	35869	Α	5547	2	451	LVAEFSAADNHILPNESAYDQK
		1	1	1	I	NIRRRVYDALNVLMAMNIISKE
1	1	1	1	1	I	KKEIKWIGI.PTNSAQECQNLEV
		1		1	1	ERQRRLERIKQKQSQLQELILQ
1	1		l	1	1	QIAFKNLVQRNR\HAEQQASRP
		1	1			PPPNSVIHLPFIIVNTSKKTVIDC
		1	1		1	SISNDKFEYLFNFDNT
5502	35870	Α	5548	37	162	
		_				

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
5503	35871	A	5549	205	616	RKLHGSQSSITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADAQVRRAVNNYDIIVMSNSF NGQSEHQVWIGGQFTFIKF\PIN
						SVSIRCRARQEGIMSSPGQQVG
5504	35872	В	5550	I	1407	
5505	35873	A	5551	3	416	MLPARMCCGIVSG*QFHTGNSY DHDYEFELGTRS*A*LKLLFS*T LPP*QLPAGSGEGPYHL.FGQLS YCHRGGEKALAALLSSPTSKTR SPSEPDPEQDEQKLRFCKRHLY GQQPRSPVEIRLQHVAIAYQTH HAYD
5506	35874	A	5552	1988	2137	LVITTLLPLACGTAK*E*VNVTS FGSRPICSTSPVLFSGL*GPVKEF DT
5507	35875	В	5553	1	561	Di
5508	35876	A	5554	1	492	
5509	35877	A	5555	3	1055	
5510	35878	Ā	5556	1	634	
5511	35879	Ā	5557	i	723	
5512	35880	A	5558	ī	384	
5513	35881	Α	5559	1	792	
5514	35882	A	5560	3	1607	HCTRMSVKWTSVILLIQLSFCFS SGNCGKVLVWAGYSHWMIN KTILDELIQRGHEVTVLASSASI LFDPNNSSALKIEIYPTSI.TKTE ENFIMOQIKEWSDLFREDFUFLADAI FSQVQEIMSIFGDITRKFCKDVV SNKKRMKKVQESRFDVIFADAI FFCSELLAEI,FNIFFVYSLSFSRG YTFEKHSGGFIFPRSVYDVVMSE LTDQMTFMERVKNIMYVLYFD FWFEIFDMKKWDQFYSEVLGR PTILSETMGKADVWLIRNSWN FOFPIPILLFINVDFVGGLICKPA KPLPKEMEDFYQSSGENGVVV FSLGSMVSNMTEERANVIASAL AQIPQKVLWRFDGDUKPDTLGL NTRLYKWIPQNIDLLGHPKTRA THIGGANGIYEAIYHGIPMVGI PLFADQPDNIAHMKARGAAVR FDFTMSTDLJAALKRVINDP SYKENYMKLSRIOHDOPVKPI. DRAVFWIEFVMRHKGAKHLRV DRAVFWIEFVMRHKGAKHLRV RAHDLTWFQYHSLDVIGFLLV CVATVIFIVTKCCLFCFWKFAR KAKKGKND
5515	35883	A	5561	2	1600	ICHCCCCIO
	1-2002	<u> </u>	1-20.		1	

Sequence   09/540/217   codon for peptide   of peptide sequence   deletion, ly-possil	possible mucleotide ble nucleotide insertion)  HCIRMSMKWTSAL SSGSCGKVLVWPT TTILDELVQRGHEV SFDPNSPSTLKFEV FEDIIKQLVKRWA SYFSQVQEIMWTFN IVSNKKLMKKLQE DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
Sequence   09/540/217   codon for peptide   of peptide sequence   deletion, ly-possil	HCIRMSMKWTSAL SSGSCGKVLVWPT CTILDELVQRGHEV SFDPNSPSTLKFEV FEDIKQLVKRWA SYFSQVQEIMWTFN IVSNKKLMKKLQE AVFPFGELLAELL VMSELSDQMTFIE
5516 35884 A 5562 2 1624 AATGKQAL LLIQI.SCYFS EFSHWMMIN TVILASSASIS YPVSLTKTE ELPKDIFIWS DILRKFCKD SRFDVVLAI KIFFVYRR LFPPSYVPV RVKMMIYV KWDGYSS KADIWLIKN	SGSCGKVLVWPT KTILDELVQRGHEV SFDPNSPSTLKFEV FEDIIKQLVKRWA SYFSQVQEIMWFFN IVSNKKLMKKLQE DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
LLIQLSCYFS EFSHWMMII TVLASSASIS YPVSLTKTE ELFKDITE ELFKDITE SRFDVVLAT KIPFVYRPRI LFPPSYVPV RVKMMIYV KWDGYSE KADIWLIKN	SGSCGKVLVWPT KTILDELVQRGHEV SFDPNSPSTLKFEV FEDIIKQLVKRWA SYFSQVQEIMWFFN IVSNKKLMKKLQE DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
LLIQLSCYFS EFSHWMMII TVLASSASIS YPVSLTKTE ELFKDITE ELFKDITE SRFDVVLAT KIPFVYRPRI LFPPSYVPV RVKMMIYV KWDGYSE KADIWLIKN	SGSCGKVLVWPT KTILDELVQRGHEV SFDPNSPSTLKFEV FEDIIKQLVKRWA SYFSQVQEIMWFFN IVSNKKLMKKLQE DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
EFSHWMIII TVLASSASI YPVSLTKTE ELPKDITFW DIL RKFCKD SRFDVVLAI KIFFYSTRI LFPFSSYPV RVKNMIYV KWDGYSE KADIWLIKN	KTILDELVQRGHEV SFDPNSPSTLKFEV FEDIIKQLVKRWA SYFSQVQEIMWTFN IVSNKKLMKKLQE DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
TVLASSASIS YPVSLTKTE ELPKDIFW DILRKFCKD SRFDVVLAT KIPPYYRRI LFPPSYVPV RVKNMIYVI K WDQFYSE KADIWLIRN	SFDPNSPSTLKFEV FEDIIKQLVKRWA SYFSQVQEIMWTFN IVSNKKLMKKLQE DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
YPVSLTKTE ELFKDITE BLFKDITE DILRKFCKD SRFDVVLAT KIPFVYRPRI LFPPSYVPV RVKMMIYV) KWDGYSE KADIWLIKN	FEDIIKQLVKRWA SYFSQVQEIMWTFN IVSNKKLMKKLQE DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
ELRADIFW DILRKFCKD SRFDVYLAI KIPFYYRRI LFPFSYPFV RVKNMIYV) KWDQFYSE KADIWLIKN	SYFSQVQEIMWTFN IVSNKKLMKKLQE DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
DILRKFCKD SRFDVVLAR KIPPYYRPR LFPPSYVPV RVKNMIYVI KWDQFYSE KADIWLIRN	IVSNKKLMKKLQE DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
SRFDVVLAI KIPFVSVPV RVKMMIYV) KWDGYSE KADIWLIKN	DAVFPFGELLAELL FSPGYAIEKHSGGL VMSELSDQMTFIE
KIPFVYRPRI LFPPSYVPV RVKNMIYVI KWDQFYSE KADIWLIRN	FSPGYAIEKHSGGL VMSELSDQMTFIE
LFPPSYVPV RVKNMIYVI KWDQFYSE KADIWLIRN	VMSELSDQMTFIE
RVKNMIYVI K WDQFYSE KADIWLIRN	
KWDQFYSE KADIWLIRN	
KADIWLIRN	
	CKPAKPLPKEME\E
	SVVVFSLGSMVSNT
	SALAKIPQKVLWR
	GLNTRLYKWIPQ
	RAFITHGGANGIY
	VGVPLLADQPDNI
	AVSLDFHTMSSTD
	NDPLYKENAMKLS
	PLDRAVFWIEFVM
	RVAAHDLTWFQY
	LACVATVIFIITKC
LFCVWKFV	RTGKKGKRD
5518 35886 A 5564 II 3210	
5519 35887 A 5565 I 835	
	ILKYLTKKYLKKN
NLRDWLRV	VANSKESYELRYF
OINODEEEE	EDED*ISFIWKILYE
	KKKKTKKKKK
5521 35889 A 5567 II 778 MAAAAAA	GDSDSWDADAFS
	GGGTAGGDRWG
	KDNWDDDDDEKK
	KISEKKKIAEKIKE
	QEEIKKRLEEPEEP
	ADKLRLKKLOEES
	GVNNAVYGIDAM
	EFGKLLKDI\ITQYE
	EVLVRDVCISLEID
	TVLCSEKOKOEKO
	GVVPGGGLKATM
	GYDGGYVODYED
5522 35890 A 5568 I 897	
5523 35891 A 5569 1 2658	
5524 35892 A 5570 1 441	
5525 35893 A 557I 3 427	

SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			sequence		
25904	1	5572	11	1052	PRLVLLKMAPLDLDKYVEIARI.
33894	l <sup>A</sup>	3372	'	932	CKYLPENDLKRLCDYVCDLLL
	l				EESNVOPVSTPVTVCGDIHGOF
	1				YDLCELFRTGGQVPDTNYIFMG
					DFVDRGYYSLETFTYLLALKAK
					WPDRITLLRGNHESRQITOVYG
					F\YDDCLTKYG\NANAWRYCTK
				1	VFDMLTVAALIDEQILCVHGGL
	1				SPDIKTL\D\QIRTIERNQEIPHKG
					AF\CDL\VWS\DPEDVDT\WAI\S
					PRGAGWLFGAK\VTN\EFGS*ST
					NLKLICRAHQLVHEGYKFMFD
					EKLVTVWSAPNYCYRCGNIASI
					MVFKDVNTREPKLFRAVPDSE
					RVIPPRTTTPYFL
	_				
35899	Α	5577	1	841	ILLWDVDGGLTQIDKYLYSSED
	l				YIKSGALLACGIVNSGVRNECD
	ł				PALALLSDYVLHNSNTMRLGSI
	ŀ				FGLGLAYAGSNREDVLTLLLPV
	l				MGDSKSSMEVAGVTALACGMI
					AVGSCNGDVTSTILQTIMEKSE
	ŀ				TELKDTYARWLPLGLGLNHLG
					KGEAIEAILAALEVVSEPFRSFA
	1			l	NTLVDVCAYAGSGNVLKVQQL
	l l				LHICSEHFD\SKEKEEDKDKKEK
	1				KDKDKKEAPADMGAHQGVAV
	l				LGIALIAMGEEIGAEMALRTFG
	1				HLLRYGEPTLRRAVPLALAL
35900	Α	5578	2	391	AFGVTEPGCYGVIDVDTGKSTL
	1	ĺ			FVPRLPASHATWMGKL/HSVLT
					SOKPSVLLTLRGVNTDSGSVCR
					EASFDGISKFEVNNTILHPEIVE
			1		CRVFKTDMELEVLRYTNKISSE
	1				AHREVMKAVKVGMKEYELER
	35894 35894 35895 35896 35897 35898 35899	of peptide sequence	of peptide hod in USNs 99/540,217  35894 A 5572  35895 A 5573 35896 A 5574 35897 A 5575 35898 A 5576 35899 A 5577	9/540,217   codon for peptide sequence   9/540,217   codon for peptide sequence   35894	

				Territoria de la companya della companya della companya de la companya della comp		
SEQ ID NO:		Met	SEQ ID NO:	Nucleotide location of first		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	of peptide sequence	noa	09/540.217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	sequence		09/340,217	scauence	or peptide sequence	deterion, v-possione aucreouge insertion)
5533	35901	Α	5579	18	1541	RRCRANMAAATGPSFWLGNET
						LKVPLALFALNRQRLCERLRKN
						PAVQAGSIVVLQGGEETQRYCT
					l .	DTGVLFRQESFFHWAFGVTEPG
	1		i	l		CYGVIDVDTGKSTLFVPRLPAS
				l		HATWMGKIHSKEHFKEKYAVD
	1	1				DVQYVDEIASVLTSQKPSVLLT
				l		LRGVNTDSGSVCREASFDGISK
	ł			l		FEVNNTILHPEIVECRVFKT\DM
						EL\EVLRYTNKISS\EAHREV\MK
				l		AVKSGEWKEYGVGKASFEHY\
		l		İ		CYSRG\GMRH\TSYT\CILRAVG
						*GTSAVLTFTGH\AGAPNDRTIQ
					ł	NGDMCLFDMGGEYYSVASDIT
						CSFPRNGKFTADQ\KAVYEAVL
ŀ	1					LSSRAVMGAMKPGDWWPDM\
		1				HRLAYRIHLEELAHMGILSGSV
						DAMVQAHLGAVFMPHGLGHF
						LGIDVHDVGGYPEGVERIDEPG
						LRSLRTARHLQPGMVLTVEPGI
l		l				YFIDHLLDEALADPARASFLNR
1				1	1	EVLQRFRGFGGVRIEEDVVVID
l				l		SGIELLTCVPRTVEEIEACMAGC
						DKAFTPFSGPK
5534	35902	A	5580	1	98	
5535	35903	A	5581	1	810	

SEQ ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	-	ŀ		sequence		· ·
	<u> </u>					
5536	35904	A	5582	1	861	MLKEIIDDTNKWKHIPCSWMG
		1				RISIVKMTILPKAIYKFNAVLIKI
1		l			i	PPSFFTELEKTILKFLCNEKRAS
ŀ		1		1		RAKARLNKKNKSGGITLLDFKR
1						YYSAIVTKTVWYWYKNRHIHQ
ł		1				RNRIENPEINPNTYSQLIFNKAN
1		l				KNIKWGNDTLFSKWCWDNWL
l						ATCRRMKLDPHLSPHTKINSRW
						IKDLILRPETTKILEDNIGKTLLD
1						VGLGKDFMTKNPKANARKAKI
						NIWDLIKLKSFFTAKGTVSRVN
						ROPTEWEKIFIIHTSDEGLLISRI
		1				YNELKQISKKK\TNNPIKKWAK
ļ.						DMNROFSKEDVOMANKYMKK
		ĺ				CSTSLIANLICREMOIKTTMOY
						HLTPARMAIIKKSKISRCWHGC
		l				GDQGTLLHCWWECKLVQPLW
		l				KTVWRFLKELKVELPFDPAIPL
İ						LGTHPEEKKSLCKKDTCTCMLL
		1				AAQFTIAKSWNQPKCPSVNEWI
						KKLCPRWLLSKWASA*NKWK
1		l				HIPCSWMGRISIVKMTILPKAIY
		1				KFNAVLIKIPPSFFTELEKTILKF
		1				
						LCNEKRASRAKARLNKKNKSG
						GITLLDFKRYYSAIVTKTVWY
ļ		1				WYKNRHIHQRNRIENPEINPNT
						YSQLIFNKANKNIKWGNDTLFS
		1				KWCWDNWLATCRRMKLDPHL
1						SPHTKINSRWIKDLILRPETTKIL
		1				EDNIGKTLLDVGLGKDFMTKN
		1				PKANARKAKINIWDLIKLKSFF
		1				TAKGTVSRVNRQPTEWEKIFIIH
5537	35905	В	5583	473	1694	
5538	35906	Α	5584	I	429	
5539	35907	Α	5585	572	1149	PPVSHSMTLGNSYLFAPNWTIT
					Į.	PAW/CNTLDPSEGFGWQASLSL
		l	ł		1	PSHQQFEHTCPEWLPTYSWPCK
						VGPDYLSEICQPECKQHFQESL
		1				TESSKONIYETCAIYVSSPGERIL
	ľ	l				NORFGPHGAFILVREYDDIRFS
		l				HSGPPSTCPNFPGPSYYTARESA
					ľ	YALKLRALEIIQISQSTKMQRNL
		1				GNPILPAIHOOPPO
5540	35908	A	5586	1	804	3.1.12.11.144.14
554I	35909	В	5587	1	1995	
2341	33709	In .	3301	l <u>'                                     </u>	1773	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5542	35910	Α	5588	174	1128	LLLDL*VD*SPSRPLEMRFRV*P
				1		MKRCTTLKKNYLSFLVYISRNI.
				1	İ	*NRVKAIM/VGKAEWKTIELPL
		l				PRKTVNOKOYRIPGGIAEIST II
				l		KELNNAGMVIPTTSPFNSPIWP
		1		l		VOKIDGSWRMTVDYCKLNOV
	İ					VTPIAATVPYVVSSLEQIN/TSPC
						T/WNRKRFCNRSRLLHKLLCHL
ļ		l				GHMTQQI*CFLRCQWHIGMLF
						GPEICGCTSLSGQKL/WKIFVSH
		l				AASFEWSPEQEKALQQVQAVV
					1	QAALPLGPYDPADPVLLEMSV
1		1				ADRDAVWILWQAPISESQWRPI
				l		GFWSKALPSSADNYSPFERQLL
		i		l	ł	ACYWTLVETERLTMGHQVTIPF
1		ı				ELPIMNWVFSDLSSPKMCHPQQ
5543	35911	Α	5589	1	1337	MIISIDAEKAFDKIQQPFMLKTL
		l				SKLEETASPSPVVATYTPQPML
	i	l		l	1	PSAFPPLSEEINPVLPETTVMAS
		1			ł	PEAVTRQDNVDSPQKPPPTPMF
						ASRPITRLKPRRAPSEEGIQRLK
					ŀ	KIGMVEWISHFRPTPLSMEGPE
		l				HILLTNTLLNRYVKAAPASLKS
						PLTALLFMSDLTVGTTFSQLQN
		1			İ	LNTMGIFGSSCDRSQVAALNHQ
		l				RQVPECKIVIDILNIWRIPHIGSL
						TGRVREIMVGKAKWKPLEQPP
					ľ	PRKIVIQKQYHIPGAITEISATIE
					ļ	DLKETGVVILTTSPFKSSIWPLQ
						KTDGSWRMTVNYHKLNQVET
		1			ł	PIAAAVPDVVSLLEQINTSPGT
		l				WYAAIDLVNVFFSIPVYKAHQK
					1	QFAFSWQGQQYTFTFLPQGYIN
				l	1	SPDITLVHYIDDIMLIGSSEQEV
						ANTLDLLPARVASWGVPYDQL
		_				T/GGRED*GLLHRWSCRICRHH
5544	35912	Α	5590	2	693	KIVN/QKQYHIRGGIAEISATIKD
		1		l		SKDTGVVIPTTSPFNSPIWPVW
						KTDGSWTITVDYHKLDQVVTPI
İ		l				AAAVPDVVSLLEQINTSPGTWY
			1	1		AAINLENAFFSIPVHKANQ/KQF
		l				AFSWQGQQYTIAVLPQ\VKFLG
		1	l	1		IHWFVACQDIPSKIKDKLLHLA
1		1				PPTNKKEAQCLVGLFGFWRQHI
			l	l		PHLRVLLQPIYQVTLKAAIFEW
	1			[		GPEQEKALQQVQAAVQAALPL
					L	GPYDPTDPMVLE

SEQ ID			SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hođ	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		ľ		sequence		
5545	35913	Α	5591	1	1011	MVSTPATLPSLPKPALMASWG
						VPYDQLTKEEKTRVWFTDGSA
				l		RYAGTTQKWTAVALQPLSRTS
		ŀ		l		LKDSSEGKSSQWAELQAVYLV
		ŀ				VHFAWKEKWPDVGLYTDSWA
		ŀ				VANGLAGWSETWEKQDWKIG
						DKEIWGRGMWMDLSEWSKAV
		1		l		KIFVSHVSAHQRVTSAEEEFNN
						QVDRPL/PVFTQWAHEQSGHSG
		1		l		RDGGYSWAQQT\GLPFTKADL
		l	1			AMATAECPICQQRPTLSPLYS
						TIPQGDQPATWWQIDYIGPLPS
		1				WKGQKFVLTVIDTYSRYRFAY
		1				PAHNASAKTTIHGLIECLIHCYG
				I		IPHSIASDQSIHF/TTKEVQ*WAH
						AHGIHWSYHVSHHPEAAGL
5546	35914	A	5592	7	278	SASCTAAFHHQMEVVYTRSGS
		1		1		SRS*R\PTIPVIAQWDYDHNGHG
						GRDGGYPWAQQHELPLTKADL
					1	ATATAECPICQQQRPSLSPRCGT
						IPR
5547 5548	35915 35916	A	5593 5594	63	237	
5549	35917	A	5595	2	739	HKMGHAQQHSIIKWK*YICDW
3349	33917	^	3393	12	139	ARAGPKGTT\APMASWGVLYD
						QLTEEEKTRAWFTDGSARYAG
1						TTOKWTAAALOPLSRTSLKGS
l				1		GEGKSSQWAELQAVHLVVHFS
						WKDKWPDVRLYIDSWAVANG
						LAGWSGTWKKHDWKIGDKEI
		1				WGRGMWMDLSEWPKPVKIFG
						SHVSAHQWVISAEEDFNNQVD
1		1				KMTCSVDITQPLSPATPVITQW
						AHKOSGHGGRDGGYTWAOOH
ĺ						GLPLTKTGLAMATAECPI
5550	35918	Α	5596	1	354	
5551	35919	Α	5597	3	592	
5552	35920	A	5598	126	365	QLAEPPHWLPD*KGAGFEWGP
						EQKKALQ*VQAAVQAALPLGP
l				l		YDPADPMVLVVSVADKDAVWI
		_				FHLSGSDRWRRTYRCL
5553	35921	A	5599	1	483	
5554 5555	35922 35923	A B	5600	141	1908	
5556	35923	В	5602	46	1533	
5557	35924	A	5603	61	448	WRFLGPWRIVSCWFCGWEERR
5551	33323	l^	15505	ľ.	1	EGSAFFVGIPARMSAARESHPH
				1		GVKRSASPDDDLGSSNWEAAY
				1		LGNEERKOKFLRLMGA/GKGEE
				1	1	DOKINEELESOYOHSMDSKLSG
						RYRRHCGLGFSEVEDHDGEGD
						RYRRHCGLGFSEVEDHDGE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5558	35926	A	5604	1	404	PWRIVSCWFCGWEERREGSAFF
		1				VGIPARMSAARESHPHGVKRSA
		1	1	l		SPDDDLGSSNWEAADLGNEER
		l				KOKFLRLMGAGKKEHTGRLVI
		l		l		GDHKSTSHFRTG\EDHDGEGDV
				l		AGDDDDDDDDDDPP*SPDDSES
		1				DSESE
5559	35927	A	5605	2	434	LGPWRIVSCWFCGWEERREGS
						AFFVGIPARMSAARESHPHGVK
		1				RSASPDDDFFLFAIMNGK*KIV
						NSHRCSVKAKSROOLGSSNWE
						AADLGNEERKOKFLRLMGAGK
		1				KEHTGRLVIGDHKSTSHFRTGE
	l .	ı	İ			ED*KINEELESQYOH
5560	35928	c	5606	909	1096	
5561	35929	A	5607	1	309	PQPAAMAAYIWVLIRHGESAW
		l			1	NLETSFSGWYDATLSLAGHKE
		1				AKRGGQALRGLFQVPLAPEAV
	1	1				GTVWCSWRTPCALKQL*PRPL
	1	1				KRRLRILADRHATOPRPOO
5562	35930	Α	5608	93	914	SQSVPHPQPAAMAAYK\LVLG\
						RHGESAWNLENRFSGWDDADL
	l .	l				SPAGQRGGERFAAQALQDAGY
		1		i		EFDICFTSV\QKRAIRTLW\TVL\
	l	1				DAFDQMWLASGEGLWGFNER
	1	1				HYWGS*PGLN*KQKLAAKIG*G
						PRLKI\WRRSY\D\VPPPPMEPDH
						PFYSNISKDRRYADLTEDQLPS
		ı			1	C\ESLKDTIARALPFWNEEIVPQI
	1					KEGKRVLIAAHGNSLRGIVKHL
	1					EGLSEEAIMELNLPTGIPIVYEL
		1				DKNLKPIKPMQFLGDEETVRKA
	1					MEAVAAQGKAKK
5563	35931	Α	5609	2	450	VNKAGGLIYQLDSYAP/RAEAE
	1	ı				KTFSYPLDLLLKLHDERVLVAF
						GQRDGIRVGHAVLAINGMDVN
					1	GRYTADGKEVLEYLGNPANYP
	1	1	l	I	I	VSIRFGRPRLTSNEKLMLASMF
		ĺ		I	l	HS\IKFVVLADP\RQAGIDSLLRK
	1		1			IYEIYSDFALKNPFYSLEMP
5564	35932	A	5610	1	663	
5565	35933	A	5611	1	2034	
-505	1-0/00	۲٠_	1	I	I	L

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
5566	35934	IA	5612	374	1106	IPVSERQGSDWRFFSVYVVNKA
				Ī		GGLIYQLDSYAPTGLRLEKTF\S
						YPLDLAGSS*HDERVLVAFGOR
	1	1				GRHPEWGHAVL\AINGM\DVNG
ļ						RYTADG\KEVLEYLG*PLLNYP
ŀ			ĺ			VSIRF\GRPRL\TSNE\KLMLGLP
	l	1				CFHSLFAIG\SQACLPGTREASR
						HLKILGRODTFK\LH\CYOTLT\G
	Į.	1				IKFVVL\ADPR\QAGI\DSLLRKI
		1				YEVIY\SDFALKNP\F\YSLEMPIR
ļ						CELFDONLKLALEVAEKAGTF
5567	35935	A	5613	1	336	
5568	35936	В	5614	60	2175	
5569	35937	Α	5615	2	198	
5570	35938	Α	5616	I	449	
5571	35939	Α	5617	I	771	
5572	35940	Α	5618	18	736	EAMSSKVSRDTLYEAVREVLH
						GNQRKRRKFLETVELQISLKNY
						DPQKDKRFSGT/VQVGTVLIPPS
1	1					PQCPRACPSPAGSR*AGGGHVG
						TDVLG*FRPPAPGRRGWTDPHP
						GS*NMRGGVGRPRPSPPASLRS
	1	1				QAGCW*M*TLRVRLGWLLRSQ
	ì					TLHRALGTPGLGVTCWCCPPK
						RRLKSTPRPKFSVCVLGDQQHC
						DEAKAVDIPHMDIEALKKLNK
						NKKLVKKLAKKYDAFLASESLI
5573	35941	Α	5619	24	698	EAMSSKVSRDTLYDAVREVLH
						GNQRKRRKFLETVELQISLKNY
				Į.		DPQKDKRFSGTVRLKSTPRPKF
	l					SVCVLGDQQHCDEAKAVDIPH
						MDIEALKKLNKNKKTGSRSWP
						KKYDAFLA/SQSPLIQADSPKSL
	1	l				GP\SLNKGRKSSPSLLTH\NKNM
		1	l			VAKVDEVKSTIKFPNWRRCLCL
	1		l	l		AVAVGHVKMTDDELVYNIHLA
						VNFLVSLLKKNWQNVRALYIK
		L_				SPMGKPQRLY
5574	35942	A	5620	I	843	

SEQ ID NO:	of peptide sequence	Met hød	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown,  *=Stop codon, /=possible nucleotide  deletion, \=possible nucleotide insertion)
5575	35943	A	5621	3	1215	LLIMADPRDKALQDYRKKLLE HKEIDGRLKELREQLKELTKQV EKSENDLKALQSV\GQIIVGEVL KQLTJEEKFIVKATNGFRYVVG GARQOL-QKVSLKPGTRIVALJD MTTLTI\MEDILPR\(\text{LV}\) PLYVYN MS\(\text{HEDPGINVSYSEIGGLS:\text{RG}\) TOUR\(\text{LY}\) PLYP\(\text{QY}\) PGVVG IIPPK\(\text{RG}\) LIX\(\text{LY}\) PSYFQRVG IIPPK\(\text{RG}\) LIX\(\text{LY}\) PSYFQRVG IIPPK\(\text{RG}\) LIX\(\text{LY}\) PSYFQRVG IIPPK\(\text{RG}\) LIX\(\text{LY}\) PSYFQRVG IIPR\(\text{LS}\) LIX\(\text{LY}\) PSYFQRVG IIPR\(\text{LS}\) LIX\(\text{LI}\) RAD\(\text{LPG}\) IIPR\(\text{LE}\) LIX\(\text{LI}\) RAD\(\text{LPG}\) IEMDEIDAIGGRRFSEGTSADRE IQRT\(\text{LMELINQM}\) DGFDTLIRV KMTMATNRPDTLDPALLR\(\text{LPG}\) LDR\(\text{LI}\) HIDLP\(\text{RQ}\) ADLDIX\(\text{LI}\) LIX\(\text{LI}\) GADLR\(\text{LY}\) CTEAGMFAIRADHD FYSTGKTSLKAV\(\text{RV}\) ADSKL ESKLD\(\text{KVP}\)
5576	35944	Α	5622	104	173	
5577	35945	A_	5623	1	1140	
5578	35946	A	5624	1	528	
5579	35947	A	5625	1	1083	
5580	35948	A	5626	I	471	
5581	35949	Α	5627	1	2322	
5582	35950	Α	5628	1	678	
5583	35951	В	5629	213	1477	
5584	35952	Α	5630	2	339	FGLHKWGLGLEASSPCGPLTPS YLGFPRPHPGTLGLGRFWPFLA LQSLSETPSHARMPRVTVARTS PETLEISPLRAAT*NHRSSGHTC FRERMLRVSCRLSLDLSSSWVR
5585	35953	Α	5631	1	783	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first codon for peptide	eodon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	or peptide sequence	determin, v-possime nacicottue insertion)
5586	35954	A	5632	92	2746	ASRMTVLQEPVQAAIWQALNF
						YAYRDAVFLAERLYAEVHSEE
				l		ALFLLATCYYRSGKAYKAYRL
				1		LKGHSCTTPQCKYLLAKCCVD
						LSKLAEGEQILSGGVFNKQKSF
	ŀ					DDIVTEFGDSACFTLSLLGHGH
				l		VQTERAAKGTAFSPKRLCLHT
				İ		PAWTPLEPLVEIGERPLPHQTFN
				i		FTS*RNFANCLHTSGTKQVTN\
				I		HVFSHRQPETVLTETPQ\DTIEL
				I		NRLNLESSNSKYSLNTDSSVSY
				l		DSA VISP\DTVPLGTG\TSILSKP
				I		VQ\NKPKTGRSLLGGPAALSPL
		ŀ		1		TPKFWGFLPIRKPP\SPG\DGS\Y
	1					LQNYTNTPPVIDVPSTGAPSKK
	1			1		TFRVLQSVARIGQTGTKSVFSQ
				1		SGNSREVTPILAQTQSSGPQTST
	1			1		TPQVLSPTITSPPNALPRRSSRL
				]		TSDSSTTKENSKKLKMKFPPKI
				1		NRKTKSKTNKGGITQPNINDSL
	l					EITKLDSSIISEGKISTITPQIQAF
						NLQKAAAEGLMSLLREMGKG
		1				YLALCSYNCKEAINILSHLPSHI
	ŀ					YNTGWVLCQIGRAYFELSEYM
				1	l	QAERIFSEVRRIENYRVEGMEI
	İ					STTLWHLQKDVALSVLSKDLT
						DMDKNSPESGTQRGRESPRMC GADSQIEKSQSSYFIQDLSRFDY
				1		VKFAVVTKIRAWCAAGNCFSL
						QREHDIAIKFFQRAIQVDPNYA
					l	YAYTLLGHEFVLTEELDKALA
						FRNAIRVNPRHYNAWYGLGMI
5587	35955	_	5633	260	678	GEFSIFFWVWN*LLLWHOETFS
338/	CCACC	A	5033	200	070	I*NLFSSH*TSITYQATEEGFDFI
	İ			i e		QMKLIHFGDSIFIYLKLLILNRK
						P**EAAISI*V*TWRSRFSHFQLF
		1				*HQTQVTNHSWFTEAR*LTDL
						KSKSPTIPCSRFKANTLF**SDP
5588	35956	A	5634	I	1452	
5589	35957	A	5635	2	1563	
5590	35958	A	5636	1	444	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amine acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peplide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5592	35960	A	5638	2	1721	RSREAAAVAAAAATTAFGCRI
3372	33900	1	3038	1	11/21	WNPCAALTMKQSSNVPAFLSK
		1		1		LWTLVEETHTNEFITWSONGOS
		1		İ		FLVLDEORFAKEILPKYFKHNN
		1		1		MASFVRQLNMYGFRKVVHIDS
		1				GIVKQERDGPVEFQHPYFKOGC
		1		1		DDLLENIKRKVSSSKPEENKIRG
		1				EDLTKIISSAQKVQIKQETIESRI
		1			I	SELKSENESLWKEVSELRAKHA
				1		QQQQVIRKIVQFIVTLVQNNQL
						VSLKRKRPLLLNTNGAQKKNL
						FOHIVKEPTDNHHHKVPHSRTE
				1		GLKPRERISDDIIIYDVTDDNAD
		1				EENIPVIPETNEDVISDPSNCSOY
				1		PDIVIVEDDNEDEYAPVIQSGEO
		1				NEPARESLSSGSDGSSPLMSSA
		ı				VOLNGSSSLTS\EDPV\TMDGFP
l	1	1				FGMDNIQSFWGRVEL\LDY\LDS
		1		İ	İ	IDCSLEDFQAMLSGRQFSIDPDL
		1				LVDLFTSSVOMNPTDYINNTKS
l		1				ENKGLETTK\NNVVQPVSEEGK
		1				ENLKSKP\DK\QLIQYTAFPLLAF
1		1		l .		LDG\NPASSV*TGRGTTASFRKF
		1		l .		CPL*DKPIEVDELLDSSLDPEPT
		1		1		QSKLVRLEPLTEAEASEATLFY
		1				LCELAPAPLDSDMPLLDS
5593	35961	Α	5639	2	251	
5594	35962	Α	5640	70	297	QLRSPLKWKKAQRQPLAIAHV
		1		1		LLLRPRKKRQNGFFTVRYARLL
		1				STLPRSWRR\KQWY*AQNHVRS
5595	35963	A	5641	3	985	PEWKWHYQSLS
5596	35964	A	5642	1	3501	
5597	35965	A	5643	i	1752	
5598	35966	c	5644	1	879	
5599	35967	A	5645	21	519	LHIPVRTLSCRFVGVCWRSTPG
		1				PVCLGISSGGCRTVDIAALQLW
l		1		İ		LRGLALPEQLLR VDPHPQACRR
	1	1				LPREPP\GPGQTFGTREPPQAVS
		1				TKEASSSNLHAPERTVAGLTFT
		1				TEQVRALEGVFRHHQYLGPLE
l						RNWLAREMQLS\RSR*KPGFKI
		L.,				AG*NTNGKCRTPS
5600	35968	A	5646	90	2401	
5601	35969	A	5647	776	1018	
5602	35970	В	5648	1	1296	
5603	35971	Α	5649	I	1257	
5604	35972	A	5650	731	4841	
5605	35973	A	5651	325	9497	
5606	35974	A	5652	1	322	
5607	35975	Α	5653	1	819	L

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5608	35976	Α	5654	56	251	
5609	35977	A	5655	149	701	
5610	35978	Α	5656	3	415	
5611	35979	A	5657	3	467	AIASPRAAGIRHELTSTMAAGK NKRLTKGGKKGAKKKAV/DNII NIGKTLVTRTQRTKIASDGLKG RVFEESLADLQND\TDGYLLRVI *VAFTTERTNQI/REVFNKLIPDS IGKDIEKACQSIYPLHDDFARK
5612	35980	A	5658	2 .	418	VKMLKKPKFELRKLMELHGEG PRVRADGKNFRLTKGGELGAR NKVVDPFSKKDWYDVKAPAM
						FNIRNIGKTLVSRTQGTKIASDG LKGRVFEARLADLQNDEVAFIK CKLITDDVHGKNCLTIFHGMDL TRDKM'CSLGKKWQTMIEAHV DVKTTDGYLL
5613	35981	Α	5659	3	121	
5614	35982	Α	5660	I	237	
5615	35983	A	5661	25	967	FSPAAGIRHEÖSLTSTMAVGKN KRLTKGIGKRGSIKKKVVDPFP KRÜDWY*RKKHPLMFHIYKNIG KTLVTQDPKGPKIAISDGLQGF VCLKVSLADLQINDEVASRKG RLITEVCFRGKNIN PLTSRIGN DLYPVTKMCSHGQKNWQTMI DSSR*MFKTNPMGYLALRLFLC /VGFT*KNRNQFRLRKAPPYAS ATQQVPPKSRKKMMEIMTPR GARQNDLEKKWVNKLIPRQAL GKDIRKGPAQSYFIPLHIDVLRL EKLKLLEGSPK*IGESSLGASM GGRAVVPGKSHLGTQTGAKVG TSLMGYEPPYPRILV

NKLGIDGTYLKITRÄLYDK.PY NIILMOGKLEAPPLETGTROG LSPLLFNIVLEVLAQAIRQEK KGIQLGKEEVKLSLFADDMI LENPIYSA,OKLLKLISNYSKY YKINVQKSQAFLYTNNRQTE IMSEPPTIATKRIKYLGIQLT VKDLFKKYKPLINKIKEDTI WKNIACSWIGRINIMKMAFP WELNNENTWTQEGEHHTLC VGWGKRGIALVDIPNVNDI MVLEVLARAIRQKKEIKGIQI KEEVKLSLFADDMIVYLENS SAQNLKLISNFSKVSGYKINV KSQAFLYTNNRQTESQIMSE FITATKRIKYLGIQLTROVKD KENYKPLLKEIREDTIKWKY CSRIGRINIMKMALPKVIYRI DIPIKLPMTFTELEKTTLKFI NQKRACIAKTILSKKNIAGGI PDFKLYYKATVKTAWYW NRDIDQWNRTEASEVTSHIY LIFYKPDKNKKWGDSLFNK CWENVLAICRKLKDPFLIP	SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
MATKAKYDKWDVIKLKSFC KETTIR VSRQPTEWEKIFAIYI DKGLISRIYKELKQIYRKKTI	5616	35984	A	5662		2142	MIILIDAEKAFDKIQQFFMLKTL NKLGIDGTYLKITRAIYOKPTA NKLGIDGTYLKITRAIYOKPTA NILINGOKLEAFPLKTGTROGCE LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESG WESPFFITATKRIKVLGIGLTS VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTVTQEGEHHTLGFV YGWGKRGGIAL VDIPNVNDKL MYLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESGIMSEP FITATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILFKVIYRRN DIPIKLPMTFFTELEKTTLKFIW NQRRACIAKTLSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIOQWNRTEASEVTSHIYNH LIFVKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KHSRWIKDLNVPRTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLKSFCTA KETTIRVSRQPTEWEKIFAIYPS DKGLISRIVKELKQIYKKYTNN DKGLUSRIVKELKQIYKKYTNY DKGLUSRIVKELKQIYKKYTNY DKGLUSRIVKELKQIYKKYTNY DKGLUSRIVKELKQIYKKYTNY DKGLUSRIVKELKQIYKKYTNY DKGLUSRIVKELKQIYKKYTNY

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Step codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
5617	35985	A	5663	1391	2742	KKRESSLTHVMRPASF*YOSOA
2011	00700	Γ.				ETQQKKRILDQYP**TLMQKSSI
		1			ĺ	K/YLAKRIQQHIKKLIHHDOVGF
ŀ		1			l	IPGMQGWFNIRKSINVIQHINRA
		l				KDKNHMIISIDAEKAFDKIQOPF
ŀ		1				MLKTLNKLELEETTVKFIWNQ
l		1				KRAHIAKSILSQKNKAGGITLR
		l			ŀ	DFKLYYKATVTKTAWYWYQN
1						RDIDOWNRTEPSEITLHIYNYLI
		1			1	FDKPEKNKQWGTDSLFNKWC
		1				WENWLAICRKLKLDPFLTPYTK
l		1				INSRWIKDLNVRPKTIKTLEENL
					l	GITIQDIGMGKDFMSKTPKAMA
l						TKAKIDKWDLIKLKSFCTAKET
		l				TIRVNRQPTKWEKIFTTYSSDK
		l				GLISRIYNELKQIYKKKTNNPIK
		ļ	l		!	KWAKDMNRHFSEEDIYAAKKH
		l	l	1	1	MKKCSSSLAIREMQIKTTMRYH
1						LTPVRMAIIKKSGNNRHAPFSIH
1						THIMFGSLYLQIQKDLSILGFW
		_				YPRGILEPIY
5618	35986	A	5664	1	1910	MTHNHHHTHTHIVHHTINIVIT
		1				TTILTTVIISSTIIIITIFVFETGAI
						KLEIRIKKLTQNRSATWKLNNL
					1	LLNDYWVHNEMKAEIKMFFET
		1				NENKDTTCQNLWDTFKAINKID
1						RPLARLIKKKREKNQIDAIKND
	İ					KGDITTDTTGIQTTIREYYKHLY
		l				ANKLENREEMDKFFDTYTLPRL
		l		1	1	NQEEVESLNRPITGSKIEEIINSL
						SIKKSPGPDGFTAEFYQRYKEE
		l			i	LVPFLLKLFQSIEKEGIILNSCCE
		l				ASIILIPKPGRDTTKKENFRPISL
i		l				MNIDAKILNKTLANRIQQHITK
		1				LIHHVQVGFIPGMQGWFNIRKS
		l				INNWKKTTLKLIWNQKRACITK
		1				SILSQKNKAGGITLPDFKLYYK
			l			ATVTKTAWYWYQNRDIDQWN
						RTEASEIIPHTYNYLSFDKPDKN
		1	l	İ	l	KKWGNNSLFNKWCWENWLAI
			l	1		CRKLKLDPFLTLYTKINSRWIK
			l	1		DLNFGTETIKTLEENLGNTIHDI
				1		GMGKDFMSKTPKAKATKAKID
1		1	l	1		KWDLIKLKSFCTAKETTIRVNR
		1	I	1		QPTEWEKIFAIYPSDKGLISRIY
1		1	l	1		KELKQVYKKKTNNPIKKWAKD
				1		TNRHFSNEDIYAANRHMKKCS
1		1	1	1		SSLAIREMQIKTTMRYHLAPVR
				1		MTIIKKSGSNRQ/W*ASGHVRC
						·

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5619	35987	A	5665	1	2460	MPHAGHARSPGHTLIKLAEWW
						MSRWMEWNPGFPLSIDAKCHK
		1				DLPRDIQFDSEKGVDFVLNYSK
						ALNQEEVESLNRPITGSEIEAIIN
		İ				SLPTQKSSGPDGFTAEFYQRYK
						EELVPFLLKLFQSIEKEGILPNSF
					ļ	YEASIILIPKPGRYTHKKNNFRP
						SLMNIDAKILNKILANRIQQHIK
						KLIHQDQVGIIPGMQSWFNIHK
		1				SINVIQHINRTKDKNHMIISIDAE
		1			1	KAFDKIQQPFMLKTLNKL\GIK
		1				YLRIQLTRDVKDLFKENYKSLL
						NEIKEDTNKWKNIPCSWIGRMN
						IIKMAI/LPKVIYRFNVIPIKLPMT
1		1			1	FFSELEKSTLKFIWNQKRARIAK
		1			1	TILSQKNKAGGIMLPDFKLYYK
	İ	1				ATVTKTA WY WY QNRDIDQWN
		ı			1	RTEPSEMTPHIYNHLIFDKPDKN
						KQWGKDSLFNKWCWENWLAI
					1	GRQLKLDPFLTPYTKINSRWIK
						DLNVRPKTIKTLEENLGNTIQDI
						SMGKDFMSKTPKAMATKAKM
						DK WDLIKLKSFCTAKETTIRVN
		l				RQPTEWEKNFAIYSSDKGLISRI
		1				YKQLKQIYKKKTNNPIKKWAK
		I				DMNRHFSKEDVYAANRHMKK
		1				CSSSLAIREMQIKTIMIYHLTPV
		1				TMAIIKKSGNNRCWRGCGEMG
		1			l	TLLYCWWDCKLVQPLWKTLW
	1	1				QFLRDLELGIPFDPAIPLLGIYPK
		1				DYKSCCYKDTCTPKLARDDQI
						HILKQHRRKELETRQKQYRAW
5620	35988	Α	5666	689	1909	LIAYQPKKSRTRWIHNQILPERI
	İ					KYLGIQLTRDVKDFLKEKYKPL
		1		i .		LNEIKEDINKWKNIPCSWIGRIN
		1				LVKMAIL/PQAICRKLKLDPFLT
		1				TYTKINSRWIKDLHVRPKTTKT
		1				LEENLGNTIQDIGMGKDFMSKT
		ı				PKAMATEAKIDKWDLIKRKSFO
		1				AAKETTTRVNRQPTDWEKMFA
		ı			ł	IYSSDKGLISRIYEELKQIYKKK
						TNNPINKWAKDMNRHFSKEDI
		1				YAANRHMKKCSSSLAIREMQIK
		1				TTVSPFAAQWVSQRYGK WQEA
		1				HPSNNDGKGYRGKPRFQSLSD
1	1	1			l	VHGPQDQKKIIKESALPPTPTFI
		1				NILMNAKTIENGQFPYLLNALK
	1	1				QQQPHDAENLFTWGKENAAIV
		1				SPCIEVSAALSQWKVPAWPQRS
	1	1				GIPNRILRSPIPGLGSWVAFLDL
L	1					VWVRGDPTALK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide lucation of first codon for peptide sequence	Nucleotide location of tast codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide detetion, \=possible nucleotide insertion)
5621	35989	В	5667	ı	1962	
5622	35990	В	5668	I	1851	
						IHHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHMIISIDAEKA FDKIQQLFMLKTLNKLGIDGTY FKIIRAHYDKPTANILINGKKLEA PLKTGTRQGCPLSPLLFNILLE VLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LKLKISNFSKVGYKINVQKSQ AFLYTINNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMFFFELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF
						IL YYKATVTKTAWYYQNBU DQWNRTQPSEITPHINYLYLIFD KPDKNKQWGKGSLFNKWCWE NWLAICRELKLDPFLTPYTKIN SKWIKDLNYRFKTTKTLESNLG TIQDIGMGMDFMSKTPKAMAT KOKIDK WDLIKLK SFCTAKETT IR VNRQPTKWEKIFITYSSDKG LISHIYNBLKQIYKKTNNPIK MXKCMSPISLAIREMQIKTTMRYH LTPWRMAIKKSGNNRCWRG GEIGTLLHCWIWINWMKKTWH IYTMEYYASIKKNEFMSFAGA*
5624	35992	Α	5670	2	1967	

668

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5625	35993	Α	5671	1039	2272	KKRESSLTHVMRPASF*YQSQA
						ETQQKKRILDQYP**TLMQKSSI
						K/YLAKRIQQHIKKLIHHDOVGF
ŀ						IPGMQGWFNIRKSINVIQHINRA
						KDKNHMIISIDAEKAFDKIQQPF
ŀ						MLKTLNKLELEETTVKFIWNQ
				1		KRAHIAKSILSQKNKAGGITLR
				1		DFKLYYKATVTKTAWYWYQN
l						RDIDQWNRTEPSEITLHIYNYLI
		ļ				FDKPEKNKQWGTDSLFNKWC
1	Ì					WENWLAICRKLKLDPFLTPYTK
		ĺ		i		INSRWIKDLNVRPKTIKTLEENL
		l				GITIQDIGMGKDFMSKTPKAMA
		1		1		TKAKIDKWDLIKLKSFCTAKET
						TIRVNRQPTKWEKIFTTYSSDK
l	l	l				GLISRIYNELKQIYKKKTNNPIK
l	1					KWAKDMNRHFSEEDIYAAKKH
		Ì			ŀ	MKKCSSSLAIREMQIKTTMRYH
						LTPVRMAIIKKSGNN
5626	35994	Α	5672	I	3477	
5627	35995	A	5673	1	2814 2093	
5628 5629	35996 35997	A	5675	1	2724	
5630	35998	A	5676	1	4680	MDKFLDTYTLPRLNQEEVESLN
3030	33990	^	3070	'	4080	RPITGSEIVAIINSLPTKKDPGPD
		l				GFTAEFYORIKYLGIOLTROVK
						DLFKENYKPLLKEIKEDTNKW
				į.		KNIPCSWVGRINIMKMAILPKVI
		1				YRFNAIPIKLPMTFFTELEKTTL
		1				KFIWNQKRARITKSILSQKNKA
		l			İ	GGITLPDFKLYYKATVTKTAW
İ		l				YWYONRDIDOWNRAEPSEIML
ŀ		l				PIYNYLIFDKPDKNKQWGKDSL
		l				FNKWCWENWLAICRKLKLDPF
		l				LTPYTKINSRWIK
5631	35999	В	5677	1	1989	
5632	36000	A	5678	1	2784	
5633	36001	В	5679	1	3573	
5634	36002	В	5680	1	2630	
5635	36003	Α	5681	5339	10577	
5636	36004	A	5682	1	873	
5637	36005	Α	5683	1	672	
5638	36006	Α	5684	1	435	L.,

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ		sequence		
5639	36007	Α	5685	1	1011	MVRFGDELGGRYGGPGGERA
						RGGGAGGAGGPGPGGLQPGQR
1		ŀ				VLYKQSIAQRARTMALYNPIPV
		Į.			ŀ	KQNCFTVNRSLFVFSEDNVVRK
1						YAKRITEWPPFEYMILATIIANC
						IVLALEQHLPDGDKTPMSERLD
						DTEPYFIGIFCFEAGIKHALGFV
						FHKGSYLRNGWNVMDFVVVL
l						TGRKAGLGCCGSGVESGGWGD
		l				RSSSPAMEQSRMENDFDELTEV
						GFRKSVITNFSELKE\DVRTHRK
	ļ					EAKNLEKRLDKM\VNRINSVEK
		l				TLNDPMELKTMARELCDACTS
					1	FSS*FNQVEEKVSVIEDQMDEM
						K*EEKFREKRVKRNEQSLQEIW
					İ	DYVKRPNLRL
5640	36008	Α	5686	I	1539	
5641	36009	Α	5687	I	756	MDDPRLNVKPLTESLETYSGKS
						KGLEGDVITDSKLNDCRCPSGT
	İ			l	1	KLPEEGLGSNICCSAIFAVLOPL
						LVIPROTGSGVDHQQTPTDLRM
i i					1	TVRRKMNKOKGIASTSTKRTK
						KDIHTKTPSVCHQHQRPKDCSP
					i	SPATEOSWMENDLEELTEIGFR
					i	RSVITNFSELKEDVRIHHKKAK
1						NLGKRLDEWLTRINSVEKTLND
	i					LMELKTMARELHDSCTSFNSRS
						NOAEEKVSVIEDOFNEIKREEK
1						FREK\RVKRN
5642	36010	Α	5688	1	1008	MVRFGDELGGRYGGPGGERA
						RGGGAGGAGGPGPGGLOPGOR
				l		VLYKOSIAORARTMALYNPIPV
				l		KONCFTVNRSLFVFSEDNVVRK
						YAKRITEWPPFEYMILATIIANC
						IVLALEOHLPDGDKTPMSERLD
						DTEPYFIGIFCFEAGIKIIALGFV
						FHKGSYLRNGWNVMDFVVVL
1	1	ĺ	1	1		TGRKAGLGCCGSGVESGGWGD
1	l	l		I		RSSSPAMEOSRMENDFDELTEV
						GFRKSVITNFSELKEDVRTHRK
						EAKNLEKRLDEWLTRMNSVEK
1	l	ĺ	l			TLNDLMELKTMARELRDACTS
-		l		1		FSSQFDQVQEMVSVIQDQISEM
		l				KREEKFREKRVKRNE/QSLQ*I
	l	l	l	İ		WDYVERPNLRL
5643	36011	A	5689		672	WDIVERFINERE
5644	36012	A	5690	1	807	
5645	36012	A	5691	i -	1617	
2042	20012		12021	1	1017	L

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	"=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				,		
5646	36014	Α	5692	1064	1893	LLEGSININKKDIYTKTQSVGRQ
						HQRPKVDKTTKMGRNQNRKA
		l				ENSKNQSASSPPKDC\SSSPAME
						QSWMENNFDELTEIGFRRSVIT
						NFSELKEDVQTHCKEAKNLKK
		1				RLDECLTRINSVEKKTLNDLME
						LKTMAQELHDTCTSFNTQFDQ
						VEERVSVIEDQINEIK*EEKFRE
		l				K\RVKINE*SCQEIWD*VKRPNI
		l				HLITVPESDGEKGTKLENTLQDI
		1				IQENFHNIARQANIQIQEIQRTA
		1				QRYSSRTATPRHIIVRFAKVEM
						KEKVLRAARKKG
5647	36015	A	5693	3	620	EAGWLLLSSVDEVMKENDELR
				1	1	DSISQLQKQILSLKSAKIALTESL
1		1				ISFRERAEIVEKQTQALIM*VAD
				1		LQQGNDQTFQGLLDTGSELTLI
						PGDPKHHCGPPGPKVRAYGDQ
						VINGVLAQVQLIVGPVGPWTHP
		1				VVISPVPECVIGIAILNSWQNPHI
ľ						GSLTGRVRAIMVGISWQGQQY
						TFTVLPQRYINFPALCHKTAKR HTARR
5648	36016	A	5694	1	1098	HIARK
5649	36017	A .	5695	2	563	IIRRAVFRWFWG*RSWGLNMIR
3049	30017	ľ`.	3093	1	303	PONTKOSNSNCLEKTOSPWCEL
						FKELYKINAFDTPDSLLMRGNE
		ŀ				FSDPIHHTFDHMWRTKEHNEA
		i				GWLLLSSVDKVMKENDELGDS
						ISQLQKQILSLKSAKIALSESLIS
		[				CRERAEIVEK*T*ALIMLVADL
1						Q*KVHAQPHHAQPRQVSTVKV
						RALIVLOEVTDP
5650	36018	A	5696	I	499	FVLVDVNNMWHRYASMLYER
	İ					RLLIICSKLSTLTACIHGFAAML
		1				YPMYWQHVYI\PVLPPHLLDYC
						CAPMPYLIGIHLSLMEKVRNMA
		ľ				LDDVVILNVDTNTLETPFDDLQ
		ŀ			İ	SLPNDVISSLKNRLKKVSTTTG
		1		1		DGVARAFLKAQAAFFGSYRNA
						LKIEPEEPITFCEEA
5651	36019	Α	5697	1	795	
5652	36020	A	5698	103	3531	
5653	36021	A	5699	1	2073 901	
5654 5655	36022 36023	A	5700 5701	148	639	
5656	36024	A	5702	148	318	REYGTPOEOLNLALLTLNFLSL
1000	30024	l^	3702	Ι.	310	PKGOMLSAAEOHLOKPAAKTE
		1				A/GRMIWORDPITKIWEIGKIIT
		1				WGRGYACVSPGONHOSVWIPS
		1				RHLKSCHGPDAKEEIPGGS
	1	i		1		TOTAL DARKELII 003

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ 1D NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5657	36025	A	5703	1	612	PITEPIKHITDIPYNSEGQAIVER MNLSLKQQLQKHKKGGK/SKD YGTPHMQLNLALLTLNFLSLPK GQILSVAEQHLQKPAAKTEAEQ CLVWWRDPITKS*EIGKITWGK GYACVSPGLTQOPIWIPSRHLK PYHEPDAEEEIPGGSRGPPPPV DSHVETDAEEEPIGHEGHLSNT ATHLGTDQEAVTAGGRKPEES KTTSINK
5658	36026	Α	5704	2	791	
5659	36027	A	5705	2301	2620	DGQQLIALHRLALRELQQAGH AGLPQQAKILFDGGSEIGKIRGL QRPRAKNRLSGRGPLREPSPK*F FGVQGRKTLNRTLKGAPH*NL AAKAGKPLSPCTSGRIRM
5660	36028	A	5706		1010	INDDIPOEAGRYRHNOAYAYSI QOGDAEDDDERIVRFHTRVTV DSDTLASDAARLTCRIEGLGNQ GSDLVLYGTSTPKNLLWVRVH VOGHRDDRFFAFDVWSPRSLI VDSCSKLEQHSTLSRAILLIYKG FCRFRNHIQTGSFPAGANQRGP LAATLSGFGGEGGSAVARLTGE KKNHPGAQYANRLSPRVGRFN AAGTTGFPTGKRAVSATQLMD FADFGTTIKQDFRLLQQTSVDR LLQLSQGQANVQQFIDEGNYTS GDNHTLRDPHYVEDKGHKYLV FEANTGTENGYQGESLFNKA YYGGGTNFFRKSQKLQSAK KRDAELANGALGHELNNDYTL KKVMKPLITSNTVTDEIERANVI FKMNGK WYLFTDSRGSKMTU GINSDIYMLGYVSNSLTGPYK PLNKTGLVLQMGLOPNDVFTFT SYSHFAVPQAKGNNVVITSYMT RGSSR'RQRP*IPCIRSTGMRK IPRSKNLYLTKRTAAARTSS VKKARSFSRALKNAMLS*FKTAP
566 I	36029	В	5707	1	1149	
5662	36030	В	5708	55	3947	
5663	36031	В	5709	4	885	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5664	36032	Α	5710	461	1560	SLQTRDLPISEPPSNRIFACWGK
	i					PAWTACCNSLRARR*RAISCCP
			<b> </b>			SH*KRIPRRRIFI*PKRTTAAART
	İ					SSVKKARSFSRALKNAMLS*RT
						APSVS*S*IMITH*KK**SR*SLO
						TRDLPISEPPSNR\FSPAGANOR
ŀ						GPLAATLSGPGGEGQSAVARLT
	ŀ					GEKKNHPGAQYANRLSPRVGR
ļ						FINAAGTTGIPDWKAGSERNAI
						NGAIALIEGFRPLTLEPSSLIVNS
	ŀ					CSKLEOHSTLSRAILLIYKGFCR
			٠ ،		ļ	FRNHHOTGFSPAGPNORGPLAA
	1					TLSGPGGEGQSAVARLTGEKK
						NHPGAQYANRLSPRVGRFINAA
	1					GTTGFPTGKRAVSATOLM
5665	36033	В	5711	1	1458	
5666	36034	В	5712	1	3573	
5667	36035	Α	5713	606	1005	GGMLCGTLSGPDGEGOSAVAR
						LTGEKKHPRGDQ*QKAPLLAR
			<u> </u>			W/RNPLMOLAO/PDFPTGKRAI
					1	DTHRSVSHAHIJITJHSSTLSSDIS
1						HTDAPNTSSNNYVIAITSPSDTA
		1				PTSRTPLHRIHHTTPIPIATLARP
5668	36036	В	5714	I	1566	
5669	36037	С	5715	29	2314	
5670	36038	Λ	5716	597	1384	ISYTVPEALSARSNPA ACQHAS
						CRPAACPVASVGSPRQPAPGGA
					1	GGHRHWPRRRWRLRQRPRPSA
ŀ	l					PGRPRRPRPRPRRHRRRPRPHP
	ŀ					HHAPPPRPSCAETRS\RRGGGRR
		ŀ				PLPRPLPPGAAGAGHREVGDK
		ļ.				AGAAGCGRRVVALAA\PVSPPS
		l				SPSSPSPSLLSAAVGVAGCFSAE
		l				LSDSRRLLAPGGEGPLARSPAR
	l	ŀ				CDPAAGSACPAGWSSRQRSRC
						ELMCAAGISCWHTGHCTWCSL
						SFMPLVLMILAASFRPVAVSSH
5671	36039	В	5717	1	3873	
5672	36040	C	5718	356	784	
5673	36041	Α	5719	1303	1664	KRRDEIIPCVLSKQLLVTFITCR
		1				ASCINESANARGEAVCVLGAR
		1	l			VV/SSFHQ*DGQQLIALHRLALR
		l		1		ELQQAVHAGLPQQAKILFDGGS
				1		EIGKIPYKSKE*PENRLSVVPVW
1	1			1		EQESTLASV

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	bod	in USSN	location of first	codun for last amino acid	*=Stup codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5674	36042	Α	5720	453	915	TVSRWAMLEHILLFSREPSNKE
				l		PET*AHSM*ADDKRFAAYKKK
		ĺ				TKGGTERWDKYGRRPANGIRT
						GENNAKTEHLRDRDQKR/PREI
						ERAR*TTEITEQEGSG*GEPVEG
		l				MRKRRAQAWSRRKSTGSQTET
		ĺ		l		RSVRVTRVGLKTASESRRIRTM
			l	l		EQN
5675	36043	В	5721	319	1469	
5676	36044	В	5722	164	3112	
5677	36045	Α	5723	I	1102	MRWTPGHEITKALQTFQRYTG
						QHVHRIGMAERMWCDRNRER
						HTVSSSGGNRLPNPEHFEAFQS
						VAQCTYNQTVQLDITAFLKTV
						KKNKHKFYPAFIHILARLMNAI
		İ		i		PEFRMAMKDVDSCSKLEQHST
		l				LSRAILLIYKGFCRFRNHHQTG
						SPAGANQRGPLAATLSGPGGE
						QSAVARLTGEKKNHPGAQYAI
						RLSPRVGRFINAAGTTGFPTGK
						RAVSATQLIYRELFPQPLVQLD
						PCSVPCMQPPTSPKSRAWVSDI
						ALLEFQKKKEMEKKKEKERK
		ŀ				ELQGGRGRRRGGGWGKGRER
		l	i			GGRGKKRRGGGEAIRDAEKAG
						RLPHPDMEIRGRVEQRVGYTIE
	1	l			}	QINHMRDVFGTRLRRAEDVFP
	1					VIGVAAHKGGVYKTSVSVHLA
						QDLALKGLRVLLVEGNDPQG1
	1					ASMYHGWVPDLHIHAEDTLLF
		l				FYLGEKDDVTYAIKPTCWPGL
						DIIPSCLALHRIETELMGKFDEC
						KLPTDPHLMLRLAIETVAHDYI
						VIVIDSAPNLGIGTINVHPAWG:
		1				AISLLEYSPGHLAGFVASIPAPL
						QLVPRWDTKPVLEDASASSRF:
						IPQRNPTHLHPTTSFPSCNPDTV
						DAWMRFLITWCLYTSPYSTLM
						GELFPFYQGMLLESTKQGSQVI
			İ	l		KVFVWTLVPNWNNTQPYSRAI
	1	1		1		LLIYKGFCRFRNHHQTGFSPAG
		_				ANQRGPLAATLSGPGGEGQSA
5678	36046	В	5724	90	6258	
5679	36047	Α	5725	837	1485	
5680	36048	Α	5726	1	2993	
5681	36049	A	5727	1	123	
5682	36050	Α	5728	I	960	
5683	36051	Α	5729	507	755	NKRGYKQMEEHSMLMGRKNO
		1		l		YRKNGHTAQGNL*IQCHPHQA
						TNDFLHRIGKNDFQVHMEPKK
	l					SPHRQVNPKPKEQSWRHHAT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequenec		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5684	36052	A	5730	274	882	PDQVDRGGAHWQTDADDPWL
		ľ.				ADHLQHCQRCGEILRHYSGGIR
						GNVSAVKCAEHHVPAFARLRN
		1				POCGDFORLDYRLFDSPGVKRR
		l				EL*TAYRFCHVAP*LMDLRSG
						WAAGAVYRYQSH*FTADRLRS
						VDMDEAGNHHSQQT\SQDQKI
						KORTFSLISGS*TTRTHGHREGN
		l				ITHRGLSRPNTARILCASKAHLG
			1	ļ		LPLRSSLP
5685	36053	Α	5731	114	329	
5686	36054	C	5732	1	1983	
5687	36055	С	5733	1	588	
5688	36056	Α	5734	1	597	
5689	36057	A	5735	1	721	MTSYNEQNKKPVTDPNEMAIH
ŀ				l		EDSNQEFKIAVVNETQRSPRSSP
				ļ		TEHLMTPPPLPTREQQPPLTVIF
				1		HYLPKSYKTAPPLSPFPDSLFGL
		1		ŀ		SQPAPRDMDEAGNHHSQQT\K
						QEQKTKHCMFSLTSGS*TMRTH
				İ		GHREGTVIHRGLLGQFSQQLIN
						KSEFSNTVCREKSGRVLQVNM
				1		ESPL*MIQDALQDQTTPKGPITV FL*LFYLDHLLRSSHKVASYLST
				1		ESRSRGSITVLFIRCSEP
5690	36058	A	5736	417	696	DRNRKANTACFOHSQVGVEO*
3090	20020	<u> </u> ^	3730	7''	0,0	EHMDTGKV*SI*YGNYEHTSTC
						ERMEIOKATTEHLNL*S*SGSFL
				l		RFTWKMLQFSKISRSFYQVLKH
		ı		İ		OOKIM
5691	36059	A	5737	325	1489	RSPTLLMHVHYIKVISWRELLLI
	50007	Γ.				WLRAANASINPG VEQSPSGDPK
		1				TVTGFPFLRLEAADWVEEASVP
1						KGVHIALSSQEQRAGDPRDLEA
						PSNLVISERTHRSFRVSWTPPSD
		į				SVDRYKVEYYPVSGGKRQEVV
						RTPGVPDLRLPAIIPOAAWLLA
1						HLPAPSAPPTELPTKHTEAQSQ
						RCWSLLLCSVTEVAAPSQVVK
						EAPPSFHTGTENGYQGEESLFN
						KAYYGGGTNFFRKESQKLQQS
				l		AKKRDAELANGALGIIELNNDY
				l		TLKKVMKPLITSNTVTDEIERA
						NVFKMNGKWYLFTDSRGSKM
						TIDENKIPRNPTYKGREGPLQGE
						LQTTAQGNKRGYKQMEEHSM
						LMDRKNQYRENGLTAQA\PQPP
İ				l		PSGI*GYTAPCFPWENLI
5692	36060	В	5738	1	873	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	Incation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5693	36061	A	5739	274	716	QACYIYTTEYYAAIKNDEF/TVL
	i				\	CRDMDEAGNHHSQQTVTRTKN
	1	1				<b>OTPHVLTHRWELNNENTWTOE</b>
			i			GEHHTPGPVMLDSAPPTLGHOT
						PGSSAFGLWDLHQRLRLPRPOT
						KGSTVGFPGSEAFKLGLGHYW
						LSFFPSLQTAYRGTLPFNH
5694	36062	В	5740	134	2283	
5695	36063	А	5741	3	872	
5696	36064	A	5742	1	480	SKLNSGDGCWSGARRGSAHSR
						SPLPSPLRPRAKMATEGLHENE
						TLASLKSEAESLKGKLEEERAK
						LHDVELHQVAERV/VGPGAVC
	İ	l				HEDQKDPQRPREQSPVHGLVQ
						R*EEDRELVTGWEGDRVGFLH
		l				HKQGARGHHALHVGDGMCLC
		ı				PIGMCHCLWWFG
5697	36065	Α	5743	3	387	AKMATEGLHENETLASLKSEA
		l		İ	1	ESLKGKLEEERAKLHDVELHQ
		1			1	VAERV/VGPGAVCHEDQKDPQ
		l		•		RPREQSPVHGLVQR*EEDRELV
		l				TGWEGDRVGFLHHKQDPDSER
						RWHMCPVGRGERAAAAELPRT
5698	36066	Α	5744	1	1575	
5699	36067	Α	5745	20	510	
5700	36068	Α	5746	1	1392	
5701	36069	A	5747	1	1560	
5702	36070	Α	5748	3	325	
5703	36071	С	5749	206	409	
5704	36072	A	5750	1	855	
5705	36073	С	5751	233	571	
5706	36074	A	5752	1	3600	
5707	36075	Α	5753	1	4137	
5708	36076	A	5754	3	1357	
5709	36077	A	5755	3	194	
5710	36078	A	5756	3	269	
5711	36079	A	5757	1	1770	
5712	36080	Α	5758	164	411	RKNRKPNTAFLTHK WELNNEN
						TWTQGGNITHQG\CWGVQG*R
		l		1		RDSIRRNT*CKCRVPGCSKPPW
		1	1			HVYTYVTNLHILHMYPRT

NO:         of peptide sequence         hod in USSN 09/540,217         location of first sequence         cudon for last sequence           5713         36081         A         5759         1         3095	st amino acid  *-Stop codon,/-possible nucleotide deletion, \( \tilde{\text{postible}} \) nucleotide insertion)  MKMADAKQKRNEQL\( \tilde{\text{RWIGS}} \)  ETDLEPPVVKRQKTKVKFDDG  AVFLAACSSGDTDEVLLLHR GADDNYANVDGLTALHOACID
sequence	MKMADAKQKRNEQLKRWIGS ETDLEPPVVKRQKTKVKFDDG AVFLAACSSGDTDEVLKLLHR
	ETDLEPPVVKRQKTKVKFDDG AVFLAACSSGDTDEVLKLLHR
5713 36081 A 5759 1 3095	ETDLEPPVVKRQKTKVKFDDG AVFLAACSSGDTDEVLKLLHR
	ETDLEPPVVKRQKTKVKFDDG AVFLAACSSGDTDEVLKLLHR
	AVFLAACSSGDTDEVLKLLHR
	DNVDMVKFLVENGANINOPDN
	EGWIPLHAAASCGYLDIAEFLIG
	OGAHVGAVNSEGDTPLDIAEEE
	AMEELLONEVNROGVDIEAAR
	KEERIMLRDAROWLNSGHIN
	DVRHAKSGGTALHVAAAKGY
	TEVLKLLIQAGYDVNIKDYDG
5714 36082 A 5760 1 591	WTPLHAAAHWGKEEACRILVD
5714 36082 A 5760 1 591	FTVTRCYAVAQEGTYFDGSGY
	AALVKEGYKVQSDVNITLEVS
	N\PRRNGVFLGISTAIVHAIGLEL
	VDGKVLFHVNNGAGRITAAYE
	PKTATVLCDGKWHTLQANKSK
	HRITLIVDGNAVGAESPHTQSTS
	VDTNNPIYVGGYPAGVKQKCL
	RSQTSFRGCLRKLALIKSPQVQS
	FDFSRAFELHGVFLHSCPGTES
5715 36083 A 5761 340 739	
5716   36084   A   5762   1234   1897	
5717 36085 A 5763 1 4070	VTPRAAWLGLGFRGSAVLGLC
	WQPRSPPSRAAGMMNRTTPDQ
	ELVPASEPVWERPWSVEEIRRS
	SQSWSLAADAGLLQFLQEFSQQ
	TISRTHEIKKQVDGLIRETKATD
	CRLHNVFNDFLMLSNTQFIENR
	VYDEEVEEPVLKAEAEKTEQE
	KTREQKEVDLIPKVQEAVNYG
	LQVLDSAFEQLDIKAGNSDSEE
	DDANGRVELILEPKDLYIDRPLP
	YLIGSKLFMEQEDVGLGELSSE
	EGSVGSDRGSIVDTE
5718 36086 A 5764 1 972	

677

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amine acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5719	36087	IA	5765	11	2193	MVPYSLLVTWLQKALGVROY
3717	30007	ſ^	3,03	ľ	2173	HVASVLCORAKVAMRPFEPKY
		1	į.			IHYDLLEKNINIVCK*LNRPLTL
		1				SEKIVYRHPDDPTSOEIERGGTY
		1				LOOWPDSVTMQD/ATAQMAM
		1				LQFISSRL/SKVTMPSTIHCDHLI
					Į.	EAQLGSEKDLHQAKDINHEVY
		1				NFLATGSVKYGLSFWKPGSGII
		1				HOILENYEYPGVLLIGTDSHTP
						NGGSLGGICIGVGGA/DAVDVM
						TGIPWELKCPKVIGVKLMGSLS
						GWTSPKDVILKVAGILTMKGG
						TGAIVEYHGPVVDSISCTGMVT
						VCNMGLEIGTTTSVFHYNLRM
		1		1		KKYMSKTCOADIANLADEFKD
		ı		1		HLVPDPGCHYDQLIEVNPSELK
		l		l		LHINGPFTPDLAHPVAEVGKVA
						EKEEWPLDI*VGLWGSCTNSSY
		l				EDMGCSAGVAKQALAHGLKC
		1				KSQFTITPCSEQIRASIEQDGYA
		1				QTLRDVGGIVLANACGPCIGQL
						HRKDINKQEKNIIVTSYNRNFM
		l l		1		GHNDTNPETHAFITSPETVTAL
						AIVGTLKFNPETNYLTGKDGKK
		l				FKLEAPDADELPQAEFGPGQDT
						YQHP\PWGTTDHISAAGP*LKFF
				l		GHLDTISNNLLSGAINIENGKAN
		1				SVHDAVTHEFGPFPDTARYKK
						YGISWVVIGD*NYGKGSSWEH
		1				AALEPRHL\GGRAIITKSFARIHE
		ı				TNLRROGLLPLTFADPADNKIH
		1				LVDKLTIQSLKDLT/PGKPLKYI
5720	36088	В	5766	3	1205	DVDADTIQUELED III GIR DATI
5721	36089	A	5767	435	1428	
5722	36090	A	5768	I	615	
5723	36091	Ā	5769	79	381	DKPQPHLQHTRTSKRLNRSSQA
3723	50071	ľ	5.00	l' -	501	FLONLLPOELATSAGNLAIRPR
						NACSLGFLVSRVPSLAATPRAP
						WNSGPRLSD*LLPRSSRLSS*RL
	ļ					TLPDRLGSPVDH
5724	36092	A	5770	38	452	TEL EXCEPTION
5725	36093	A	5771	435	524	
5726	36094	A	5772	284	411	
5727	36095	A	5773	i i	354	
5728	36096	В	5774	I	942	
5729	36097	Α	5775	1	417	
5730	36098	A	5776	88	279	EDLGRSQSESLGPEFQG*VVAIE
		1		1	1	TIWPTEPKIFTICLSGSHSQSPW
		1		1		NSGPRLSD*LLPRSSQLSS*RLT
1	1	1	1	1	1	LPNRLRSLQDHHRCSR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5731	36099	A	5777	206	816	FIDSMLSPSRYQ*LSSQNWKKL
3,31	150077	ľ	3,,,,	200		L*ISYGTKNEPA*PKQS*AORTK
		l				LEASH*LTSNCTTSLH*SKQHGT
						GTKTEKKT*AIPFRT*AWAKTS*
		l				LKHQKQWQQKPK*TKKIKYLG
		l				IQLTTDVKDLFKENYKPLLNEI
		1				KEDTNKWKNIPCSWIGGINIMK
	ŀ	l				MAILPKVIYRFNALPIKIPMTFF
	,	l				TELEKTTLNFIWNQKRARIAKTI
	į.	ì				LSTKNKAGGITLADFKLYYKPT
						LVKTAWYWYQNREENLGNTIQ
		i				DIGMGKNFMTKTPKAMATKA
l						KIDKRDLIKPKSFCIAKETTIRM
		l l				NRQPTEWEKLFAIYPSDKALIS
						GIYKDLKQIYKKKNNPIKKWA
						KEMNRHFSKEDIYAANRHVKN
		_				AHHHWSSEKCKSKPQ
5732	36100	A	5778	502	600	
5733	36101	Α	5779	51	452	ADKQLQQSLRIQNQCTKITSILI
		l				HQQQTNREPNHE*TPIHNCFKE
l	ł	1				NKIPRNPTYKGCEGPLQGELQT
		l				TAQGNKKGYKQMEEHSMLMG
1						RKNQYRENGHTAQELEKTKVH MEPKKSPHRQVNPKPKEQSWR
		1				HHTT
5734	36102	A	5780	381	528	LPPPLPAGLC**DOOONSNAPLI
3/34	30102	l^	3780	361	328	H*EKERPPDDSYRIFLPRYHFHD
						DRI
5735	36103	Α	5781	I	477	
5736	36104	Α	5782	180	496	TPIHNCYKENKIPGNPTYKGCE
					1	GPLQGELQTTAQ*NKRGQKQM
						EEHSMLMDRKNKYHEN/EPYSP
1	ł				1	R*FIDSMPSPSNYQ*LSSQNWK
						KLL*GPYGTKKEPT*PRQS
5737	36105	Α	5783	1	533	MGPEICTSDKLSDEADVTVLEV
		1				LARAIRQEKEIKGIQLGKEEVKL
ŀ						SLFADDMIVYLENPIVSAQNLL
	İ	ĺ				KLISNFSKVSGYKINVQKSQAF
						LYTNNRQTESQIMSELPFTIASK
						RIKYLGIQLTRDVKDLFKENYK
		1				PLLKEIKEEHSIKWKNIPSSWVG
						RISIMKTAILPKVYIRIKDDEWN
	1				1	IYRRYTEFRSLHHKLQNKYPQV
	1				1	RAYNFPPKKAIGNKEAVLCHG
	1				1	R*HDCISRKPHRLSPKSP*ADKQ
	1				[	LQQSLRIQNQCAKITSILIYQ*QT
	1				I	NREPNHE*TPIHNCFKENKIPRN
	1					PTYKGCEGPLQGELQTTAQGN
						KRGTFHQMEEHSILMGRKNQY
L	l				L	HENGHTAQGLHPDKRR

SEQ ID	SEQ ID NO:		SEQ ID NO:		Nuclcotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5738	36106	A	5784	599	870	TPANQQHYRRMTLQLKENQTN RKRQQKQHQQKRPHKNPIQRS ATSKIKGDGSIQP*MLPWGQSP QKALTLATAPEQRKDTPPVRGL SLQD
5739	36107	С	5785	I	1170	
5740	36108	A	5786	317	960	IKWPYCPROFIDSMPSPSSYQRL SSQNWKKLL'SSYGTKKEPTSP SQS*AKRTKLEASRYLTSNYTT RLQ*PKOHGTGTKTEI*INGTQO SPQK*OPBYTYNYLIFINKPEKK QWGKDSLFNKWDMDEVGNIH SQQTITRTGNQTPHYFTHRWEL NNEITWTQGAGHHTPGPVVGL GAGRGIALREIPNANDELMVQQ TNMAHIYLGKPARCADV
5741	36109	Α	5787	903	1050	LPPPLPAGLC**DQQQNSNAPLI H*EKERPPDDSYRIFLPRYHFHD DRI
5742	36110	A	5788	281	491	SFGYIPSNGMAGSNGISSSRSLR NRHTDFHNG*TSLQSHQQCKSV PISPHPLQHLLFPDFLMIAILTGV R
5743	36111	Α	5789	1	381	
5744	36112	Α	5790	1	3231	
5745	36113	A	5791	1312	1463	KGSATCSPPQANATTTTALQML GGIPWGNACGIFTRPPPQTYLN THLSTR*RPLLLLLKCVR*KGSA TCSPPQANATTTTALQMLGGIP WGNACGIFTRPPPQTYLNTHLS TR
5746	36114	Α	5792	811	1065	IS*VSFMSITH:*WKKEQQLLG CWLA*M*SMLICV*RERI*THKL E*LIILCI*RMKKILEIQKGMFKL LPY*TKRIMLK/TLNRQLNSTVS SLISRVDSLEKSNTKLIEELAIA KNNIIKLQEENHQLRSENKLIL MKTQOHLEVTKYDVETELQTY KHSRQGLDEMYNEARRQLRDE SQLRQDVENELAVQVSMKHEI ELAMKILEKDIHEKQDTLIGLR QQLEEVKAINIEMYQKLQGSED GLKEKKEIIVRLYWSALCG
5747	36115	Α	5793	1	1353	
5748	36116	Α	5794	78	503	TKELLHSKRNYHQSEQATYRM GENFCNLLI*QRANIQNLQ*TQT NLOEKNKQPHQKVGEGYQQTL LKRRHLCSQKTHEKMLIITGHQ GNTNQNIHEIPSHTS*NGDH*K VRKKQGHG*SWKPSFSANYRK DKKPNTSCSHSQ

SEQ ID NO:	of peptide	hod	SEQ ID NO: in USSN	location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5749	36117	Α	5795	2	200	YGLMIRTIPVDPTIRTTSVSLTV
				İ		RLATMNPRSRPAPVDT\APGPP
						HLHKNQKSSQHSQYLDLTSYC
5750	36118	Α	5796	76	195	
5751	36119	A	5797	1	2445	
5752	36120	Α	5798	207	475	TNLQEKNKQPHQKVGKGYEQT
						LLKRKHSCSQQTYEKMLIITGH
						QRNANQNHNDIPSHSS*NNDH*
						KDRKQQMLERM*RNRNAFTLL VGV
5753	36121	В	5799	1	681	
5754	36122	Α	5800	1	798	
5755	36123	С	5801	78	245	
5756	36124	Α	5802	16	491	EPYPDRPREPKRDPEWSWGLW
		1		l		DKGGL\VLSLGRTRTEAHTALS
	1	1				RLRASMWIDRSTRAVSVHFTLY
	1					NPPTQLFTSVSLRVEILPTGSLV
	1	1		ŀ		PSSLVESFSIFRSDSALQYHLML
		1				PQLVFLALSLIHLCVQLYRMMD
				l		KGVLSYWRKPRNWLEVASLVS
				1		FSFEK
5757	36125	Α	5803	3	2791	
5758	36126	Α	5804	219	392	
5759	36127	Α	5805	1	1044	
5760	36128	Α	5806	1	360	*
5761	36129	Α	5807	1	528	
5762	36130	Α	5808	127	360	
5763	36131	Α	5809	1	421	GRRSRLAMRPLSMSYSFDLSDV
			ŀ			TTPESTKNLVESSMVNGGLTSQ
			ł	1		TKENGLSTSQQVPAQRKKLLR
		1		1		APTLAELDSSESEEETLHKSTSS
		ı	1	1		SSVSPSFP\EEPVL\EAVFTRKKP
			l			PKFLPISSTPQPERRQPPQRRHSI
	-	_		<u> </u>		EKETP
5764	36132	A	5810	328	1086	
5765	36133	A	5811	1	2076	
5766	36134	A	5812 5813	901	450	
5767	36135	A	5814	17	1506	
5768 5769	36136 36137	C	5814	24	330	ARDQPI/PKKGTVEGFEPADNK
3 /69	36137	A	3813	24	330	CLLRATDGKKKISTVVSSKEVN
						KFQMAYSNLLRANMDGLKKR
	1		l			DKKNKTKKTKTSSSSSSSSSPA
			l			AATAATTAATTAATAAQ
5770	36138	A	5816	1	2247	AATAATTAATTAATAAQ
5771	36138	A	5817	1	339	
5772	36140	A	5818	3	463	
5773	36140	A	5819	3	83	
5774	36141	A	5820	1	642	
5775	36142	A	5821	2	583	
5776	36144	A	5822	193	409	
2//0	20144	I'A	10022	1173	1707	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*-Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5777	36145	Α	5823	3	425	
5778	36146	Α	5824	1	450	
5779	36147	В	5825	82	2096	
5780	36148	В	5826	1	1554	
5781	36149	Α	5827	129	522	LCTDNIEITSKVHLHCSHHGAG
		1				LGTCSPLCLSLPPPPWAPVOPEP
1	l			1		PR*APPPAPORPVPSTIOGRKRL
		ı				OLHS*SO*DH/DAHAKVCSFTPE
		1			İ	PARPRTHOKEETPNTSEHOKKO
		1		1		TPDTPPLRTVTLTARLHGF
5782	36150	Ι_	5828	1	541	
5783	36151	A	5829	i	714	
5784	36152	A	5830	188	287	KELPSGGHYNCRAPSSPHPAGS
15704	30132	ľ.	15050	100	207	S*SGHQPNSQQ
5785	36153	A	5831	71	689	SPVLDDCPOGPLPSEESW/EOPV
3763	130133	l^	2021	l''	007	TROYPLRPEVHKGLONIVKHLK
1		1		İ		APGLVRKCSSHCNTPILGVOKP
		1		ŀ		NGQWRLVQDLRLINEAVVPLY
	1	1				PVVPNPYTLLSOTPEEAEWFMV
		1		i		LDLKDAFFCIPLHSDSQFLFAFE
	1	1				DPTDHTSQITWMVLPQGFRDSP
	l l	1		l	l .	
	1	1		İ		YLFGQALAQDLGHFSSRGTLVL
		1				QYADDLLFATSSEASCQQATLD
5786	36154	В	5832	45	1148	LLNFLANQ
5787	36155	C	5833	233	319	
5788	36156	c	5834	11	133	
5789	36157	A	5835	215	849	IKRLPLMKRMWL*LOPESLEIA
3/89	30137	l <sup>A</sup>	2632	213	049	GILVO*MIE*OPKKGTNSIPVSK
		1				PSP/VVQKPNGQWRQVQDLRLI
		1			1	SDAVIPLYPAVSNPYTLLSOILE
	İ	1			1	EAEWFTVLDLKDAFFCIPLRSD
		1				
1		1				SQFLLAFEDPTDHTSQLTWTVF
		1				TQGFMDTPHLFGQSLAQDLGH
		1				FSSPGTLVLQYVDDLLLAKQQA
l		1				TLDLLNFLANQGYKLSKLKAQ
		<del> </del> —		l		LCELLVFSSCARMHS
5790	36158	Α	5836	1	449	MNKELGISSYKFCGMGRKTSVS
1	1	1	l			AAKSVSATIPISRVQGLLQVLG
1	1	1	l			QEVFLLLCQDQEEQAKREKRD
1	1	1	l			QRKATALAMALRQTNLGGSER
		ı				IENGAGQSPSRACYQCGLQGHF
1	1		l			KKDYPTR/EPAAPCPLC*GNHW
						KMHCPRGQRSCDSHLAITHL
5791	36159	Α	5837	1	723	
5792	36160	Α	5838	186	602	
5793	36161	Α	5839	1	843	
5794	36162	В	5840	1	1779	
5795	36163	Α	5841	1	1182	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5796	36164	Α	5842	23	302	LSQWKNRWTRTFLASLSVIANI
					\	LEPLLNILHVAVWLMLPN*S*V
		l				KKQVIM\FWNWWVLGLTDFKN
						EATDPRVCSWPCWLRSEAADL
		1				CGECYSS
5797	36165	В	5843	1	2622	
5798	36166	Α	5844	279	1024	
5799	36167	Α	5845	3	3619	
5800	36168	В	5846	1	1898	
5801	36169	Α	5847	1	420	
5802	36170	Α	5848	1	1632	
5803	36171	A	5849	1	597	KYLTKKTQAASVEAVKMLDEI
						LLQLSASVPVDVMPGEFDPTNY
	l .					TLPQQPLHPCMFP/LATAYSTLQ
	1					LVTNPYQATIDGVRFLGTSGQN
						VSDIFRYSSMEDHLEILE*LRVR
						HISPTAPDTLGCYPFYFCGNTPS
		1				FGSKIIRGPEDQTVLLVTVPDFS
İ						ATQTACLVNLRS/LACQPISFSG
						FGAEDDDLGGLGWAPDSKKW
5804	36172	Α	5850	1	1490	RDAARRALNLLGLGEAVWTKO
				l		VRSVAMFSEQAAQRAHTLLSPF
					1	SANNATFARVPVATYTNSSQPF
					1	RLGERSFSRQYAHIYATRLIQM
						RPFLENRAQQHWGSGVGVKKL
						CELQPEEKCCVVGTLFKAMPL
1						QPSILREVSEEHNLLPQPPRSKY
						IHPDDELVLEDELQRIKLKGTID
1		1				VSKLVTGTVLAVFGSVRDDGK
	1					FLVEDYCFADLAPQKPAPPLDT
	1					DRFVLLVSGLGLGGGGGESLLC
l		İ	1		į.	TQLLVDVVTGQLGDEGEQCSA
						AHVSRVILAGNLLSHSTQSRDSI
						NKAKYLTKKTQAASVEAVKM
						LDEILLQLSASVPVDVMPGE\FD
1						PTNYTLPQQPLHP\CMFPLATA
1						YSTLQLVTNPYQATIDGVRFLG
		1	1			TSGQNVSDIFRYSSMEDHLEILE
1		1				WTLRVRHISPTAPDTLGCYPFY
1		l				KTDPFIFPECPHVYFCGNTPSFG
1		1				SKIIRGPEDQTVLLVTVPDFSAT
1	1	1				QTACLVNLRSLACQPISFSGFG
		l _				AEDDDLGGLGLGP
5805	36173	В	5851	13	441	
5806	36174	Α	5852	3	279	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5807	36175	A	5853	23	841	FEKAKEPRRAEEKKKEVPAYPET LKKKI*RNFAELKIKRLRKKFA QKMLQRARRKFIHEKAKHYH KEYRQMYRTEILMAIRMARKA GNFYYPAEPKLAFVIRIGINGY SPEVRRIVLOLLRLRQIFNCNILL *SSTKASINMLRDCRSHILAWG VPQILKSVNELIYKIRGYGKINK KRIAUTDNVALIARSLGKYGIL LAWEDLIBIETYTYGKIRKEAN NFPVGPSNLSSPPRWK*KKTT HPCKKVEDAGNREGRTRSNRP YLEGMDLRCLP
5808	36176	С	5854	57	287	
5809	36177	Α	5855	1	450	
5810	36178	A	5856	1	549	
5811	36179	А	5857	3	581	EQRKIPLVPENLLKKRKAYQAL KATQAKQALLAKKEQKKGKG LRFKRLESFLDSWRQKRDKV RLFRLEVKPHALELPDKHSLAF VVNIERIDGVSILLVQRTIARIRL KKIFSGVPKVTPQNLKMI.RIV EPYVTWGFPNLKSVRELILKRG QAIKVKNKTIPLTDMTVIEEHLG ECYSLGVSWGKPROSIKL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
l				sequence		
5812	36180	₩	5858	l	2652	MFGRSRSWVGGGHGKTSRNIH
5812	36180	Α	2828	1	2652	
	ì			t		SLDHLKYLYHVLTKNTTVTEQ
	l					NRNLLVETIRSITEILIWGDQND
ł						SSVFDFFLEKNMFVFFLNILRQK
	i					SGRYVCVQLLQTLNILFENISHE
1		1				TSLYYLLSNNYVNSIIVHKFDFS
	į.			·		DEEIMAYYISFLKTLSLKLNNH
	i					TVHFFYNEHTNDFALYTEAIKF
				}	İ	FNHPESMVRIAVRTITLNVYKV
				1		DNQAMLHYIRDKTAVPYFSNL
						VWFIGSHVIELDDCVQTDEEHR
						NRGKLSDLVAEHLDHLHYLND
					ŀ	ILIINCEFLNDVLTDHLLNRLFLP
						LYVYSLENQDKVFLIIHHAPLV
	1	l				NSLAEVILNGDLSEMYAKTEOD
		1				IQRSSVLPTLSSLWQGSHLSLNQ
						LOSGLHKCSSHLCGAQAAADS
		l				VTGEIPAIRSLEWLISAGSKART
						FFFLKMLIGFWEKVDCEYORR
						QVLSTRLQEALPSNRLTDVAAV
						HSSCMLGFGSTAPRGSWIGDPA
						AVHLPLPGELAEHLGSKGTTTV
						TKHOPOAKPSIRCFIKPTETLER
						SLEMNKHKGKRRVOKRPNYK
						NVGEEEDEEKGPTEDAOEDAE
						KAKGTEGGSKGIKTSGESEEIE
						MVIMERSKLSELAASTSVQEQN
						TTDEEKSAAATCSESTOWSRPF
				1	i .	LDMVYHALDSPDDDYHALFVL
	1			i		CLLYAMSHNKENLLKKRKAYO
						ALKATQAKQELLAKKEQKKGK
						GLRFKLLESFLHDYWQQKPDK
5813	36181		5859	1	405	
3813	30181	A	3839	1	405	LEISIMAASISGYTFSAVCFHSA
			l			NSNADHEGFLI.GEVRQEETFSIS
	1	1	1	1		DSQISNTEFLQVI\KVIGWYRFR
	1	1	l	l		RNTQQQMSYREQVLHKQLTRI
	1					LGVPDLVFLLFSFISTANNSTHA
	L	_	l			LEYVLFRPNRRYNQRISLAIPN
5814	36182	В	5860	1	843	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hođ	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5815	36183	A	5861	3	1260	EISIMAASISGYTFSAVCFHSAN
						SNADHEGFLLGEVROEETFSISD
						SQISNTEFLQVIQIYNHQPCSKL
						FSFYDYASKVNEESLDRILKDR
						RKKVIGWYRFRRNTQQQMSYR
						EQVLHKQLT\RILGVPDLVFLLF
						SFISTANNSTHALEYVLFRPNRR
						YNQRISLAIPNLGNTSQQEYKV
						SSVPNTSQSYAKVIKEHGTDFF
						DKDGVMKDIRAIYQVYNALQE
						KVQAVCADVEKSERVVESCQA
						EVNKLRRQITQRKNEKEQERRL
						QQAVLSRQMPSESLDPAFSPRM
l					1	PSSGFAAEGRSTLGDAEASDPP
						PPYSDFHPNNQESTLSHSRMER
		l			1	SVFMPRPQAVGSSNYASTSAGL
l			1			KYPGSGADLPPPQRAAGDSGE
						DSDDSDYENLIDPTEPSNSEYSH
						SKDSRPMAHPDEDPRNTQTSQI
5816	36184	Α	5862	1	742	
5817	36185	Α	5863	1	3063	MSLEVDRSVETMCSGDEILLPD
				1		LPKADVADPLWGPFPVQNCLS
				ł		LARSDSREQGLVLVMESRNRE
				l		VVPPGVSYSKDGAKSLKGDVP
						ASEVTSKDSTFSQFSPISSAEEC
		l		l		GDDEKIKVDDPLTRRTCNQASG
		l				SAPQQDYDKLKAFGGENSSKT
		1		ĺ		GLSPSGNMEKNKVVKREAEAN
		1		ł		SINLSVYEPFKVRKAEDKLKEN
		1				SDNVLENRVLDGKLSSEKNDT
		l				CLPGTAPSKTKSSSKLSSCSSAI
		L				MALSAKKAASDSCKEPV
5818	36186	Α	5864	2	626	LCQHNRIKHKGIRKVYACSHCP
	1	l				DSRRTFTKRLMLEKHVQLMHS
		1				LKDPDLKE/TDRCHQ*GGNRNK
		l				RRH/LSSPVPSGSWKNQFSR/CA
		l				MCGFTTENLLQFHEHIPQHKSD
	Į	l		l		SSSYQCQECGLWYTSHVSLSRH
		1		l		LFIVHKLKEPQPVSKQNGAGED
				l	1	NQQENKPSHEDESPNGTVSDRK
		1		I	1	CKVCVKTFETEAALNTHMRIH
	1	1	l		I	GMAFIKSKRMSSAKK

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5819	36187	A	5865	11	765	MORDVYISHVRKEHGKOMKK
		1				QPCCORDKPFSSSHSLCWHNRI
	1			1		KHKVIRKVYTCSHCSDSRGTFT
						KOLMLEKHVOLTHGIKDPDLK
		1				E/TDRRHQ*GGNRNKRRPQGPQ
	1					SOVEVERTGSGVQASQ\GAITO
						PLKKLKINVFKVHKCARA\GFT
		1				TENLLOFHEHIPOHKSDGSSYO
		l				CREHLFVVHKLKEPOPVSKON
						GAGEDNQQENKPSHEDESPNG
	İ	l		l		AMSDRKCKVCAKTFETEAALN
1		ļ				THMOTHGMAFIKSKRMSSDEK
5820	36188	Α	5866	878	1095	AFFLDTLYTQFSRC*SRAFVPFA
						HPTAMACSSRR/LIRVOEODAA
ļ						QVTHQSFKDDLCVVLGDTLHH
İ		l				RFFLIFRH
5821	36189	Α	5867	1	1137	
5822	36190	Α	5868	1	1380	
5823	36191	Α	5869	55	558	
5824	36192	Α	5870	1	897	
5825	36193	Α	5871	1	565	
5826	36194	В	5872	22	1696	
5827	36195	Α	5873	295	522	
5828	36196	Α	5874	3	3678	IPAPVSGRPPPGLLAEGKLSGPR
		l				PMCRTRLGSHTAASAPARMWL
	-					FHTLLCIASLALLAAFNVDVAR
		1				PWLTPKGGAPFVLSSLLHQDPS
		1				TNQTWLLVTSPRTKRTPGPLHR
						CSLVQDEILCHPVEHVPIPKGRH
		1	•			RGVTVVRSHHGVLICIQVLVRR
		1			ŀ	PHSLSSELTGTCSLLGPDLRPQA
		1		1		QANFFDLENLLDPDARVDTGD
		l				CYSNKEGGGEDDVNTARQRRA
				l		LEKEEEDKEEEEDEEEEAGT
				1		EIAIILDGSGSID
5829	36197	Α	5875	ł	3189	

SEQ ID	SEQ ID NO:			Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	delction, \=possible nucleotide insertion)
5830	36198	A	5876	1119	2463	LRAGGPGQGGKGPAHPGRRVD
		l				ELLLGHPTAVGCAKGTDCPTPT
		l				PGGLWV*GVQEESSDLPTAVDS
						SRPDIRDQA WASVHWELYVHG
						SSFINT*GERGAGY/AVITW/STV
			l			VEARSMPQGTSAQKAELIAFIR
			İ			ALELSEALAKTVRQRCVSCRQ
						HHARQGPAVPPGIQAYGAAPFE
						DLQVDFTEMPKCGDIRKIVTGD
1						VNTPAILGVVSSSPPSHIGNNITE
						DPELQPILAGLSLSMYLVTVLR
						NLLIILAVSSDPHLHTPMCFFLS
İ			İ			NLCWADIGFTLATVPKMIVDM
1						QSHTRVISYEGCLTRISFLVLFA
						CIEDMLLTVMAYDCFVAICRPL
1			l			HYPVIVNPHLCVFFLLVYFFLSL
	J	l				LDSQLHSWIVLQFTIIKNVEISN
l						FVCDPSQLLKLACSDSVINSIFM
		1		i	1	YFHSTMFGFLPISGILLSYYKIVF
		1				SILRISSSDGKYKAFSTCGSHLA
5831	36199	В	5877	I	1830	
5832	36200	С	5878	109	245	
5833	36201	В	5879	I	801	
5834	36202	В	5880	171	288	
5835	36203	В	5881	49	502	
5836	36204	В	5882	1	639	
5837	36205	Α	5883	1	821	MSGQFDFLLWTPEEDNSDESD
		l				AEGEHGDGAEEEAPPPVPRPGP
		İ				KPAGLGRRPCPYEQAQGGDGP
		1			1	EEQWMSFCWDIPRKSGAPRERI
		1				TLRRHLEDCGCKVSKKKAQICR
1						QQKDPQEESPAQFYERLCEAYG
						MYTPFDPDSPENQRMIHMALV
						RQSAEDMRRKLQKQAGLAGM
1					l	NPSQLLERASQVFVNRDAV/TP*
					1	GKQQREWRERG*YDSQYRRGG
						TQPCDIVPNIRRERR*YHSQYRR
					1	RARPPGPH*SERGALRPGSLPRQ
						AA*RVPSGPADGQ
5838	36206	Α	5884	1	1860	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5839	36207	A	5885	2745	3732	IRIGKNYFKVHMEPKKSPHROV
						NPKPKEQSWRHHTT*LQTILOG
						YSNONSMPGPTPO\PSTPAPGG
		l				NLRNPOSSDLLQVTKOQGOAL
	1	l		İ		AIQREAPLHRIPAPEAIPWYFQP
						QPATQLGSPPVDPPSSAMM/SR
		l				RAHRSRGPDROGYPLOGD*PGE
	1					PRPOEH*RGHSQERLPSSEKOTE
	ŀ	l				ICPPAQATQHPEEPDAHQPYKH
	ŀ					LFQVCAHQGHPVAQRRN*PGY
		l				WERYHSAEDPELQPILAGLSLS
		1				MYLVTVLRNLLIS
5840	36208	В	5886	1	2379	
5841	36209	В	5887	1	6741	
5842	36210	В	5888	165	928	
5843	36211	Α	5889	56	2028	
5844	36212	В	5890	1335	3804	
5845	36213	Α	5891	365	1573	
5846	36214	Α	5892	1	1491	
5847	36215	A	5893	25	458	140001111010001111111111111111111111111
5848	36216	Α	5894	11	1194	MGGNAADKFRAGVELALQSG
		l		1		NKVCVCSPRTTISGDAVAPRSV
						LPGCRHIPGEISQHSHCWAGRS
						LSSRKRGSLFRRMGFIKVVKNK
						AYFKRYQVKFRRR\RKGKT\DY
	İ		ŀ	i		YARKR\LVIQDKNKYNTPKY\R
						MIV\RVTNRDI\ICQMLYA/RRIE
			İ			GDMIVCAAYCTPNLPKIWV*RV
						GLTNYAAAY\CTGLLL\ARRLL
			l			NRFGMDKIYEGQV\ELTGDEYN
						VESIDGQPGAFTCYLDAGLAR\
						TTTGNKVFGAPEGKLWMGGLS
						IPHSTK\RFPG\YDSE\SKEFNA\E
						VTSGKHIMGPKCLQNYM\RYL
						ME\ED\EDAYKK\QFS\QYIK\NS
l	İ		j			VT\PDMM\EEMYK\KAHAAIRE
						ESSSMEKKAQGKKFKKKRWNR
						P\KMSLAQKKDRVAQKKASFL
50.40	2/217	١.	5005		1101	QSSRSGLLESLTPAIFP
5849 5850	36217 36218	A	5895 5896	21	1191	PRSSVRPAGGESSTCPPSWAAS
2820	30218	l <sup>A</sup>	2090	21	139	RSCTTSHGCGHQ*CAGTGTQTR
		1	l	1		i
5851	36219	Ā	5897	1	1062	
5852	36220	A	5898	1	246	
5853	36221	A	5899	1	642	
5854	36222	A	5900	2	648	
5855	36223	A	5901	1	555	
5856	36224	В	5902	151	513	
2320	1-322	10	10.02	1	15.5	L

SEQ ID	SEQ ID NO:	Talet	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon fur last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
5857	36225	A	5903	1	2915	VSLAFCQPLSLSLSPLLPLASSL
		1				APERTHLPGPGSLLLSPPSFPAR
	ŀ	1			1	PREPRGCVTAAPPDKMDTAEE
				İ		DICRVCRSEGTPEKPLYHPCVC
	l	1				TGSIKFIHQECLVQWLKHSRKE
	İ	1				YCELCKHRFAFTPIYSPDMPSRI.
	İ					PIODIFAGLVTSIGTAIRYWFHY
		1				TLVAFARWEVVLLPACRIYKCL
						FLGSVSSLLTLPLDMLSRKNLL
	i	1				ADCLQGCF\VVTCTLCAFISLV
	ŀ	1				WLREQIVHGGAPIWLEHAAPPF
		1				NAAGHHQNEA
5858	36226	Α	5904	3	907	
5859	36227	В	5905	102	406	
5860	36228	В	5906	I	5241	
5861	36229	Α	5907	I	519	
5862	36230	A	5908	I	3067	TRDAAMAEAALEAVRSELREF
		1			,	PAAARELCVPLAVPYLDKPPTP
		1				LHFYRDWVCPNRPCIIRNALQH
		1				WPALQKWSLPYFRATVGSTEV
		1				SVAVTPDGYADAVRGDRFMM
		1				PAERRLPLSFVLDVLEGRAQHP
		1				GVLYVQKQCSNLPSELPQLLPD
		1				LESHVPWASEALGKMPDAVNF
		1				WLGEAAAVTSLHKDHYENLYC
-		1				VV\$GEKHFLFHPPSDRPFIPYEL
		1				YTPATYQLTEEGTFKVVDEEA
L		1_				MEKAEVSRTCLLTVRVLQA
5863 5864	36231	A	5909 5910	I I	429 690	
5865	36232 36233	A	5911	1	376	
5866	36234	A	5912	1	471	
5867	36235	A	5913	i	606	
5868	36236	IA	5914	3	2756	SPGGRTPAARDSIVREVIONSKE
1000	50250	ľ	3714	ľ	2,30	VLSLLQEKNPAFKPVLAIIQAG
		1		1		DDNLMQEINQNLAEEAGLNITH
		1				ICLPPDSSEAEIIDEILKINEDTRV
		1				HGLALQISENLFSNKVLNALKP
		1				EKDVDGVTDINLGKLVRGDAH
ł	i	ı				ECFVSPVAKAVIELLEKSGVNL
		1			1	DGKKILVVGAHGSLEAALQCLF
		1			1	QRKGSMTMSIQWKTRQLQSKL
	ł	1				HEADIVVLGSPKPEEIPLTWIOP
ł						GTTVLNCSHDFLSGKVGCGSPR
						IHFGGLIEED
5869	36237	A	5915	3	404	RLKEKKLVKEVIAVSCGPAQCQ
15007	1 323	Ι΄.	1	Γ	1	ETIRTALAMGADRGIHVEVPPA
1			1	1		EAERLGPLQVARV/AVVTADLR
						LNEPCYATLPNIMKAKKKKIEV
1			1			IKPGDLGVDLTSKLSVISVEDPP
		1				QRTAGVKVETTEDLVAKLKEIG
			1	L		CHARLES AND AND AND AND AND AND AND AND AND AND

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5870	36238	A	5916	1	334	
5871	36239	А	5917	88	870	IAD DYRVLIVAVKEVIDY AVKIR VKPDRTGVVTDGVKHSMNPFC EIAVEEAVRLKEKLIVKEVIAVI SCCPAQCOETIRI TALAMGAID RGIHVELVPPAEAERF/GVPLQV ARVLGQAWQRRRILDLVILLGK QAUACTDCRQTGOMTAGFLD WPQGTFASQVTLEGDKLKVER EIDGGLETLRLKLPAVVTADLR LNEPRYAVIL PNIMKAKKKIE VIKPGDLGVULTSKLSVISVEDP PQRTAGVKVETIEDLVAKLKEI
5872	36240	Α	5918	1	774	
5873	36241	Α	5919	1	1557	
5874	36242	Α	5920	1	759	
5875	36243	Α	5921	305	638	
5876	36244	Α	5922	364	540	
5877	36245	Α	5923	9	111	
5878	36246	Α	5924	1	594	
5879	36247	Α	5925	169	594	
5880	36248	Α	5926	37	936	
5881	36249	В	5927	91	2043	

691

SEQ ID			SEQ ID NO:		Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		02/340,217	sequence	or behine sederate	percentage macratomy
5882	36250	Α	5928	[1	2298	MSRKGPRAEVCADCSAPDPGW
						ASISRGVLVCDECCSVHRSLGR
						HISIVKHLRHSAWPPTLLQMVH
					ĺ	TLASNGANSIWEHSLLDPAOVO
						SGRRKANPQDKVHPIKSEFIRA
						KYQMLAFVHKLSCRD\DDGVT
						AKDL\SKAN*HSSVR\TGKPWK
						TCLRLLS\LGA\QANFFHPEKGT
						TPLHVAAKAGQTLQAEL\LVVY
					1	GADPGSPDVNGRTPIDYA\ROA
						GHHELAERLVEC\QYE\LTERLA
						FYLCGRKPDHKNGHYIIPOMAD
						SLDLSELAKAAKKKLQALSNRL
			1			FEELAMDVYDEVDRRENDAV
						WLATONHSTLVTERSAVPFLPV
						NPEYSATRNQGRQKLARFNAR
						EFATLIIDILSEAKRROOGKSLSS
	İ		1			PTDNLELSLRSQSDLDDQHDYD
1						SVASDEDTDQEPLRSTGATRSN
						RARSMDSSDLSDGAVTLQEYL
						ELKKALATSEAKVQQLMKVNS
						SLSDELRRLQREIHKLQAENLO
						LRQPPGPVPTPPLPSERAEHTPM
			1			APGGSTHRRDRQAFSMYEPGS
			l			ALKPFGGPPGDELTTRLOPFHS
			}			TELEDDAIYSVHVPAGLYRIRK
					ł	GVSASAVPFTPSSPLLSCSQEGS
					ł	RHTSKLSRHGSGADSDYENTQS
						GDPLLGLEGKRFLELGKEEDFH
						PELESLDGDLDPGLPSTEDVILK
						TEQVTKNIQELLRAAQEFKHDS
1					ľ	FVPCSEKIHLAVTEMASLFPKRP
5883	36251	A	5929	1	924	T T GOOD TO TE TO THE TOTAL THE
5884	36252	A	5930	214	387	RRAFHPTPVTSARSTLHSFGQL
3004	30232	l^	3330	217	1507	RLPHSM*SGGTLLISMMQANQS
						LSLEFSKWTSFPLD
5885	36253	A	5931	1	1639	ESELI SKW ISI I ED
5886	36254	A	5932	i	1098	
5887	36255	A	5932	1	546	NSSQVLQF*YLWVNEAPFRLLT
3007	30233	^	3933	ļ'	340	MPOPYPOINITADOLWGSVAVL
						V*MH\NGLPGLCI*AWEKTTSG
			ŀ	l	1	GEOYPSSSAIKQGPKEPYADFIA
			ŀ			
		1	[			RLQESLKKVIADLAAQDIVLWL
			1			LAFDNANPECQAALRPIRGKAH
	i					LVDYTKVCDGIRDKLHKATLL
	Ì					AQAMAGLRMGKGNTPFPGACF
	L				L	NCGKHGH

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5888	36256	A	5934	T .	648	MGQVWGLVHFTLEVFHTGDEE
5000	50250	ľ.		i		EOEYSEVTEDVTEHVYLPAKA
ł						KVAKEEEAGIQQARQEGDLEA
						WOFPVRIHPPDOOENITATFEPF
1		1				PFKLLKELKQAINQYGPGSPFV
			l			MGLLKNVTVSSQMIPTDGDPLT
						RACLTPAQFLQFKTWWADEAS
						IOAARNAWAOPOINITADOLLG
						VGGWAGLDAQFVMQDDAIEQ
						LRGVCIRAREK\IT*CGEOYPSF
5889	36257	A	5935	120	254	
5890	36258	C	5936	366	479	
5891	36259	A	5937	1	933	
5892	36260	A	5938	1	840	MGKVWGLVHSTLELFHTDVEE
		ŀ				EGEYNEVTEEVTKHVYLPAKA
		ŀ				KAAKEGEVHPYHSAPPHYYFE
		ŀ			i	ENDPPDLSFLEDTGTPRLAAAA
						TTKANA\KQPLLLSPSMHR/PLP
	ļ	l				TRPLLAG\QATALPQGV*PLIAP
		l l				PTRPHLEHCSTQ*RPQPAPTLGE
1		1				ITPVTVPQAPLHPRAVQPW/HST
						PTRSWLQAVMPGIAPPSRSPPW
1						AVQLRILTYLGCLSTTPAAVQS
		l				LSQPPASVRQARVPQAPASSLC
		1				QEKPPSPPPVAPHGAAAAARPP
						SYHSSCASVAVVAANVLIG
5893	36261	Α	5939	I	134	MGQVW*KSQSPKA*EPGVSCP
						RAGRREASVPRWYSS
5894	36262	Α	5940	I	1158	
5895	36263	Α	5941	I	673	MGIALGSPTTGPKAMKQNLSIG
		1				PAGILLPQPVMTPGCPAAAPPV
1		1				APRCGYVLSEDAWGNLQGLCT
1		1				GLSCGQPVAPWATDSGGAQDP
		1				VALLPPFPSRGLLGPSCMQRSQ
						VVKGGRQSEISSQNKKVIADLA
			ŀ			AQDIVLQLLAFDNANPDCQAA
			ł			LRPIRGKAHLVDFIKACDVIGGI
		1	1		1	PNLLLHPRGLRAITIAVFGKQ\IR
			l			TSGSNPLRSTFLSRSRSISKNCSA
						EV
5896	36264	A	5942	i .	1182	

SEQ ID	SEO ID NO.	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
ŀ				sequence		
5897	36265	A	5943	1056	2128	TQPPTWGQIKKLSQMVEENLR
						KAGQLVTMNNLMVAMIVVITT
			ľ	ŀ		TEEQEYSEVTEEVTEQVYLPAK
						<b>AKVAKEGEVHPYPSAPPHYYFE</b>
						EKEWPDPPDLSFLEDTRQKVVA
						PVTVRAAPRATVLSSIQAGIQQ
						AR*EGDLEAWQFPVRIHPPDQQ
1						GNIIVTFEPFPFKLFKEFKQAVN
						QYGPGSPFVMGLLKNVAVSSW
1						MIPTDWDALTRACLTPAQFLQF
			l .			KTCAMKQGPREPYVDFIARLQE
ŀ						SLKKMIADSAAQEIVLQLLAFD
						NAHPDCQAALRPIRGKAHLVD
		1	ł			YVKACDGIGEYTPSTYEKKVN
			ļ			CKTASCRSFRRYPEEGIVITGDD
						SSMRVVVPEDLPVGQDVEVED
						RDIDDPDPV
5898	36266	A	5944	1	300	RESIDES EST
5899	36267	A	5945	1	373	
5900	36268	A	5946	1	2976	
5901	36269	A	5947	287	544	
5902	36270	A	5948	831	4555	
5903	36271	C	5949	108	434	
5904	36272	C	5950	145	402	
5905	36273	A	5951	3	1104	GSRPGGHTLQSHRGRHAQGLR
						SPLLAPVCLGCGTWGQRRLFW
			l	1		SLKI*RLLCWF/CRRLQINCKNK
	1					PAIPRGPT/GPSEKSGLLLQDQG
	İ					DTTNTEEENSKSLENIFGRVIKE
						NFQSLVRDLDI\QYKKHKEHPG
						NSSQKDHHLGTLSSGYPKLRQR
			ŀ			KES*ELSDRSTRKISQS/YNLYTP
			l			NTGAPRFIKQLLTDLRNEIDSNT
						IIVGYFSTPLTALDRSSRQKVND
						ETVDLNYTLEQMDLTEIYRTFH
						PTTTEYTFYSTVHGTFSKIDHMI
						CHKMSLNEFKKTEIISSTLSDHS
						GIKLEINSKMNLONHANTWKL
		1				NNLLLNEHWVKNEIKMEIEKFF
						KLNDSNDTTYONLWDMAKAV
						LRGKFIALNTYIKKMM
5906	36274	В	5952	1	2367	EKGKI IALITI TIKKIVIVI
5907	36275	A	5953	21	132	WREGAROCOEDPAEFLSD*DW
3907	302/3	<u>۱</u> ^	2223		132	ADPGPPHNAPGQNWH
5000	26276	-	5954		1471	ADIGITANATOQNWH
5908	36276	A	3734	ı	1461	L

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5909	36277	A	5955	31	1802	SAWWNSRELLDPOSRSRSGFCF
				1		*EYPPTSGTEOESVSGNRALCSS
	ŀ	l		i		LRMNGDQNSDVYAQEKODFV
ŀ		l		ŀ		OHFSOIVRVLTEDEMGHPEIGD
						AIARLKEVLEYNAIGGKYNRGI
		l				TVVVAFRELVEPRKQDADSLO
	ļ	l				RAWTVGWCVELLQAFFLVAD
	l	l				DIMDSSLTRRGOICWYOKPGV
	ľ	ı				GLDAINDANLLEACIYRLLKLY
	ŀ					CREOPYYLNLIELFLOSSYOIEI
1	ľ	ı				GADPGPPHSPPRAMWILSDSLK
		l				RGTNLLSSTRQLSTPSTFL
5910	36278	A	5956	<del> </del>	532	RUNEAEQKYKDIQDKLQIISEET
3910	30278	Ι^	3930	l'	332	
		1				NARAPECMALKADVVAKKRA
ŀ		1				YNEAEVLYNRSLNEYKALKKD
İ	1	l				DEQLCKRIEELKK/RVLTN/RLE
Ì		1				PERLERQKKISWLKERVKAFQN
ļ		l				QENSVNQEIEQFQQALEKDKEE
ŀ		1				HGKIKREKLDVKHALSYNQRL
	l	1				LKELKDSKTDRLKRFGPNVPAL
						LEAIDD
5911	36279	A	5957	121	475	
5912	36280	A	5958 5959	131	2891 3101	
5913	36281	A		I31	292	CORURNII I LOOM OND VILLED
5914	36282	A	5960	44	292	CQDYRWLLASSVLCWLY*KTQ
	Ì	ı				QSDTEDLLCSAPTGPPNPEEDD
				I		GKS*PEKCRQMT*KKWSINCKC
	ŀ			I		
					***	FFASSHNTTLSIGLFLR
5915	36283	В	5961	26	239	FFASSHNTTLSIGLFLR
5915 5916	36283 36284	B	5961 5962	26 131	239 3121	FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY  LLPSGAPERGSPGKEHPEERVV
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY  LLPSGAPERGSPGKEHPEERVV  TAPPSSSQSAEVLGELVLDGTA
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY  LLPSGAPERGSPGKEHPEERVV  TAPPSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLRP
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQUK KATSAATVQRAGSQPASQGLD
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY  LLPSGAPERGSPGKEHPEERVV  TAPPSSSQSAEVLGELVLDGTA  PSAHHDIPALSPLLPEEARPKHA  LPPKKKLPSLKQVNSARKQLRP  KATSAATVQRAGSQPASQGLD  LLSSSTEKPGPPGDPDPIVASEE
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY  LLPSGAFERGSPGKEHPEERVY  TAPPSSSQSAEVLGELVLDGTA PSAHDIPALSPLLPEEARPKHIA  PSAHDIPALSPLLPEEARPKHIA  KATSAATVQRAGSQPASQGLD  LLSSTIEKFGPFGDPIPVASEE  ASEVPLWLDRKESAVPTTPAPL
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY  LLPSGAFERGSPGKEHPEERVV  APPSSSQSAEVLGELVLDGTA  PSAHHDIPALSPLLPEEARPKHA  LPPKKKLPSLKQVNSARQGLP  KATSAATVQRAGSQPASQGLD  LLSSSTEKPGPPGDPDPVASE  ASEVPLWLDRKESAVPTTPAPL  QISPFTSQPYVAHTLPQRPEPGE
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY  LLPSGAPERGSPGKEHPEERVV  TAPPSSSQSAEVLGELVLDGTA  PSAHHDIPALSPLLPEEARPKHA  LPPKKKLPSLKQVNSARKQLRP  KATSAATVQRAGSQPASQGLD  LLSSSTEKPGPPGDPDPIVASEE  ASEVPLWLDRKESAVPTTPAPL  QISPFTSQPYVAHTLPQRPEPGE  PGPDMAQEAPQEDTSPMALMD
		_				FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSSQSAEVLGELVLDGTA PSAHDIPALSPLLPEEARPKHA LPFKKKLPSLKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPDIVASEE ASEVPLWLDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTISTHIT
5916	36284	_	5962	131	3121	FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY  LLPSGAPERGSPGKEHPEERVV  TAPPSSSQSAEVLGELVLDGTA  PSAHHDIPALSPLLPEEARPKHA  LPPKKKLPSLKQVNSARKQLRP  KATSAATVQRAGSQPASQGLD  LLSSSTEKPGPPGDPDPIVASEE  ASEVPLWLDRKESAVPTTPAPL  QISPFTSQPYVAHTLPQRPEPGE  PGPDMAQEAPQEDTSPMALMD
5916	36284 36285	A	5962 5963	131	3121	FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY LLPSGAPERGSPGKEHPEERVV TAPPSSSQSAEVLGELVLDGTA PSAHDIPALSPLLPEEARPKIL PSKKLFLSKQVNSARKQLRP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPFGDPDIVASEE ASEVPLWLDRKESAVPTITAPL QISPFTSOPYVAHTLPORPEPGE POPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTISTIII TTVITTEQAP
5916	36284	A	5962	131	3121	FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY LLPSGAFERGSPGKEHPEERVV APPSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLLP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPDIVASE ASEVPLWLDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTISTIII TTVITTEQAP PSVVLDINVSFNHWSAIFLTMEN
5916	36284 36285	A	5962 5963	131	3121	FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY  LLPSGAPERGSPGKEHPEERVV  TAPPSSSQSAEVLGELVLDGTA PSAHDDIPALSPLLPEEARPKHA  LPPKKKLPSLKQVNSARKQLRP  KATSAATVORAGSQPASQGLD  LLSSSTEKPGPPGDPDPIVASEE ASEVPLWLDRKESAVPTTPAPL  USPFTSGPYVAHTLPGREPGE PGPDMAQEAPOEDTSPMALMD  KGENELTGSASEESQETTISTHIT  TTVTITEQAP  PSVVLDINVSFNHWSAIFLTME\ PPCHRVRSHAMESR*GSVLP*N
5916	36284 36285	A	5962 5963	131	3121	FFASSHNTTLSIGLFLR  LVSFLLFQDALPEGDASPLGPY LLPSGAFERGSPGKEHPEERVV APPSSSQSAEVLGELVLDGTA PSAHHDIPALSPLLPEEARPKHA LPPKKKLPSLKQVNSARKQLLP KATSAATVQRAGSQPASQGLD LLSSSTEKPGPPGDPDIVASE ASEVPLWLDRKESAVPTTPAPL QISPFTSQPYVAHTLPQRPEPGE PGPDMAQEAPQEDTSPMALMD KGENELTGSASEESQETTISTIII TTVITTEQAP PSVVLDINVSFNHWSAIFLTMEN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
	1	<u> </u>	ļ		Land	Anna de Constantino di I
5920	36288	Α	5966	3	688	GTSAGDGCPHPHTVLWPPDIMF
	1	1				PKKDVPVKKPAGPSISKPAAKP
	1					AAAGAPPAKTKAEPAVPQAPQ
	1				Į.	KTQEPPVDLSKVVIEFNKDQLE
				1		EFKEAFELFDRVGDGKILYSQC
	1					GDVMRALGQNPTNAEVLKVLC
	1		l			NPKSDEMNVKVLDFEHFLPML
				1		QTVAKNKDQGTYEDYVEGLRV
						FDKEGNGTVMGAEIRHVLVTL
			1	Ì		GEKMTEEEVEMLVAGHEDSNG
ŀ						CINY\EELVRMVLNG
5921	36289	A	5967	54	540	AVYMCDLTENOTADLIPST\EF
						KEA\FQLFDRTGDGKILYSQCG
ł		1				DVMRALGONPTNAEVLKVLGN
				Į.		PKSDEMNVKVLDFEHFLP\MLQ
l						TVAKNKDOGTYEDYVEGLRVF
						DKEGNGTVMGAEIRHVLVTLG
						EKMTE\EDVHMLVAGHEDSNG
						CINYEAFVRHILSG
5922	36290	A	5968	1	405	CHAILM VIGHESS
5923	36291	A	5969	93	506	
5924	36292	В	5970	43	615	
5925	36293	A	5971	2	598	TRTSLHAALFSWDPVGTSLETFI
3723	30273	,	3771	[	370	SHLEVKKGMLVGIVGKVGCGK
						SSLLAAIAGELHRWEOVOCGG
						HTLH*APEQMLRGHVAVRGLS
						KGFGLATQEPWIQFATIRDNILF
						GKTFDAQLYKEVLEACALNDD
		1				LSILPAGDQTEVGEKGVTLSGG
						QRARIALARAVYQEKELYLLD
	0.000					DPLAAVDADVANPPACTGCNP
5926 5927	36294	В	5972	137	371 1398	
	36295	A	5974	1	915	
5928	36296	A		1		
5929	36297	A	5975	40	564	
5930	36298	A	5976	62	280	
5931	36299	A	5977	17	744	
5932	36300	Α	5978	1	537	
5933	36301	A	5979	242	576	AANSLYKGSNSAALIILVGP*IS
	1					CLTHPVYMK*APS*TICLLYSM
						VILKALFFPQNINFIFLPVKSRHS
5934	36302	Α	5980	924	3473	
5935	36303	Α	5981	1	604	
5936	36304	A	5982	288	732	RNCIANYDFLILPTSF*WCSFFV
l		1	1	1		LLFLFLSLSLSSLKLHSDLDKGE
	1	1		1		GTAKYTLSGDGAGP\VFTIDETT
	1	1	l	1		GD\IHAIRSL\DREEKPFYTLR\A
	1	1		1		Q\AVDIETRKPLEPESEF\IIKVQ
	1	1				DINDNEPKFWGWDLMVATGP
1	1	1	1			QKWSPVG*VGQIKIL
5937	36305	A	5983	1	1510	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5938	36306	Α	5984	1	603	
5939	36307	Α	5985	250	505	GFSPTWQ*MNTHPSLMCFSPSR TTGSAAAN*RGQQKSGVPFWS* SHVKGKDQIPVPICPCTTAPVT MESTCIC*PTHVSCKTLMV
5940	36308	Α	5986	3	131	RVLVPDIRGAI*AVPKSPSIKSYF ALPRALFLLPPYPDDLGI
5941	36309	Α	5987	1	913	
5942	36310	Α	5988	5	177	
5943	36311	Α	5989	3	383	
5944	36312	A	5990	1	1323	
5945	36313	Α	5991	342	594	
5946	36314	Α	5992	ı	321	
5947	36315	Α	5993	3	601	
5948	36316	Α	5994	1	1023	
5949	36317	Α	5995	1	606	
5950	36318	Α	5996	]	1536	
5951	36319	Α	5997	2	1394	
5952	36320	Α	5998	371	1045	
5953	36321	Α	5999	3	360	
5954	36322	Α	6000	l	636	
5955	36323	С	6001	1	861	
5956	36324	Α	6002	1	711	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
5957	126226	<del>-</del>	10002	110	2446	AGSPPRADAAAGLWERGHLLS
5957	36325	Α	6003	18	2446	
		l				AAVAAMGKRDRADRDKKKSR
l		l				KRHYEDEEDDEEDAPGNDPQE
i		l				AVPSAAGKQVDESGTKVDEYG
						AKDYRLQMPLKDDHTSRPLWV
	l	l l				APDGHIFLEAFSPVYKYAQDFL
	1	l				VAIAEPVCRPTHVHEYKLTAYS
						LYAAVSVGLQTSDITEYLRKLS
		1				KTGVPDGIMQFIKLCTVSYGKV
		1				KLVLKHNRYFVESCHPDVIQHL
		l		i		LQDPVIRECRLRNSEGEATELIT
		l				ETFTSKSAISKTAESSGGPSTSR
i		l				VTDPQGKSDIPMDLFDFYEQM
						DKDEEEEEETQTVSFEVKQEMI
		1				EELQKRCIHLEYPLLAEYDFRN
		1				DSVNP\DINIDLKPTAV\LRPYQE
						KSLR\KMFGNGRARSGVIVLPC
		l				GAGKSLVGVTAACTVRKRCLV
1						LGNSAVSVEQWKAQFKMWSTI
1	İ					DDSQICRFTSDAKDKPIGCSVAI
		ı				STYSMLGHTTKRSWEAERVME
		1				WLKTQEWGLMILDEVHTIPAK
l	ŀ					MFRRVLTIVQAHCKLGLTATLV
l		1				REDDKIVDLNFLIGPKLYEANW
		1				MELQNNGYIAKVQCAEVWCP
l		1				MSPEFYREYVAIKTKKRILLYT
1						MNPNKFRACQFLIKFHERRNDK
1		ı				IIVFADNVFALKEYAIRLNKPYI
						YGPTSQGERMQILQNFKHNPKI
1						NTIFISKVGDTSFDLPEANVLIQI
			1		1	SSHGGSRRQEAQRLGRVLRAK
		l				KGMVAEEYNAFFYSLVSQDTQ
5958	36326	Α	6004	1	933	
5959	36327	A	6005	]	879	
5960	36328	Α	6006	1	727	
5961	36329	A	6007	1	1509	
5962	36330	Α	6008	1	1698	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5963	36331	A	6009	2465	2751	VPTSSAPMPWPSRQWERSSRT MTVISSSQLMALCPP*TAQVLA AAPA*LGASSAARGIPPQAGKT QKIETDIATMQLCANKLDKKDF FGKSDPFLYFYRSNEDGTFTICH KTEVYKNTLNPVWQPFSIPVRA LCNGDYDRTVKIDVYDWDRD GSHIDFIGEFTSYRELSKAQNQ FTVYEVLNPRKKCKKKKYVNS GTVTLLSESVDSEFTFVDYIKGG TUQLNFTVAIDFTASNGETRIMSE KVGGNPLQPTSLHY MSPYQLS AYAMALKAVGEHQDYDSDKL FPAYGFGAKLPPEGRISHQPLIN NNDEDPNCAGIEGVLESYFQSL
5964	36332	Α	6010	1	1059	
5965	36333	Α	6011	255	405	
5966	36334	Α	6012	251	1199	
5967	36335	Α	6013	1	1791	
5968	36336	Α	6014	335	984	
5969	36337	A	6015	1	127	LPLRLSYEIYLYFTF*KPEHNKS HFLESHLIRNTRSALNTRK
5970	36338	Α	6016	1	774	

699

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
5971	36339	ĪΑ	6017	186	2699	PRGAKPAVPAGPERPGPGPGPC
1277	30337	ľ.	0017	1.00	2077	SPRPMVLPTCPMAEFALPRHSA
	1					VMERLRRRIELCRRHHSTCEAR
	1			l		YEAVSPERLELERQHTFALHOR
		1				CIOAKAKRAGKHROPPAATAP
		1		l		APAAPAPRLDAADGPEHGRPA
				l		THLHDTVKRNLDSATSPONGD
						QQNGYGDLFPGHKKTRREAPL
		l		l		GVAISSNGLPPASPLGQSDKPSG
						ADALQSSGKHSLGLDSLNKKR
		ŀ				LADSSLHLNGGSNPSESFPLSLN
		ŀ				KELKQEPVEDLPCMITGTVGSIS
		ľ				QSNLMPDLNLNEQEWKELIEEL
						NRSVPDEDMKDLFNEDFEEKK
		i				DPESSGSATQTPLAQDINIKTEF
	i					SPAAFEQEQLGSPQVRAGSAGQ
	1	1				TFLGPSSAPVSTDSPSLGGSQTL
	1	1				FHTSGOPRADNPSPNLMPASAO
		1				
	1	1				AQNAQRALAGVVLPSQGPGGA
		1				SELSSAHQLQQIAAKQKREQML
						QNPQQATPAPAPGQMSTWQQT
						GPSHSSLDVPYPMEKPASPSSY
						KQDFTNSKL/PHDA*CE*EFPSA
	ŀ					RRPLPPAQPCEPAESPATE*LES
						ELRE/YTRGLCW\IRQYKTPFSL
						QSGLWARQPGVWPEQASPDGL
	į .					SSPAAVPYKSRAELPVSDEAKA
						RKYAFPITGSTWPGAEPFQCPC
						ASPGYQCWDPAACRVRGQLPQ
						QLPLSQQPATGRCNEAASVAFG
						PTETKGAAAKAFTATAVPSEAT
						APSRGTGEATVSAPSDPPTTPVP
5972	36340	Α	6018	1	1062	
5973	36341	Α	6019	3	566	ASRPPVTLRLVVPASQCGSLIG
-						KGGCKIKEIRESTGAQVQVAGD
						MLPNSTERAITIA GIPQSIIECVK
1						QICVVMLESPPKGVTIPYRPKPS
					İ	SSPVIFAGGQAYTIQGQYAIPQP
						DLTKLHQL\AMQQC\HFPMTHG
						\NTGFQWALES\SFPEV\KGYW\
1		1				AGLDASAQTTSHELTIPNDLIGC
						IIGRQGAKIN
5974	36342	Α	6020	2	531	TLRSSWQVVRTGTAQAATVRG
			İ		1	FPPHPPRP\SASTLTLEGPPLEAY
	1		l		1	TIQGQYAIPQPDLTKLHQL\AM
		1	1	1	1	QQSHFPMH/GDGIHSDYSAG\LD
1		1			l	ASA\QTTSH\ELTISKRILIGLA*S
					ŀ	GRSRAPKINGGSRQMSGAQI\KI
			1	1		ANPV\EGSTD*GRFTITGSAASIS
		1		1		LAQYLINVRLSSETGGMGSS
		Ь.	L		L	2.10.2

SEO ID	SEO ID NO:	Mot	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
İ		1		sequence		
		<u> </u>		1.00	1369	DI VILLE DE LA CALLACTA DE LA CALLAC
5975	36343	A	6021	181	1369	PLKVQLPRTLLDMDTGVIEGGL
						NVTLTIRLLMHGKEVGSII\GKK
					İ	GESVKKMREESGARI\NISEGNC
1		1				PERII\TLAGTH*LPSFKAFAMI\I
		1				DKLGRRDISSSM\TNSTAAQLGF
1		l		1		PVTLKLG\APAS\QCGSLIGKGG
		l			į.	CKIKEIRESTGAQVQVAGDMLP
	[	1		1	1	N\STEAGHHYLLGIPQSII\ECV\K
		l		1		QILRGSCWETLFPSSPPKGVTIP\
						YRPK\PSSSPV\IF\AGGPGQVPA
						QAATVRAFPTPPRPCGSTLTWE
		l				GPPLEAYTIQGQYAIPQPD\LTK
						L\HQL\AMQQSHFPMTHGNTGF
	1					SG\IESSF\PEVKGYW\AGL\DAS
						AOTTSHELTI\PNGFDWAGIIGA
		1			1	FKGAKIN\EIROMSGAQIKIANP
		1				VE\GSTDRQVTITGSAASISLAQ
	1			1		YLINVRLSSETG\GMGNN
5976	36344	A	6022	1	690	T DATE THE COURT OF THE COURT O
5977	36345	A	6023	li -	399	
5978	36346	A	6024	3	397	
5979	36347	A	6025	3	249	
5980	36348	A	6026	1177	477	
5981	36349	A	6027	49	451	
5982	36350	A	6028	1	1305	
5983	36351	A	6029	1	568	
5984	36352	A	6030	207	1053	PLTFGPARWRETPPSLYKEFSG
		1				LFGSFFLSSAWGAHNLRALFLL
						LPSSRIQPTPWVFGDLKSPAGL
						OVLNDYLADKSYIEGYVPSOA\
	ł					DVAVFEAVSSPPPADLCHALR
		1	1			WYNHIKSYEK\EKASLPGVKKA
1						LGKYGPADVEDTTGSGATDSK
						DDDDIDLFGSDDEE\ESEKPKRL
				l		REERLAQYESKKAKKPG\LVA
		ł	l			KSSILLLVKP\WD\DETDMAKLE
		1				ECVRSIQADGLVWGSSKL\VPV
						GYGIKKLQIQCVVEDDKVGTD
		_				MLEEQITAFEDYVQSMDVAAF
5985	36353	A	6031	1	211	
5986	36354	Α	6032	27	241	EVFGSWWQVPHEWLGSVLVV
	1	1	1	1	l	MSEFLFH*LM*ELVLKRV*CLS
	1	l		1		HLSLAPFLAM*YACSSSSPSTMI
						VSFFFF
5987	36355	Α	6033	1	588	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
	0.000	Ļ	1000	1000	Linna	LIFCGCWLFASLTVMEAAHFFE
5988	36356	A	6034	279	1333	
		1				GTEKLLEVWFSRQQPDANQGS
	į.		i			GDLRTIPRSEWDILLKDVQCSII
		1				SVTKTDKQEAYVLSESSMFVSK
		1				RRFILKTCGTTLLLKALVPLLKL
		1	l			ARDYSGFDSIQSFFYSRKNFMK
	1	1				PSHQGYPHRNFQEEIEFLNA1FP
						NGAGYCMGRMNSDCWYLYTL
1		1				DFPEER\VISQPDQTLEILMSELD
ļ		1	l			PAVMDQF*HEDG\VTAKDVTRE
		1	1			SGIRDLIPGSVIDATMF\NPCGYS
						MNGMKS\DGTYWT\IHITPEPEF
						SYVSFETNLSOTSYDDLIRKVV
			1			EVFKPGKFVTTLFVNQSSKCRT
		l				RLGLPQK\IEGFKR\LDCQEGWF
		1				KDSNFFF\TSFAKKQQQQQS
5989	36357	A	6035	1	687	- months and a state of the sta
5990	36358	A	6036	i	894	
5991	36359	В	6037	1	1458	
5992	36360	Ā	6038	1	1062	
5993	36361	A	6039	1	1218	
5994	36362	Α	6040	277	3508	RSGRIAWAQEMDAAGRGCHLL
	1		i e			PLPAARGPARAPAAAAAAAAS
						PPGPCSGAACAPSAAAGAGAM
ŀ		1				NPSSSAGEEKGATGGSSSSGSG
						AGSCCLGAEGGADPRGAGSAA
						AAGAAALDEPAAAGOKEKDEA
		l				LEEKLRNLTFRKQVSYRKAISR
		1				AGLOHLAPAHPLSLPVANGPA
1		1				KEPRATLDWSENAVNGEHLWL
1						ETNVSG\DLCYLGEENCQVRFA
	İ	1				KSALRRKCAVCKIVV/HTTACIE
1		1				ELEKINFRCKPTFREG\GS
5995	36363	A	6041	45	155	ELEKINFRCKF I FREG (G3
5996	36364	A	6042	1	979	
5997	36365	A	6043	3	1042	
5998	36366	A	6044	2	401	
5998	36367		6045	1	5772	
6000	36368	A	6046	16	5678	VTSGRLLFYFRSMGPGCDLLLR
6000	36368	A	6046	16	3678	
						TAATITAAAIMSDTDSDEDSAG
		1	l			GGPFSLAGFLFGNINGAGQLEG
		l				ESVLDDECKKHLAGLGALGLG
		1				SLITELTANEELTGTDGALVND
					1	EGWVRSTEDAVDYSDINEVAE
1	1	1			1	DESRRYQQTMGSLQPLCHSDY
			i		1	DEDDYDADCEDIDCKLMPPPPP
	1	1	1	1	I	PPGPMKKDKDQDSITGEKVDFS
		1			1	SSSDSESEMGPQEATQAESEDG
	1	1	1	1	I	KLTLPLAGIMQHDATKLLPSVT
					1	ELFPEFRPGKVLRFLR
6001	36369	Α	6047	l	354	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6002	36370	Α	6048	I	666	
6003	36371	Α	6049	129	456	TYPAVGESSRRPERSRGVPGPD AAAESHFRPGRISNPLHRAGEQ GHARAEGSGVFRPHRGRGLRL LFVQAPDQVDAPVHG*VAPPAI GARDAQTCRSHECPRTRPLDEV
6004	36372	A	6050	1	1095	
6005	36373	Α	6051	171	619	
6006	36374	Α	6052	1	621	
6007	36375	В	6053	1	181	
6008	36376	Α	6054	1	905	
6009	36377	Α	6055	1	855	
6010	36378	Α	6056	2	244	
6012	36380	A	6058	133	5421	FGKLYAWTVONILNVLMDASK KFKELGIQPVPLQTITSENPLGP SLGSIPQARFLLMMLSMLTLQF SANNLDLLLNSGTLALTQTALF LIVLPDVELLIPOHLL*MGYSL LPVLALLLAQHRSFGPSCDNVE EDMNASAQGASATVLATTRKE VMRGVDWKWGDVGEAEQTER NIHPTTMMFTSTINLLQTLCLP/ RVHAEIMQSEATKTLCGLLQIL VESGTTDKTRME
0.012	33300	^			,	FFTGONCRNNEKVTLVRIADLE NHNNDGGFWTVIDGKVYDIKC FQTQSLTENSILAQFAGEDPVV ALEAALQFEDTRESMHAFCVG QYLEPDQEGVTIPLGSLSSPLI DTERNLGLLLGLHASYLAMSTI LSPVEIECAKWVQSSIFSGGLQI SQHHYRYNEEKDEDHCSSPGGT PASKSRLCSHRRALGDHSQAFL QAIADNNIQDHNVKDFLCQIER YCKOCHLTPIMF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Mct hod	SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		, ,
6013	36381	A	6059	1	2607	MMGHSSAIPLTATPGELKGOSP
0015	50501		000,	ľ		TKMPDPELGCQGAKSQGCSRN
						ARHOKARSMPLQDQHLALAIL
						LELAVORGTLSOMLSAILLLLO
						LWDSRAQETDNERSAQGTSTL
			l			LLSLLQTFQSIICSKDTPPSEGN
1			ĺ	1		MHLLSGPLSPSESFLRESFFTVO
			l			NCRNNEEVTLICKADLENHNK
						DGGFWIVIDEKVYDIKDFOTOS
			l	l		LTGNSILAQFAGENPVVALEAA
				l		FEFEVTRESMHAFCVGQYLEVR
				l		LYALSDAEDGRG\TL*WLOSSIF
l						SG/GLQTSQIHYSYNEEKDEDH
1				I		CS/SPVGTPASKSR\CSHRWALG
						DHSOAFLOAIADNNIODHNVKT
1				1		HOEOGRSYKEVCTPVIERLRFL
	1					SNELRPAVGNDLSIISEFKLLSSL
						PRWRRIAOKIIRERRKKRIPKKP
						ESTADEEKIGNEESDLEEACILP
						HSPINVDKRPIAIKSPKTITSENP
						LGPSLGSIPQARFLLMMLSMLT
		l		l		LOHSANNLDLLLNSGTLALTOT
						ALRLIGPSCDNVEEDMNASAQ
				l		GVSATVLEATRKETAPVHLPVS
						GPELAATMKIGTRVMRGVDW
				l		KWGDQDGPPPGLGRVIGELGE
ļ.			İ	İ		DGWIRVQWGTGSTNSYRMGK
					1	EGKYDLKLAELPAAAQPSAEDS
				l		DTEDDSASPNRLVYREQHRSW
				l		CMLGFVRSIALTPQVCGALSSP
				l		OWITLLMKVMKGHAPFPAASL
1				l		QRQRWVAVSLPHALVKSGTVP
6014	36382	A	6060	1	7297	QUQUE TITTE STREET TO STATE
6015	36383	A	6061	32	259	SLRVTPGGRNVSEKKDRKKTG
10015	33303	ľ.	""	l	[ ·	R/PPELERKSHTERLYLEEGSAE
						PA*VGRRAPESVNDRGGAIQRA
						QRGQPAPPLPR
6016	36384	A	6062	3	437	QROQUALTER
6017	36385	A	6063	1	425	MTELPTLWKPLKNSPMFRVIAR
10017	33303	<u> </u>	0005	l.	1	AFCVTFILVSTHOEMLTITSENP
						LGPSLGSIPQARFLLMMLSMLT
						LOHSANNLDLLLNSGTLALTOT
						ALRLIGGTPVELPAELAAPAFR
			1	l		AAAA/VDKNPRRRGOKVAVAK
			1	l		SGGDRGKKSR
		L	L			BOODROKKSK

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6018	36386	Α	6064	2	14566	RRGGRALRVRPETWEEAGEKM
		1				PSESFCLAAQARLDSKWLKTDI
		1				QLAFTRDGLCGLWNEMVKDG
		1				EIVYTGTESTQNGELPPRKDDS VEPSGTKKEDLNDKEKKDEEET
		1			1	PAPIYRAKSILDSWVWGKOPDV
		1				NELKECLSVLVKEQQALAVQS
		1				ATTTLSALRLKORLVILERYFIA
		1				LNRTVFOENVKVKWKSSGISLP
		1				PVDKKSSRPAGKGVEGLARVG
		1				SRAALSFAFAFLRRAWRSGEDA
		ŀ				DLCSELLQESLDALRAL
6019	36387	В	6065	75	581	
6020	36388	A	6066	517	5495	ESFFTGQNCRNNEKVTFVRIAD
		ŀ				LENHNNDGGFWTVIDGKVYDI
		1				KDFQTQSLTENSILAQFAGEDP
						VVALEAALQFEDTRESMHAFC
		1				VGQYLEPDQEGVTIPDLGSLSSP
						LIDTERNLGLLLGLHASYLAMS
1		1				TPLSPVEIECAKWLQSSIFSGGL QTSQIHYSYYEEKDEDHCSSPG
1		1			1	GTPASKSRLCSHRRALGDHSQA
	1	1				FLQAIADNNIQDHNVKDFLCQI
		1				ERYCROCHLTTPIMFPPEHPVEE
						VGRLLLCCLLKH
6021	36389	Α	6067	1	1851	
6022	36390	Α	6068	53	423	YHLTLLIHGTKVSATRPGHCSP
		1			1	GKLPSWVPISLQCTPSSPECRSV
		1				*RQL*HGHMHELLYIITKADSVI
		1				TASCLISRSEW\WGDGGTVSLV
		1				QRFVDYGSSQCQRPHRTGCASS SAPQRASSVAPG
6023	36391	A	6069	1	49	EWSGTRTWWRPWSCRT*CRT
6024	36392	A	6070	1	726	_
6025	36393	A_	6071	368	485	
6026	36394	Α	6073	I	414	
6027	36395	Α	6074	3	535	RRREFPAKERESASMSSPEE*P/
		1				DMAKGAPPSQPPPNSVPAD/CS
1		1				RSVRLSSSNFEESLRPTEDDEGQ
1	1	1		1		EGQDSMSRAKANWLRAFNKV
	1			1		RMQLQEARGEGEMSKSLWFKG
	1			1		GPGGGLIIIDSMPDIRKRKPIPLV SDLAMSLVQSRKAAITSALASS
		1				TLNNEELKNHVYKKTLQALIYP
		-				ISC
6028	36396	Α	6075	I	222	
6029	36397	Α	6076	2	284	NGIPDFSNTTLLRGLQMPGARG
1		1				PCCGSQRHINLLMGTGVFLVK
	1	1			1	MKA/NEFFFLDSETRLCKIAPEG
	1	1				WREQPQKTSMNTFTLFLRIKFF
						VSHYGLL

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
6030	36398	A	6077	91	749	
6031	36399	c	6078	1	380	
6032	36400	Ā	6079	li -	877	MPRPDLAPALLVAVLVLLYLL
0032	30400	ľ	0077	,	l"''	VSAAAPAPSSDSTPENVCPVET
	1	1				TINFIWELSSPHNTSAVLLVVF
	1					HKGPSPKFEVKLKKNANGLGFS
	1	ĺ				FVOMEKESCSHLKSDLVRIKRL
						FPGHPAEENGAIAAGDIILAVN
		l				GSPRKASSSRCRGSWAMOLSV
		1				QAGPSFASYYPAAVEVLHLLRG
		1				APQEVTLLLCRPPPGALPELEQE
	1					WQGQKYKCAWAIVNEAEVEE
l		1				VVEVAGTVEFFGDQ\GA*CHHP
		1				ACSGKPLGWHGGLSRKCPRLFF
		1				RGATRVTGAQGLKEVKQQSFR
						SNMMWLGLRL
6033	3640I	Α	6080	1	1683	
6034	36402	В	6081	66	1214	
6035	36403	Α	6082	1	5694	
6036	36404	Α	6083	3	483	SSLTSSMEDPAAPGTGGPPANG
		1				NGN\GGGKGKQAAPKGREAFR
						SQRRESEGSVDCPTLEFEYGDA
						DGHAAELSELYSYTENLEFTNN
	ŀ					RRCFEEDFKTQVQGKEWLELE
	l .					EDAQKAYIMGLLDRLEVVSRE RRLKAARAVLYLAOGTFGECD
			ĺ			SEVDVLHWSRY
6037	36405	Α	6084	1	2646	SEVDVLHWSKI
6038	36406	A	6085	115	1289	FSPLEPRLCSLGGWGALOAGEP
0020	20400		0005	1113	1207	COPSRAGCGREGATMGCTLSA
						EERAALERSKAIEKNLKEDGIS
						AAKDVKLLLLGAGESGKSTIVK
						QMKIIH\EDGFSGEDVKQYKPV
ł	ŀ					V\YSNTIOSL\AAIVRAMDTLGIE
						YGDKERKADAKMVCDVVSRM
						EDTEPFSAELLSAMMRLWGDS
						GIQECFNRSREYQLNDSAKYYL
						DSLDRIGAADYQPTEQDILRTR
						VKTTGIVETHFTFKNLHFRLFD
		1				VGGQRSERKKWIHCFEDVTAII
l				1		FCVALSGYDQVLHEDETTNRM
1						HESLMLFDSICNNKFFIDTSIILF
l		1		1	1	LNKKDLFGEKIKKSPLTICFPEY
l						TGPNTYEDAAAYIQAQFESKNR
l	1	1		1		SPNKEIYCHMTCATDTNNIQVV
L						FDAVTDIIIANNLRGCGLY
6039	36407	A	6086	1	1053	

SEQ ID		Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6040	36408	Α	6087	2	377	IYDGFDGFAKGQIKEIGWTDVG
		1	l	1		GWTGQGGSILGTKRVLPGK/Y
						MEEIATQMRTHSINALLIIGGFE
		1	l		i	AYLGLLELSVFVTLKLFYQHFM
		l	ŀ	l		HVLLTLIPNRRVPICPTSPSACC
						LWSVSHAFRCAYEQN
6041	36409	Α	6088	1	591	
6042	36410	Α	6089	ı	2391	PGRAAPLGLLAMDADDSRAPK
		1				GSLRKFLEHLSGAGKAIGVLTS
						GGDAQGMNAAVRAVVRMGIY
						VGAKVYFIYEGYQGMVDGGSN
						IAEADWESVSSILQVGGTIIGSA
						RCQAFRTREGRLKAACNLLQR
				ļ		GITNLCVIGGDGSLTGANLFRK
			l			EWSGLLEELARNGQIDKEAVQ
						KYAYLNVVGMVGSIDNDFCGT
						DMTIGTDSALHRIIEVVDAIMTT
		ŀ				AQSHQRTFVLEVMGRHCGYLA
		ŀ	l			LVSALACGADWVFLPESPPEEG
		i i				WEEQMCVKLSENRARKKRLNI
						IVAEGAIDTQNKPITSEKIKELV
						VTQLGYDTRVTILGHVQRGGTF
		ŀ	ŀ			SAFDRILASRMGVEAVIALLEA
i			l	l		TPDTPACVVSLNGNHAVRLPL
		ŀ				MECVQMTQDVQKAMDERRFQ
		1				DAVRLRGRSFAGNLNTYKRLAI
l		ŀ		]		KLPDDQIPKTNCNVAVINVGAP
		1				AAGMNAAVRSAVRVGIADGH
		1				RMLAIYDGFDGFAKGQIKEIGW
		i i				TDVGGWTGQGGSILGTKRVLP
		l				GKYLEEIATQMRTHSI\NALLIIG
		l	l			GF\EAYLGLLELSAAREKHEEFO
1	1	ŀ				VPMVMVPATVSNNVPGSDFSIG
		1		1		ADTALNTITDTCDRIKQSASGT
1		1	l	l		KRRVFIIETMGGYCGYLANMG
				l	1	GLAAGADAAYIFEEPFDIRDLQ
1			l	l	1	SNVEHLTEKMKTTIORGLVLRN
			l	l		ESCSENYTTDFIYOLYSEEGKG
				1		VFDCRKNVLGHMQQGGAPSPF
6043	36411	A	6090	l	459	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6044	36412	Α	6091	1930	5781	RAKSPANIIMTGSNSHITILTLN
						VNGLNSPIKRHRLASWIKSQDP
						SVCCIQETHLMCRDTHRLKIKG
		1				WRKIYQANGKQKKAGVAILVS
	Į.					DKTDFKPTKIKRDKEGHYMMV
						KGSIQQEELTILNMYAPNTGAP
	l .				İ	RFIKQVLSDLQRDLDSHTLIMG
						DFNTPLSTLDRSTRQKVNKDTQ
	1					ELNSALHQADLIDIYRTLHPKST
l						EYTFFSAPHHSYSKIDHILGSEA
					1	LLSKCKRTEIITNYLSDHSAIKL
						ELRIKNLTQSR
6045	36413	Α	6092	1	3654	
6046	36414	A	6093	1	5127	
6047	36415	Α	6094	T	3663	
6048	36416	Α	6095	1	3210	MVKGSIQQEELTILNIYAPNTG
1						ALRFIKQVLRDLQRDLDSHTIIM
						GDFHTPLSTLDRSTRQKVNKDI
						QELNSALHQEDLIDIYRTLHPKS
						TEYTFFSAPHHTYSKIDHIVGSK
						ALLSKCKRTEIITNCLSDHSAIK
						LELRIKNLTQNRSTTWKLNNLL
	1	l		į		LNDYWVHNEMKAEIKMFFETN
						ENKDTTYQNLWDTFKAVCRGK
	1			1		FIALNAHKRKQERSKIDTLTSQL
						KELEKQEQTHSKASRRQEITKIR
- CO 40	0	<u>.                                    </u>	1001		5000	AELKEIETQ
6049	36417	A	6096	1	5073 3489	MGDFNTPLSTLDRSTROKVNK
6050	36418	Α	6097	l' .	3489	DTQELNSALHQADLTDIYRTLH
	1					PKSTEYTFFSAPHHTYSKIDHIV
		1				GSKALLSKWKRTEIITNYLSDH
		1				SAIKLELRIKNPTOSRSTTWKLN
ĺ					i	NLLLNDYWVHNKMKAEIKMFF
						ETNENKDTTYQNLWDAFKAVC
		1		ŀ		RGKFIPLNAHKRKOERSKIDTL
		1			1	TSQLKELEKQEQTHSKASRRQE
		1			1	ITKIRAELKEIETOKTLOKINESR
						SWFFERINKTDRPLARLIKKKR
l		1				EKNOIDTIKNDK
6051	36419	A	6098	1	3235	EKINGIDTIKNDK
0031	30419	Α_	0090	1	3233	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown.
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6052	36420	A	6099		3070	MATLIPLLFHKHPHLTORYOFN
0052	30.20	l'`	0033	ľ	50.0	VRGGCPTSTSAIATLDPRTAVER
						LMSVFQTSAPWPFWGFTHQTP
				1		VPOPLKVKIHSSADTAADIOAN
						RVWSGPPANSKRPAAEEGKLT
						NRKDIHTKNPSVRHHHQRPKV
1	ļ.					DKTTKTGKKORRKTGNSKKOS
				}	1	ACPPPKERSSSTATEQSWTEND
		ı				FDKLREGFRRSNYSKLQDEIQT
		l				KGKEVENLEKSLDECITRITNTE
		1				KGLKKLENYVKNEETSGANAI
		l		1		NWKKGINKIDRPLARL
6053	36421	A	6100	1	3297	NWKROINKIDRFEARE
6054	36422	A	6101	1	2563	MKAEIKMFFETNENKDTTNON
1005.	50122	ľ.		ľ		LWDAFKAEEVESLNRPITGAEI
		İ				GAIINSLPTKKSPGPDGFTAEFY
		l				ORYKEELVPFLLKLFOSIEKEEI
1		ı				LPNSFYEASIILIPKPGRDTTKKE
						NFRPISLMNIDAKILNKILANRI
						QQHIKKLIHHDQVGFFPGMQG
		1		1		WFNIRKSINVIQHINRAKDKNH
				Ì		MIISIDAEKAFDKIOOPFMLKTL
						NKLGIDGTYFKIIRAIYDKPTAN
		1				IILNGOKLEAFPLKTGTROGCPL
		1		1		SPLLFNILLEVLARAIRQEKEIK
		1			-	GIQLGKEEVKLSLFADDMIVYL
						ENPIVSAONLLKLISNFSKVSGY
l					l	KINVQKSQAFLYTSNRQTESQI
				1		MSELPFTIASKRIKYLGIOLTRD
						VKDLFKENYKPLLKEIKEDTNK
		1				WKNIPCSWVGRINIVKMAILPK
l	1				-	VIYRFNAIPIKLPMTFFTELEKTI
						LKFIWNQKRAHITKSILSQKNK
1		1				AGGITLPDFKLYYKATVTKTA
1						WYCYQNRDIDQWNRTEPSEITP
		1				HTYNYLIFDKPEKNKOWGKDS
1	l			l		LFNKWCWENWLAIWRKLKLD
1		1				PFLTPYTKINSRWIKDLNVRPKT
1		1		1		IKTLEENLGITIQDIGMGKDFMS
1	1	1		1		RTPKAMATKAKIDKWDLIKLK
1	1	1	1	1		SFCTAKETTIRVNRQPTTWEKIF
		1	1	1		ATYSSDKGLISRIYNELKQIYKK
1	1	1	1	İ		KTNNPIKKWEKDMNRHFSKED
1	1	1	1			IYAAKKHMKKCSSSLAIREMQI
						KTTMRYHLTPVRMAIIKKSGNN
6055	36423	Α-	6102	1	3417	
3000	155725	<u>'`</u>	10.02	·		<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6056	36424	Α	6103	i i	3579	MPGHNLKWKLNRGTVLIETGI
		l				QLSTSTILGSASEPPSAPIPKAQV
						SSTEKLRNCIDDLKPFPALASEL
		l	i			SRRAKALQIAGFPPMKVPRDTI
						SKVCLDKTVGKLCHSGEESRK
		1				CTLICNNKHYPIQDNLQGYKTQ
l						NKFLNKEILELSALRRNAERRE
	ľ					RDLMAKYSSLEAKLCQIESKYL
						ILLQEMKTPVCSEDQGPTREVI
1	1					AQLLEDALQVESQEQPEQAFV
		ı				KPHLVSEYDIYGFRTVPEDDEE
				1		EKLVAKVRALDLK
6057	36425	A	6104	1	4371	
6058	36426	Α	6105	Ī	1825	MVKGSIQQEELTILNTYAAHTG
		1				APRLIKQVLSDLQRDLDSHTIIM
İ						GDFNTPLSTLDRSTRQKVNKDT
		1				QELKSALHQADLTDIYRTLHHK
						STEYTFFSAPHHIYSKIDHILGSK
						ALLSKCKRTEHTNYLSDHSAIK
i				l		LELWIKNLTQNHSTTWELNNLL
		İ				LNDYWVHNEMKAEIKMFFETN
				ŀ		ENKDTTYHNLWDTFKAVCRGK
				l		FIPLNAHKRKQERSKIDTLTSQL
						KELEKQEQTHSKASRRQEITKIR
		l				AELKEIETQKTLQKINESRSWFF
				l		ERINKIDRLLARLIKKKREKNQI
						DAIKNDKGDITTDPTEIQTTIRE
						YCKHLYANKLENLEEMDKFLD
	i					TYTLPRLNQEEVESLNRPITGAE
		1				IVAIINSLPTKKSPGPDGFTAKF
		1				YQRYKEELVPFLLKLFQSIEKE
	i	1				GILPNSFYEASIILIPKPGRDTTK
	i	1				KENFRPISLMNIDAKILNKKLA
		1		ĺ		KRIQQHIKKLIHHDQVGFIPGM
						QGWFNIRKSINVIQHINRAKDK
				l		NHMIISIDAEKAFDKIQQPFMLK
1	1					TLNKL\GIKYLGIHLTRDVKDLF
l						KENYKPLLKEIKEDRNKWKNIP
						CSWVGRINIVKMAILPKNILITL
		_				QLLLVLPELSTLIPLWLPALAGQ
6059	36427	Α_	6106	1	4449	

SEO ID	ISEO ID NO:	Tales	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6060	36428	IA.	6107	824	3693	AWKGTTDRSTRQKVNKDTQEL
0000	30420	l^	0107	024	50,55	NSALHOADLIDIYRTLHPKSTE
						YT/FFSAPHHTYSKIDHIVGSKA
	1					LLSKCKRTEITNYLSDHSAIKL
	1			ı		ELRIKNFTQSRSTTWKLNNLLL
						NDYWVHNEMNAEIKMFFETNE
				1		NKDTTYONLWDAFKAVCRGK
						FIALNAHKRKOERSKIDTLTSOL
	1	1		l		KELEKOEOTHSKASRROEITKIR
		1				AELKEIETOKTLOKINESRSWFF
						ERITKSDRPLARLIKKKREKNOI
						DTIKNDKGDIT
6061	36429	A	6108	1	3297	
6062	36430	В	6109	112	3300	
6063	36431	A	6110	3	3316	
6064	36432	Α	6111	I	3457	
6065	36433	Λ	6112	I	3170	MVKGSIQQEELTILNIYAPNTG
						APRFIKQVLSDLQRDLDSHTLI
ļ.		l				MGDFNTPLSTLDRSTRQKVNK
					i e	DTQELNSALHQADLIDIYRTLH
						PKSTEYTFFSAPHHTYSKIDHIL
		1				GSKALLSKCKRIEIITNYLSDHS
						AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKTEIKMFF
						ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKEERSKIDTL
				1		TSOLKELEKOEORHSKPSRROE
		1				ITKMRAELKEIETQ
6066	36434	В	6113	1	4753	TRANSCEREIQ
6067	36435	В	6114	1	3384	
6068	36436	Α	6115	1	3345	
6069	36437	Α	6116	I	3780	
6070	36438	A	6117	1	3720	
6071	36439	Α	6118	1	3894	
6072	36440	Α	6119	1	3335	MVKGSIQQEELTILNIYAPNTG
		1				APRFIKQVLSDLQRDLDSHTLI
l		1				MGDFNTPLSTLDRSTRQKVNK
l						DTQELNSALHQADLIDIYRTLH
		1				PKSTEYTFFSAPHHTYSKIDHIV
l		1				GSKALLSKCKRTEIITNYLSDHS
						AIKLELRIKNLTQSRSTTWKLN
						NLLLNDYWVHNEMKAEIKMFF
						ETNENKDTTYQNLWDAFKAVC
						RGKFIALNVYKRKQERSKIDTL
						TSQLKELEKQEQTHSKASRRQE
(0.00	26111	١	(120	ļ	2000	ITKIRAELKEIETQ
6073 6074	3644I 36442	A	6120	I	3780 3852	
6074	36442	A	6121	I	3345	
6076	36444	B	6123	1	6136	
6077	36444	В	6124	1	3924	
0077	20442	$\Gamma_D$	0124	1.	J/67	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6078	36446	В	6125	295	4185	
6079	36447	Α	6126	1	405	
6080	36448	Α	6127	1	1059	
6081	36449	Α	6128	2	518	EKATCDENDSVSNIATEIKEGQ
	1	l		1		QSV\HVSPQKQSAWKVIFKKKV
				1		SLLNIATRITGGGKSGTVSSQKQ
			ĺ	1		PPSKATSDKTDSALNIATEIKDG
	1	1				LQCGTVSSQKQPALKATTDEED
	4					SVSNIATEIKDGEKSGTVSSQKQ
		1				PALKATTDEKDSVSNIATEIKD
		1				GEKSVTVSSQKQPASK
6082	36450	A	6129	I	843	
6083	36451	Α	6130	1	432	
6084	36452	A	6131	2	835	CGSAQAAAAAAEEATEKIPAL
						RP/ASAVGAAGALAVLRDPRA
l	1					WREAGSKS/PETPFS*CQGA/HG
		1				GGQFCPSGTAFPGKMKVMMR
	1	l				KRKKKGQCLPGICRSLKRRKSP
		l				RSPGM/IGYSTLSIPPEMLASYQ
						SYSSTFHSLEEQQVCMA/G*HR
		1				QMPGADKPVRACQRVLAGVW
						AGFTMRHQSRLY*ECSICGVIFR
						HRCVAHLLGRAIGAGLFVITPA
		ı				GERGMCCKAIKLGNARVFPVT
		1				TL*NDGQCQACMHAG/TTLEDP
	1					GKNYISSSPSSSSSSSSPSSPRVPS
6085	36453	С	6133	278	446	
6086	36454	Α	6134	1	1152	
6087	36455	Α	6135	1	639	
6088	36456	Α	6136	12	1436	
6089	36457	Α	6137	367	1056	
6090	36458	A	6139	I	4263	
6091	36459	Α	6140	1	1311	
6092	36460	Α	6141	1093	1358	MQKKPLTKFNNPSC*KLSIN*V
		l				LMGRISK*VTTTATTTTTTTT
			1			TITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
		1				TTTTTTMGPTLPLIPIGLGS
6093	36461	Α	6142	1	699	
6094	36462	Α	6143	1	489	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ļ.		sequence		
6095	36463	Ā	6144	5	916	ALGGTPMLGKLAMLLWVOOA
0093	30403	l^	0144	ľ	710	LLALLLPTLLAOGEARRSRNTT
			İ			RPALLRLSDYLLTNYRKGVRPV
		1		1		RDWRKPTTVSIDVIVYAILNVD
		l				EKNOVLTTYIWYRQYWTDEFL
1		1				OWNPEDFDNITKLSIPTDSIWVP
ľ		1		1		DILINEFVDVGKSPNIPYVYIRH
ļ		1		1		OGEVONYKPLQVVTACSLDIY
l		1				NFPFDVONCSLTFTSWLHT/SPG
		1			,	HOHLFVALARKGEIRQECLHEP
	1	1		l		GRVGVAGGAALLSGVOHGKO*
		1				LLCRNEVLCGHPPAAPLLCGOP
						ATAOHLPHGHGHRGLLPAPOO
						WREGLFONYTPPGLLGLPDHRF
6096	36464	A	6145	5	756	WIGGEL GITTITI GEEGEL BING
6097	36465	A	6146	1	471	
6098	36466	A	6147	184	1097	ALGGTPMLGKLAMLLWVQQA
00,0	100,00	ľ				LLALLLPTLLAQGEARRSRNTT
		l	1			RPALLRLSDYLLTNYRKGVRPV
		l	1			RDWRKPTTVSIDVIVYAILNVD
		1				EKNOVLTTYIWYRQYWTDEFL
		İ				OWNPEDFDNITKLSIPTDSIWVP
		l				DILINEFVDVGKSPNIPYVYIRH
						QGEVQNYKPLQVVTACSLDIY
ĺ		1			1	NFPFDVQNCSLTFTSWLHT/SPG
	1					HQHLFVALARKGEIRQECLHEP
		1				GRVGVAGGAALLSGVQHGKQ*
		l				LLCRNEVLCGHPPAAPLLCGQP
		l				ATAQHLPHGHGHRGLLPAPQQ
		1				WREGLFQDYTPPGLLGLPDHRF
6099	36467	Α	6148	3	672	
6100	36468	Α	6149	3	398	LRKIKIDLGKFSDNPDGYIDVLQ
		l				GLRQSFDLTWRDIMLLLDQSLT
	1	1		l	I	PNEKSAAKTAAREFGDLWFV/S
			1	1		FQN*SCKTTNRSSNGAPDAVHD
					1	*D/PTADPWTGPLAHALMLMTL
	1	1	1		I	KAPLTRKSQLHDPYYAPIQQEA
		_				v
6101	36469	Α	6150	1	420	

NO:	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
		of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
		sequence		09/540,217		of peptide sequence	delction, \=possible nucleotide insertion)
GNKDPGGTLERGKVEDASC   TSRTLKETSGKAEHRKKQDG   CSPQGKNALKMYSGEFDPYS   CVPFSLSDLKQLKIDLGRFSD   DGYIDVLQGLGGSPGLTWRE   MILLLDGTLTPNERNATITAAI   FGDLWCLSQVDRMTTEERI   FPTGQQAVPSADPH*DTESEI   DWCCRHLLTCVLEGLRKTRK   AVNFSVMSTVTQGKEENPTA   ERLREALRKHTSLSPDSIEQO   LKIKFITRSAADIRKQTSKVHI   PGAKLKTPY   FGRALKKTPSLSPDSIEQO   LKIKFITRSAADIRKQTSKVHI   PGAKLKTPY   FGRALKTPY					sequence		
GNKDPGGTLERGKVEDASC   TSRTLKETSGKAEHRKKQDG   CSPQGKNALKMYSGEFDPYS   CVPFSLSDLKQLKIDLGRFSD   DGYIDVLQGLGGSPGLTWRE   MILLLDGTLTPNERNATITAAI   FGDLWCLSQVDRMTTEERI   FPTGQQAVPSADPH*DTESEI   DWCCRHLLTCVLEGLRKTRK   AVNFSVMSTVTQGKEENPTA   ERLREALRKHTSLSPDSIEQO   LKIKFITRSAADIRKQTSKVHI   PGAKLKTPY   FGRALKKTPSLSPDSIEQO   LKIKFITRSAADIRKQTSKVHI   PGAKLKTPY   FGRALKTPY	6102	36470	A	6151	ti -	878	TLLPPRPGVGSDYPNIPGCPMW
CSPQGKNALKMYSGEFDPVR							GNKDPGEGTLERGKVEDASOR
CVPFSLSDLKQLKIDLGRFSD   DGYIDVLQGLGQSFDLTWRE   MILLDQTLTPNERNATITRAI   FGDL WCLSQVNDRMTTEERI   FPTGQAQVPSADPH*DTESSE   DWCCRHLLTCVLEGLRKTRK   AVNFSVMSTVTQGKEENPTA   ERLREALRKHTSLSPDSIEGO   LKIKFITRSADDIRKQTSKVHI   PGAKLKTPY			l				TSRTLKETSGKAEHRKKODGK
CVPFSLSDLKQLKIDLGRFSD   DGYIDVLQGLGQSFDLTWRE   MILLDQTLTPNERNATITRAI   FGDL WCLSQVNDRMTTEERI   FPTGQAQVPSADPH*DTESSE   DWCCRHLLTCVLEGLRKTRK   AVNFSVMSTVTQGKEENPTA   ERLREALRKHTSLSPDSIEGO   LKIKFITRSADDIRKQTSKVHI   PGAKLKTPY							CSPQGKNALKMYSGEFDPVRV
MILLDOPTLTPNERNATTIAAI   FGDLWCLSQVNDRMTTERRI   FPTGQQAVPSADPH*DTESSE   DWCCRHLITCVLEGLRKTRR   AVNFSWMSTVTQGKEENPTA   ERLREALRKHTSLSPDSIEGQ   LKIKFITRSAADIRKQTSKVHI   PGAKLKTPY	ŀ		1				CVPFSLSDLKQLKIDLGRFSDNP
FGDL.WCLSQVNDRMTTERRI	ŀ						DGYIDVLQGLGQSFDLTWRDI
PFTGQQAVPSADPH*DTESSED   DWCCRHLLTCVLEGLRKTRK   AVNPSWMSTVTQGKEENPTA    ERLREALRKHTSLSPDSIEQO    LKIKFITRSAADIRKQTSKVHI    FGAKLKTPY			1				MLLLDQTLTPNERNATITAARE
PFTGQQAVPSADPH*DTESSED   DWCCRHLLTCVLEGLRKTRK   AVNPSWMSTVTQGKEENPTA    ERLREALRKHTSLSPDSIEQO    LKIKFITRSAADIRKQTSKVHI    FGAKLKTPY	l						FGDLWCLSQVNDRMTTEERER
AVNFSWASTVTOGKEEMPTA   ERLREALRKHTSLSPDSIEGQ   LKIKFITRSAADIKKQTSKVHI   PGAKLKTPY	i		ĺ				FPTGQQAVPSADPH*DTESEHG
BERLEALRKHTSLSPDSIEGO							DWCCRHLLTCVLEGLRKTRKK
LKIKFITRSAADIRKQTSKVH    PGAKLKTPY							AVNFSVMSTVTQGKEENPTAFL
PGAKLKTPY							ERLREALRKHTSLSPDSIEGQLI
Section   Sect							LKIKFITRSAADIRKQTSKVHLR
Section							PGAKLKTPY
Section   Sect							
STOPPING   STOPPING					-		
SIV*GKDTPLNAIVIHEVYEE   AAVDGRLWAGDQILEVNGV    RNSSHEEAITALMQTPQKVRI    VYRDEAHYRDEENLEIFPVDI    6107 36475							
AAVGGR.WAGDQILEVNOV. RNSSHEAITALMQTPQKVRI	6106	36474	A	6155	]1	335	
RNSSHEEAITALMQTPQKVRI   VYRDEAHYRDEENLEIFPVDI   6108   36476   A 6157   109   4991   6108   36476   A 6157   109   4991   6108   36476   A 6158   3   862   6110   36478   A 6159   1   1857   6111   36479   A 6160   3   100   6112   36480   A 6161   1   537   6113   36481   A 6162   125   1184   6114   36482   A 6163   875   1506   LSIYLVTQKAA/SSEWGPEQE ALQEVQAAVQAALILEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WARAGLEPYDP GPVVLEVSLADRDAWSLW-WYTAGALOPISRKSLKDSEG SSGWAELRAVHLAWW-WK KWPDVRLDTDSWAV/ANGLEPYDP GPVVLEVSLADRDAWSLW-WYTAGALOPISRKSLKDSEG SSGWAELRAVHLAWW-WK KWPDVRLDTDSWAV/ANGLEPYDP GTRI GTRI GTRI GTRI GTRI GTRI GTRI GTRI			1				
VYRDEAHYRDEENLEIFPVDI							
\$\frac{6107}{6108}		l					
6108   36476	(100	06106	١.	(156	100	4407	VYRDEAHYRDEENLEIFPVDLQ
6109   36477   A   6158   3   862							
Set   Set							
			-				
			_				
ALQEVQAAVQAALILEPYDP. GPVVLEVSLADRDAVWSLW APIGESQQRPLGFWSKALPSS DHKACHAQQHSIIKWKWYIH RARAGPEGTNSSARYAATM* WYTASALQPLSRKSLKOSSG SSQWAELRAVHLAVHVAWK KWPDVRLDTDSWAV/ANGL/ WSGTWKEHDRKIGDKEVWG GTRI 6115 36483 A 6164 I 1566 6116 36484 A 6165 I 1098 6117 36485 A 6166 I 538 6118 36486 A 6167 410 625 LTLVPFSFSVVLTPLPKGNTIR *TGIL*GWNLSWKGTLGFSVT							LSIYLVTOKAA/SSEWGPFOEK
GPVVLEVSLADRDAVWSLW    APIGESQQRPLGFWSKALPSS    DHKACHAQQHSIIKWKWYIII    RARAGPEGTNSSARYAATM    WITASALQPLSRKSLKDSSEG    SSQWAELRAVHLAVHVAWK    KWPDVRLDTDSWAV/ANGL/    WSGTWKEHDRKIGDKEVWG    GTRI     6115   36483   A 6164   I   1566     6116   36484   A 6165   I   1098     6117   36485   A 6166   I   538     6118   36486   A 6167   410   625     LTLVPFSFVVLTPLPKGNTIR    *TGIL*GWNLSWKGTLGFSV		30.02	l' .	0.05	10.5	1.2.0	
APIGESQQRPLGF WSKALPSS   DHKACHAQQHSIIK WKWYIH RARAGPEGTNSSARY AATM* WTTASALQPLSRKSLKDSSEG SSQWAELRAVHLAVHVAWK KWPDVRLDTDSWAVIANGL/ WSGTWKEHDRKIGDKEVWG GTRI     1566							
DHKACIAQORSIIKWKWYIH    RARAGPEGTNSSARYAATM*							
RARAGPEGTNSSARYAATM   WITASALQPLSRKSLKDSSEG   SSQWAELRAVHLAVHVAWK   KWPDVRLDTDSWAV/ANGL/   WSGTWKEHDRKIGDKEVWG   GTRI   G115   36483   A 6164   1   1566     G116   36484   A 6165   1   1098     G117   36485   A 6166   1   538     G118   36486   A 6167   410   625   LTLVPFSFSVVLTPLPKGNTIR   *TGIL*GWNLSWKGTLGFSVVL   *TG			l				
WITASALQPLSRKSLKDSSEG   SSQWAELRAVHLAVHVAWK   KWPDVRLDTDSWAVANGLA   WSGTWKEHDRKIGDKEVWG   GTRI   GTRI   36483   A 6164   I   1566     6116   36484   A 6165   I   1098     6117   36485   A 6166   I   538     6118   36486   A 6167   410   625   LTLVPFSFSVVLTPLPKGNTIR   *TGIL*GWNLSWKGTLGFSVT		1					
SSQWAELRAVHLAYHVAWK   KWPDVRLDTDSWAV/ANGL/  WSGTWKEHDRKIGDKEVWG   GTRI		i	l				
KWPDVRLDTDSWAV/ANGL/ WSGTWKEHDRKIGDKEVWG GTRI     1	1					0	
WSGTWKEHDRKIGDKEVWG  GTRI							
GTRI  6115 36483 A 6164 I 1566 6116 36484 A 6165 I 1098 6117 36485 A 6166 I 538 6118 36486 A 6167 410 625 LTLVPFSFSVVLTPLPKGNTIR *TGIL*GWNLSWKGTLGFSVT							WSGTWKEHDRKIGDKEVWGR
6116 36484 A 6165 I 1098 6117 36485 A 6166 I 538 6118 36486 A 6167 410 625 LTLVPFSFSVVLTPLPKGNTIR *TGIL*GWNLSWKGTLGFSVT							
6117 36485 A 6166 I 538 6118 36486 A 6167 410 625 LTLVPFSFSVVLTPLPKGNTIR *TGIL*GWNLSWKGTLGFSVT			Α		1		
6118 36486 A 6167 410 625 LTLVPFSFSVVLTPLPKGNTIR *TGIL*GWNLSWKGTLGFSV1							
*TGIL*GWNLSWKGTLGFSVT	_		_				
	6118	36486	Α	6167	410	625	
	1		1				*TGIL*GWNLSWKGTLGFSVTA
	1		1				QPSSGTPRTALGSRTTKPLLVSL
LQV							LQV

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop endon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
6119	36487	Α	6168	821	1428	QVTDVQDFPLKCKIQWRRTVR
						GDLQ/PFTRVTVHWGKGNDQT
		l				FQGLLDTGSELTLIPGDPKRHC
						GPPVKIGAYGGQIINGVLAQVQ
	ļ	l				LTVDAVGPWTHPVV/I/SPVPECI
						IGIDILSSWQ/NSHIGSLTGRVRA
	ł					TMVGKAKWKPLELPLPRKIVN
l	l				İ	QKQYHIPGGIAEIGATIKDLKDT
l		i				G\VIPTSPFNSPI*PMQKTDGSW
						RMTVDYL
6120	36488	Α	6169	203	850	DVEHVGKMRRRWRRRVVVAD
						GNVVKPMSCAGDLQ/PFTRVTV
1		1				HWGKGNDQTFQDLLDTGSELT
1		l		ł		LIPGDPKRHCGPPVKIGAYGGQI
	1	1	1			INGVLAQVQLTVDAVGPWTHP
1	l	ŀ				VV/I/SPVPECIIGIDILSSWQ/NSH
	1					IGSLTVHLSSDPKGCHSEWGPE
ŀ						QEKALQEVQAAVQAALILEPY
				1		DPAGPVVLEVSLADRDAVWSL
	1					WQAPIGESQORPLGFWSKALPS
6121	36489	A	6170	1	864	
6122	36490	A	6171	1	205	VPDFPAKPIOGPHFNSRYL/REA
						VHGEAVHAPFIAGQPLT**ELM
i	1					SIFPOFOFFLYRRLDSHSGOSWQ
		1				1
6123	36491	Α	6172	1	3039	
6124	36492	Α	6173	1	1364	MIISIDAEKAFDKIQQPFMLKTL
i					1	SKLEETASPSPVVATYTPQPML
		l			1	PSAFPPLSEEINPVLPETTVMAS
1		1				PEAVTRODNVDSPQKPPPTPMF
		l				ASRPITRLKPRRAPSEEGIORLK
				1		KIGMVEWISHFRPTPLSMEGPE
		1				HILLTNTLLNRYVKAAPASLKS
		1				PLTALLFMSDLTVGTTFSQLQN
1		1	ł			LNTMGIFGSSCDRSQVAALNHQ
				l	İ	ROVPELIIGIDILSSWONPHIGSL
				l		NGRGYINSLALCHNLIRRDLDR
1	1	1				FLLPODITLVHYIDHIMRLDSVK
1		1		1		DKWLHLAPPTTKKEAQCLVGL/
		1	1			FGFWRQHIS\LWRQPLACYWAL
	1					VETEHLTMGHQVTMQPELPIM
						NWLLSDPSSYKPAPMASWGVP
	1	1				YGQLTEEEKTRAWFTDGSARY
1	1	1				TETTRKWTAVAIQPLSRTSLKD
		1	1			SNEGKSSHQQAKNGITVLAGVI
	1		1	l		DPDYQDEISL/LTPQWRCHPGSS
		_				VWRASSLGISHPP
6125	36493	A	6174	114	1996	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6126	36494	A	6175	I	475	MGRNQNRKAENSKNWNASSP KEHNSSPAREQNWREDEFNELT EVGFRRSVITNFSDLKEHVLTH CKEAKILEKRLDKWLTKITSVE KS/CK*PDG/J**KPQYENFMKHT QASIADLIKRKKRYQ**LKIKLM K*SKKTR**EKKYKLPSENTTN
		1				TSMQIY
6127	36495	A	6176	179	393	NKRGYKQMEEHSMLMDKKNQ YYENGHTAQGN*AGEGNKGYS IRKTGSQIVPLCR*HDCISRKPD CLSPKSP
6128	36496	A	6177		710	IAARELRDECTSFSSOFHQLEER VSVIEDDMNEMKQEEKFREKGI KRSEQSLQEIWDYMERPNLCLI GVPESDGENGIKLEDTLQDIIGK DFPNLGROANIQQEIGRMPQR YSSRRATPRHIVERTTKEIQTTIR EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPITGS EIEAIINSLPTKKSPRPDGFTAEF GIEPAISTENSFYEASIILIPKLGRDTTK KENFRPISAINIDAKILNKILAN QMQNIKNLIRHDQAGFIPGMQ CWFNIRKSINVIQHINISTROKN HMISIDAEKAFYKIQOPFILKT NKLENKIPRNPTKYKGEGPJEK ENYKLIMLKAFAYKIQOPFILKTL NKLENKIPRNPTKYKGEGPJEK ENYKLIMLKAFAYKIQOPFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILKTL NKLENKIPRNPTKYKGEGFILTN VERNYKLENKIPRNPTKTTLEENL ONTIGDIGMGKDEMKYPKAM TURNSWIKGLNVPRKTITCHEENL ONTIGDIGMGKDEMKYPKAM TURNSWIKGLNVPRKTITCHEENL ONTIGDIGMGKDEMKYPKAM TURNSWIKGLNVPRKTITCHEENL ONTIGDIGMGKDEMKYPKAM TURNSWIKGLNVPRKTITCHEENL ONTIGDIGMGKDEMKYPKAM TURNSWIKGLNVPRKTITCHEENL ONTIGDIGMGKDEMKYPKAM TURNSWIKGLNVPRKTITCHEENL ONTIGDIGMGKDEMKYPKAM TURNSWIKGLNVPRKTITCHEENL ONTIGDIGMGKDEMKYPKAM TURNSWIKGLERFGSI
6129	36497	Α	6178	464	724	IGEVLLDNILQRVFQLGSILPITF RYTNQT*IWSWTLFWLVSY
6130	36498	A	6179	1	2022	
6131	36499	A	6180	i	882	
6132	36500	c	6181	i i	1935	
6133	3650I	Ā	6182	i	672	
6134	36502	В	6183	140	2195	
6135	36503	A	6184	26	354	

peptide juence		SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	cedon for last amino acid of peptide sequence	Amino add sequence ( Netluknown,  "Stop ordon," possible nucleotide  deletion, "possible nucleotide insertion)  SLEDAMSLKDDDSGDHDQNEE NSTQKDGEKEKTERDKNQSSS KRKAVPVGPAEHPLQYNYTTW SRRTPGRFTSGSVEQNIKQIG TFASIVEQFWRFYSHMVRPGDL TGHISDFHLFKEGIKPMWENDDA KNKOJGKWIRLJAKRGFGSRCW
	A		sequence		SLEDAMSLKDDDSGDHDQNEE NSTQKDGEKEKTERDKNQSSS KRKAVVPGPAEHPLQYNYTFW YSRRTPGRPTSSQSYEQNIKQIG TFASIVEQFWRFYSHMVRPGDL TGHSDFHLFKEGIKPMWEIDDA
504 .	Α	6185	<u> </u>	747	NSTQKDGEKEKTERDKNQSSS KRKAVVPGPAEHPLQYNYTFW YSRRTPGRPTSSQSYEQNIKQIG TFAS\VEQFWRFYSHMVRPGDL TGHSDFHLFKEGIKPMWE\DDA
504	Λ	6185	86	747	NSTQKDGEKEKTERDKNQSSS KRKAVVPGPAEHPLQYNYTFW YSRRTPGRPTSSQSYEQNIKQIG TFAS\VEQFWRFYSHMVRPGDL TGHSDFHLFKEGIKPMWE\DDA
504	^	6185	86	747	NSTQKDGEKEKTERDKNQSSS KRKAVVPGPAEHPLQYNYTFW YSRRTPGRPTSSQSYEQNIKQIG TFAS\VEQFWRFYSHMVRPGDL TGHSDFHLFKEGIKPMWE\DDA
					KRKAVVPGPAEHPLQYNYTFW YSRRTPGRPTSSQSYEQNIKQIG TFAS\VEQFWRFYSHMVRPGDL TGHSDFHLFKEGIKPMWE\DDA
					YSRRTPGRPTSSQSYEQNIKQIG TFAS\VEQFWRFYSHMVRPGDL TGHSDFHLFKEGIKPMWE\DDA
					TFAS\VEQFWRFYSHMVRPGDL TGHSDFHLFKEGIKPMWE\DDA
					TGHSDFHLFKEGIKPMWE\DDA
					NENC/CEMINDIAPEGEGERCIM
					HAVIAGOE MAINTENANCE OBLICAM
					ENLILAMLGEOF\MVGEEICGG
					CGVCPAFQEDIIS\IWNKTASDQ
		1			ATTARIRDTL\RRVL\NLPANTI
					MEYKN
505	Ā	6186	23	127	
		6187	2	419	
					AVFFFFFFFFFFFFFFFFFFF
300	^	0107	1,7	[575	FFFFFFFFFFSSSSSSFFFFSFFL
					FFFFKLKELRLVI*PLNPEN*ESC
- 1		1			PLFSPVNLDMP*TFKDKRWKV
ŀ					NWARSTSROOLLESARTKSWA
					EREGGTRWRAW
500		(100	227	420	KNFLPNCSAKELFFFFFFFFFF
509	A	6190	221	420	LLLLLLYFKF/MI*WFYKHLAF
					PLLAFILSPTAL*RGVFHH
-10		(101	400	500	PLLAFILSPIAL-ROVFHH
512	A	6193	2	109	FTFWHDFAAAGTGCSFPCLVLP
					SWW*QNLSAFACL
513	A	6194	110	377	QWISRQKPYKPEKRGDQYSTFL
		1			*EC*ILVPPLFWLVGFLPRDPLL
1					V*WAYGCP*HFFLHFNLGESNN
	_				YVSWGCSS
			1.		
	Α				
0.10			1		
519	Ā	6200	716	1001	SMPASTHLILVGSCSWKMVIVL
					PLVTHFLFTALTVPWNLPWVEL
					YWNM*TM*LRSMKESLMATIF
					TLPELKA\VLHEKLQ*LQSTEDL
		1			*HGLLGG
520	Ā	6201	5772	5971	TANIIMTGSNSHITILTLNVNRL
				1	NARIKRHRLENCIKSODPSVCCI
					*ETHLMCRDTYRLKIKGWSN
521	A	6202	1	974	
			1		
5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	107 108 110 111 112 113 115 115 116 117 118 119	107 A 108 A 109 A 100 A 100 A 101 A	107 A 6188 108 A 6189 109 A 6190 110 A 6191 111 A 6192 112 A 6193 113 A 6194 115 A 6196 116 A 6197 117 A 6198 118 B 6199 119 A 6200	107	100

SEOID	SEO ID NO:	Tatas.	SEO ID NO:	Nucleatide	Nucleotide Insetion of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			İ	sequence		
6155	36523	IA.	6204	51	424	MAPKODPKPKFQEGERVLCFH
0133	30323	^	0204	[31	424	GPLLYEAKRVKVAIKD/ITREI/H
		l		ł		SYITVVGIKIGMNGFRRAKYSN
		ĺ				TWTPICRNSENFKKPISKFVL*T
		l	1			EY*GEMPVD*FWTWNEOWRSC
						WLPCLYNDTSDLSAGV
6156	36524	A	6205	h	3827	MOKAIRLNDGHVAPLGLLARK
0130	30324	A	0205	l'	3827	
1		l	l		ł	DGTRKGYLSKRSSDNTK WQTK
						WFALLQNLLFYFESDSSSRPSG
1		l	İ			LYLLEGCVCDRAPSPKPALSAK
		ł				EPLEKQHYFTVNFSHENQKALE
						LRTEDAKDCDEWVAAIAHASY
						RTLATEHEALMQKYLHLLQIVE
					ì	TEKTVAKQLRQQIEDGEIEIERL
			Ì			KAEITSLLKDNERIQSTQTVAPN
						DEDSDIKKIKKVQSFLRGWLCR
		l				RKWKTIIQDYIRSPHADSMRKR
						NQVVFSMLEAEAEY
6157	36525	Α	6206	I	900	
6158	36526	С	6207	172	501	
6159	36527	Α	6208	499	848	KIRVPAAVAGLSPPLGPWSLRS
						PSQPERCCPWRNSSWWTAPRTS
			ł			IITAAKGVSPARLSSISCTTRGS
						WVKTPTPTRARMVIASSNLERP
						SALSRM*PTSQSMTRKRWWRL
		<u> </u>				WPSTTL
6160	36528	A	6209	3	495	SCAQTFPKLDTFLEHIKSHQEEL
						SYRCHLCGKDFPSLYDLGVHQ
				!		YSHSLLPQHSPKKDNA/CLQVF
		1				PCERYLRRHLPTHGSGGRFKCQ
		1				VCKKFFRREHYLKLHAHIHSGE
		1				KPYKCSVCESAFNRKDKLKRH
		1		ì		MLIQYDEVRQGLGMVPGTQKV
						LNKCFCHNVKKKK
6161	36529	Α	6210	667	2142	
6162	36530	Α	6211	1	396	
6163	36531	A	6212	213	446	
6164	36532	Α	6213	101	580	VAGVGSLPRSMEDDAPVIYGLE
		l l				FQARA\LTPQT\AETDAIRFLVG
		ŀ				TQSLKYDNQIHIIDFDDENNIIN
						KNVLLHQS/AGEIWHISASPADR
		1				GVLTTCYNRTSDSKVLTCAAV
		1				WRMPKELESGSHESPDDSSSTA
			1	l		QTL\ELLCHLDNTAHGNMACV
				l		VWEPMGDG
6165	36533	A	6214	I	933	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in HSSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			ŀ	sequence		
6166	36534	A	6215	3	404	RLKEKKLVKEVIAVSCGPAOCO
0.00		`		ľ		ETIRTALAMGADRGIHVEVPPA
						EAERLGPLQVARV/AVVTADLR
						LNEPCYATLPNIMKAKKKKIEV
						IKPGDLGVDLTSKLSVISVEDPP
						QRTAGVKVETTEDLVAKLKEIC
6167	36535	A	6216	1	408	QUITTOVICTE I ESSTANDADIO
6168	36536	Ā	6217	88	871	MADVRVLVAVKRVIDYAVKIR
						VKPDRTGVVTDGVKHSMNPFC
						EIAVEEAVRLKEKKLVKEVIAV
						SCGPAQCQETI\RTALA\MGA\D
		l				RGIHVE\VPPAEAERF/GVPLQV
						ARVLGOLAKK\EKVDLVLLGK
		1				QA\IACTDCNQ\TGQMTAGFLD
						WPQGTF\ASQVTLEGDKLKVER
		1				EIDGGLETLRLKLPAVVTADLR
ļ		1				LNEPRYA\TLP\NIMKAKKKKIE
		l		l		VIKPGDLGVDLTSKLSVISVEDP
		l		l		PORTAGVKVETTEDLVAKLKEI
6169	36537	A	6218	1	1023	I QKING TKYEI IEBETAKEKEI
6170	36538	Α	6219	110	842	
6171	36539	Α	6220	I	122	
6172	36540	Α	6222	I	1257	MNDATAVQEGSQMYSWQKLT
		l		l		PTGPFIMQPEGMGRLFAINKMA
						EGPFPEHYEPIETPLGTNPLHPN
1				ŀ		VVSNPVVRLYEQDALRMGKKE
		1		ł		QFPYVGTTYRLTEHFHTWTKH
						ALLNAIAQPEQFVEISETLAAAK
		1				GINNGDRVTVSSKRGFIRAVAV
				ŀ		VTRRLKPLNVNGQQVETVGIPI
		1				HWGFEGVARKGYIANTLTPNV
		l				GDANSQTPEYKAFL/GQHREGV
		l				RN*LHHAAFSGA*LOCFQYAH
		1				NSRKNN
6173	36541	Α	6223	737	941	WLRMMEHRILFPLWKRESKKA
		1				HYVOSSVLLCLGMLR*KYKGK
						KGKKERKKKDEKRKGNGKKRI
						KIHSI
6174	36542	Α	6224	I	1072	
6175	36543	Α	6225	1	585	
6176	36544	A	6226	1	930	
6177	36545	A	6227	28	392	AGEVPLQLPPAAVCSACLQRPA
						LWWNSSFFL*SCLHALFH*VDL
		1				QSLIAFLLLD*SSY*YLCMLHEV
	1	1	1	I		LVLCFSAPSGHLCSSLS*LF*LAI
1		1	l		1	HLTFFQGS*LPCIGLEHASLAQR
		L				SLLLPTF
6178	36546	Α	6228	1	271	SAIVTFVCFMKFSCCVFQLHQV
			l			FHVL\FKLVILVSSSCNLFSRFLA
			1		1	SLHWVTTCSFSSEEFVITHLLKP
1		1		[		APVNSSNSFSVQFCSLAGKEL

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6179	36547	Α	6229	11	1089	MGWRPRWLPYLYWGFOSDLC
	l .					PHCKRKAQEEDSLAAQAASHP
	l					RLSANSKNNSWGKOYSYALFK
		ŀ				AMRHMLCIGYGRQAPAAVSDV
						WLTMLSM\IVGATCYAMFIGH/
						ATALIQVLDCSRRQYQEKVVLP
						REHPNIGSSQEGGTWHQTVGL
						QQTSDKFDANDPILKDQTQEW
		1				SGSATFTSDGKIRLFYTDYSGK
						HYGKQSLTTSAANTGTENGYQ
		1				GEESLFNKAYYGGGTNFFRKES
		ı				QKLQQSATTRDAELANGALGII
	l	l				ELDNDSPLKKRGATQRSSEENI
		l				TLKAYKRDVRSLLMLTRNEDV
	1					ADSLNSSKKRQNYQLPSIRSVT
		1				RCKKIGVCAKGIGCGQGTHYLS
						VSILNTADRDRRKLGFTRTSMY
6180	36548	В	6230	1	1140	
6181	36549	Α	6231	3	204	GSDYELGLW*PWLTSEATDLH
				1		GECYSS*SGASGVVRSSLWARG
1					1	LAGFRSEAADLRGRESVAVTN
6182	36550	Α	6232	I	1296	
6183	36551	В	6233	1	1686	
6184	36552	Α	6234	I	627	
6185	36553	A	6235	570	736	SATFGRSSRSGCSG\FPAASRRG
						RLPLSPPPWPAV\RVYPCGMLD
		Ļ.				NKASAAHPPKKK
6186	36554	A	6236	11	103	OLODO A PROPERTO MANAGEMENTO MANAGEMENTO
6187	36555	A	6237	699	887	GLQPPAPRETRPLY*TLAWNLH
						FLFVSPLDSCDLVRSVLTCLSPP
61.00	0.000	ļ.	(222	-	803	GNSPSFDMHRYQLPCVH
6188	36556	A	6238	2	1277	YKETYLIHLFHTFTGLSIAYFNF
6189	36557	A	6239	2	12//	GNQLYHSLLCIVLQFLILRLMG
					i	RTITAVLTTFCFQMAYLLAGYY
ļ.		1			i	YTATGNYDIKWTMPHCVI.TLK
			1			LIGLAVDYFDGGKDQNSLSSEQ
		1				QKYAIRGVPSLLEVAGFSYFYG
	1					AFLVGPQFSMNHYMKLVQGEL IDIPGKIPNSIIPALKRLSLGLFYL
						VGYTLLSPHITEDYLLTEDYDN
		1				
	1				1	HPFWFRCMYMLIWGKFVLYKY
		1		1		VTCWLVTEGVCILTGLGFNGFE
1		1			1	EKGKAKWDACANMKVWLFET NPRFTGTIASFNINTNAWVARYI
1	1	1		1	1	
l	1	1				FKRLKFLGNKELSQGLS\MLFLF
1	1	1				LWHGLHSGYLVCFQMEFLIVIV
1	1		1	1		ERQAARLIQESPTLSKLAAITVL
	3					QPFYYLVQQTIHWLFMGYSMT
	1					AFCLFTW\DKWLKVYKSIYFLG
ı	I	1	1	1	1	HIFFLSLLFILPYIHK\AMVPRKE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6190	36558	A	6240	56	324	
6191	36559	Α	6241	68	487	
6192	36560	Α	6242	52	457	
6193	36561	Α	6243	263	787	SLEV*KWPGVACRLQL*P/MVP
				İ		APKS*ESKSAGSLNTPSAICRDA
	i					SGRGLARPWLRKSKCLACHLV
						DTRSKTAGGLAPVPSAHLISVR
		i				EREPGLCAVLVSQLEFRVGVGL
						VGPTLGARREPCWPQAMGDLA
	1					PEPVAALRLISRRALPAFPWGR
		i				ARDLQPAMPEPPTHSMGSCAPE
		1				PPR
6194	36562	Α	6244	3	236	
6195	36563	С	6245	1	1608	
6196	36564	В	6246	1	1083	
6197	36565	A	6247	823	1055	KQKDGTGAPWSRGRRSSGRLG
1						THRSPRRGWEAQAWRAAGPET
						CPAGRQLRPGEKSSAAPG*RSR
						RKDAYEMDTAKKK
6198	36566	В	6248	1	390	
6199	36567	A	6249	27	363	
6200	36568	В	6250	1132	1268	
6201	36569	A	6251	11	489	
6202	36570	A	6252	356	638	
6203	36571	A	6253	1	507	
6204	36572	A	6254	80	336	
6205	36573	В	6255	100	912	
6206	36574	В	6256	821	2992	
6207	36575	A	6257	2	602	
6208	36576	Α	6258	1	519	
6209	36577	A	6259	3	228	STGVPVSQ\RTCLLEKASVLFNT
1						GALYTQIGTRCDRQTQAGLESA
						IDAFQRAADMSPPGLTRRSLGP
(210	0.6570	١.	(2(0		0.02	TRWHQGTPH
6210	36578 36579	A	6260	1	963	
6212	36580		6262	1	397	
6212	36581	A	6263	1	2625	
6214	36582	A	6264	11	241	SLOHLNPATFLPVSKSPVKHNC
6214	36582	A	6264	11	241	VEVLDSVYSSGPNHRDHP*TSV
		1				
		1				DWELYMDGSSFTNPCKVTLKK
6215	36583	A	6265	1	1662	TTSPAPVTPGS
6216	36583	B	6266	1	897	
6217	36585	A	6267	3	258	
6217	36586	A	6268	1	279	
6219	36587	A	6269	1	258	
6220	36588	A	6270	1	639	
6221	36589	В	6271	li .	1935	
6222	36590	A	6272	698	1643	
0222	130390	Ι^	10212	1070	11043	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleoride
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6223	36591	Ā	6273	91	386	IFDFLFLLYVSGCNS1AEPOHFT
						TTVTRCSPTVAFVEFPSSPOLKN
		l				DVSEEKDQK\KP\ENEMSGKGG
		1				SWVLFTKGEVQEWRESGLNPT
						KFNMGPLIYS
6224	36592	Ã	6274	1	2538	
6225	36593	Α	6275	1	471	
6226	36594	Α	6276	152	520	CPLTLLLPSRGAGLGTCSPPCLS
	İ					LPPTPWAPVRPEPPRRAPPPAPR
	1					RPVPSTGKEQTTQGLRNASARR
		1				GTGRQLHL\SPGVGSTG*SQGL
6227	36595	Α	6277	831	1449	HPGQWLRRVCWVSSGAGPLAL
		l				CSISCPALAAFPRVGLGTCSPPC
	1	l				LSLPPTPWAPVRPEPPRRAPPPA
		l				PR/PPSPIDHPRAEEYE/PHGAGL
	ļ.					AGSSTCSPSAESTG*SQLGS*VV
						RVRGFILEVSETKNPPIPDTFGL
	ŀ	1				PPGSSSAASTLVQVTRL*ISAISL
	1	1				PHLLSRPCSNTARGPVPAPVPG
		1				AAVRAPAAGGRWCGGARGRG
		1				RRGGGH
6228	36596	С	6278	I	426	
6229	36597	Α	6279	I	535	MKHSGAQLASPSGS\PLGPQVE
		l				LPASPVPCACTSQPLGGRWDW
	1					APWSRGWCSSGRLGPHRSPWS
	1	l			i	GWE\LRHGGLQVPSPAPREGS*
	1	l				GPARNP/GTAPGRPAAPS\GGPP
	1	l				SPRPPRTPAGPQALRAAPVP\LA
	1	1				PLPPHLPAS*GSGLQPWPA*KE
		1				APTVQCQAEGLLKCRQSGSPGR
						GGAESE
6230	36598	В	6280	I	1743	
6231	36599	Α	6281	I	428	GTREEHLKRSGREIALPIEACV
	1					MLLLETGMKEEGLFRIGAGASK
	1	1				LKKLKAALDCS\ILTWDEFYSD
	1	1				PHAVAG\ALKSYLRELPEPLMT
		1			1	FNLYEEW\AQVASVQDQGQKT
		1				FKDLWRTCQKLPPQNFVNFRY
	L	L.	-	L		LIKFLAKLAQTSDV
6232	36600	Α	6282	135	512	LPFRGAGLETCSPPCLSLPPPPW
	1				l	APVRPKPPR*APPPAPRRPVPST
	1	1	1		I	TQGSLGPHCFYEL*HSP*RSAAS
	1	1			l	LLKPARP*AHREERTTP/GRSAL/
	1	1			İ	TSCNTHREGLQ/PSLRKKETPNT
		L	<u></u>		L	SEHQKEQTPDAPP

SEO ID	ISEO ID NO:	Talat	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
6233	36601	ĪĀ.	6283	698	2233	IQAAMQAAPQFGPSTED*CCPIT
0233	50001	ľ.	0203	10,0		SEAPWAIMDAKLR\LKPPSHPPL
						VSPHLNPQVWDTSSPSLATEHA
						SLTISLKPNHPYPAQSQYSIPOH
		l				ALKGSKPVITRLLEHGLLKPINS
		1				
					ŀ	PYNSPILPVQKLDKSYRLVQHL
				1		CLIYQIVLPIHPMVPNPYTLLSSI
		1			ŀ	PFTTHYSVLDLKHAFFTIPLYPS
İ	1	1		1		SQPLFAFTWTDPDTHQAQQITL
				1		AVLPQCFIDSPHYFSQAQISSSS
		l		1		VTYLGIILMKTHIGLGAVEQGV
ļ						VLVGEARAAQEPMEWVGGSG
ł						MVGCRSRALPRGKAAKARREI
		l				ERSAVTIVPVLDFNPAFHIIPDTT
1	ŀ		i	1	İ	PDHHDCISLIHLTFTPFPHISFFP
						VPHLEHTWFIDGSSTRPNCHSP
l		1			i	AKAGYAIVSSTSIIEATALPRST
l		1				TSQQAKLIAYTDSKCAFHILHH
		l				HAVIWEERNFLTMQGASIINAF
		l				LIKTLLKDILLPKEAGVIHCKGH
						QKASDPITQDNAYADKVAKKQ
						LAFOLLSLTAVFLLLIRPLSPTSP
						LKLPLINLFPHKANDS
6234	36602	Α	6284	I	1239	
6235	36603	Α	6285	1	477	QRPPHGVFVLGVAGRVHGPEL
						ASHKAGPQLGDVGVCAGQGG
						QVGPLVLQPVVEHIQQLPG/AG
	ľ	1				HCAHQ*QGSPS*SSLPRPERSLQ
		1				CRRPQGATATIRSTWWGPRGP
i		1		l	i	VCTAALVPLCWPGWPVQKDEL
						QAVRSHSALASAMQTCSLAGP
		l				GLGSSHARLTA
6236	36604	Α	6286	1	1134	
6237	36605	Α	6287	673	836	
6238	36606	A	6288	1	225	
6239	36607	A	6289	1	468	
6240	36608	Α	6290	495	1637	ESQVLSNVSPHVKV*NMASWE
						GKDLTVPQPDTRKGSVLRRISK
1						RGRNASCS*DKRKASVSCLSLG
ļ						NGMSRYKTRLYAPSTEIGKNRL
						RAGGGTCGQQYCFVKH
6241	36609	Α	6291	1	507	
6242	36610	A	6292	215	389	
6243	36611	A	6293	1	255	
6244	36612	В	6294	69	1055	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6245	36613	A	6295	23	1596	IKPQRWGETRAEMLKILKTREP
						FLLQRIASPRQQWNKAGQRRS
						WFFERL/NKIDRLLARLIKKKRE
	l					KNQIDAIKNDKGDITTDPTEIQT
						TIREYYKHLYANKLENLEEMD
	l					KFLDTYTLPRLNQEELESLNRPI
	l	ŀ				TGSEIEAHSSLRTKKSPGPDGFT
				ł		AEFYQRYKEELVLFLLKLFQSIE
						KEGILPNSFYEASIILIPKPGRDT
	İ					TKKENFRLISLMNIDVKILNKIL
						ANRIQQHIKKLVHHDQVGFIPG
						MPDWFNICKSINIIHHINRTNGK
	1					NHMIISIDAEKAFEKIQQCFMLK
	1	!				TLNKLGIDGMYLKIIRAIFDKPT
	1					ANVILNGQKLEAFPLKTGTTQG
						CPLSPLLFKIVLEVLARAIRQEK
				i		EIKRIQLGKEEAKLSLFADDMIV
	1			ĺ		YLENPIVSAQNLLQLRSNFSKV
		l				LGYKINMQKSQAFLYTKNKQT
		1				ESQIMSELPFTIATKRIKYLGIQL
		1				TRDVKSLFKENYKPLLSKIKED
		1				TNKWKNIPSSWIGRISIAKMAIL
						PKVIYTFNAIPIKLPMTFFTELEK
6246	36614	Α	6296	1	1488	
6247	36615	Α	6297	1	1401	
6248	36616	Α	6298	2	1256	
6249	36617	В	6299	84	955	

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SEQ ID	SEQ ID NO:	Mct	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		Sequence		
6250	36618	ĪΑ	6300	735	2718	RSFPRSRPSPFLLLSRYLRIHMV
		l				FSVLPFGLQNPKYLLSGSLOEK
		į				FRTPGINSHKTLDPNRVIIKVRR
1		l				RLEKEKALRAYVGKSEVRNMI
		1		1		LRERCKL*KKREKNQIDTIKND
ŀ	l	[				KGDITTDATEIQTTIREYYKHLY
		l				ANKLENLEEMDKFLDTYILPRL
		i		1		NQEEVESLNRPITGSEIEAIINSL
		1				PTKRSPGPDGFTAEFYQTYKEE
İ		1				LVPFPLKLFQSTEKEGILPNSFY
						EASIILIPKPGRDTTKKENFRPIS
						LMNIDAKILNKILANRIQQHIKK
		ŀ				LIHYDQVGFIPGMQGWFNKRK
1		l				SINVIQHINRTNDKNHMIISIDAI
		1				KAFDKIQQPFMLKTLNKLGIDG
		1				TYLKVIRAIYDKPTANIILNGQK
		[				LEAFPLKTDTRQGCPLSPLLFNI
		l				VLEVLARAVRQEKEIEGIQLGK
		1				EEVKLSLFADDMIVYLENPIVS
		1				AQNLLKLISNFSKVSGYKINIQ
		l				SQAFLYTNNRQTESQIMSELPFT
		l				TASKKIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPC
		1				SWVGRINIMKMAILPKVICRFN
į .		1				
		1				AIPIKLPMPFFTELETTTLKFIWN
		1				QKRARKSILSQKNKAGGITLPD FKLYYKATVTKTAWYWYQNR
		1				DIDOWNRTEPSEIMPHIYNYLIF
		1				DKPEKNKQWGKDSLFNK*CWI
						NWLAIWRKLK
6251	36619	В	6301	tr	2907	
6252	36620	A	6302	1	2358	
6253	36621	Α	6303	1	1866	
6254	36622	Α	6304	1	885	
6255	36623	Α	6305	1	1059	MKNNSESFEPLLLIPRQRGSGV
		1				DLQQTPTDLQLRVLTVRRKTN
		ı				KQDIHTKTPTVRHHHQRPKNP
		1				WDTFKAVCRGKFIALNAHKRK
		İ				QERSKIDTLTSQLKEVEKQEQT
	ļ	1				QSKASRRQEITKIRGELKEIETQ
						KTLQKINESRSWFFEKINKIDRL
		1				LARLIKKKREKNQIDTIKNDKE
		1	1			DITTDSTEIQTTIREYYKHLYAN
		1	1			KLENLEEMDKFLNIYTLPRLNQ
						EEVESLNRPITGSEIEAIINSLPT
			1	1		KKSPGPDGFTAEFYQSYQEELV
		1	1	1		PFLLKLFQSIEKEGILSNSFYKA
			1	1		NIILIPKPGRDTTKKENFRPISLM
			1	1		NIDAKILNKIL/ANRIQQHIKKLI
		<b>!</b>		ļ	1.00	HHDQVGFIPGMQGWFNI
6256	36624	Α	6306	1	1692	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6257	36625	В	6307	I	2871	
6258	36626	A	6308	2	2315	
6259	36627	Α	6309	ı	1210	MMSFHELSVHTAIDGHSHSSCS
						AWCSPIDRDYFEQENNSSSSCC
						CCCYHCHRKHCGGKGLSFPGE
					i	MPLSPGHFNKMMYSVSELMQG
						SGSGTFIPLPAELSLWLLVTNTK
						GQRMIKNDAEIQTTIREYYKHL
						YANKLENLEEMDKFLDTYTLP
ŀ						RLNQEEVESLNRPITSSEIVAIIN
						SLPTKKSPGPHGFTAEFYQRYK
						EELVPFLLKLFQSIEKEGILPNSF
l						YEASIILIPKPGRDTTKKENFRPI
						SLMNSDAKILNKILANRIQQHIK
		l				KLIHHDQVGFIPGMQGWFNICK
					1	SINVIQHINRTKDKNHMIISIDAE
		1		ŀ		KAFDKIQQPFMLKTLNKL\GIK
						YLGIQLTWDVKDLFKENYKPL
						LKEIKEDTNKWKNIPCSWVGKI
						NIMKMAIPPKATSPLESYKREK
6260	36628	A	6310	<b>)</b> 1	2745	MEGEMNEMKREGKFREKRIKR
						NEQSLQEIWDYVKRPNLRLIGV
						PESDGENGTKLENTLQDIIQENF
						PNLARQANVQIQEIQRTPQRYS
						SRRATPRHIIVRFTKVEMKEKM
				-		LRAAREKDRSTRQKVNKDTQE
						LNSALHQADLIDIYRTLHLKSTE
					1	YTFFSAPHHTYSKIDHILGSKAL
	1			1	į	LSKCKRTEIITNYLSDHSAIKLE
					1	LRIKNLTQNRSTTWKLNNLLLN
				[		DYWVHNKMKAEIKMFFETNEN
L		L_				KDTTYQNLWDTF

SEQ ID NO:	SEQ ID NO: of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	Nuclcotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6261	36629	A	6311			MGDFNTPISTLORSMRQKVNK DTOFELNSALDAOLLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITTNYLSDHS GSKALLSKCKRTEIITTNYLSDHS AIKLELRIKNITONRSTTWELN NLLLADYWVINEMKAEIKMFA CRGKFVALNAHKRKQEGSKID TLTSQLKELEKQEQTHSKASRR QETIKVRAELKEIETOKTLQKIN ESRSVARLIKKKBEKNOJDAIKN DKRDITIDFTEQTTHEYYKHL YANKLENLEEMDKFLDTYTLP RLNQEEVESLNRPITGSEIVAIIN SLPTKKSPGPGFTAEFYQRYK EELVPFLLKLFOSTEKEGILPNS FVEASILIPKFOROTTKEKSHFAP ISLMNIDAKILNKILAKRIQQHI QKLIHHDQVGFPGMGGWFNIC SKINVQHINKTDKNHMISID AEKVFDKIQQRFMLKTLNKLU EVLARAVROPKKIKGIQLGKE ELKLSLFADDMIVYLENPIVSA QNLLKLISNFSKVSEYKINVQKS QNLLKLISNFSKVSEYKINVQKS QNLLKLISNFSKVSEYKINVQKS QNLLKKLISNFSKVSEYKINVQKS QNLLKKLISNFSKVSEYKINVQKS QNLLKKLISNFSKVSEYKINVQKS WGRINVKMIGUTENDVKDLFKFE WVGRINVKMILPSTPTLASKRIKVLGIQLTRDVKDLFKF WVGRINVKMALPKVIYRFNAI PIKLPMTSFTELEKTTFKFIWMH KGARIAKSILSQKNKAGGITLPD
	1	1				FKLYYKATVTKTAWY

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence	ŀ	
6262	36630	IA	6312	2	2143	SSDGSWWTGFQWREWROAGR
				_		SVNSWDNPKQEVRASSKDKSR
						GSIQEAMRMQSSAKLLCSAWT
		1				LAYSIAVRTLSSDSEGQPPLVIH
		ĺ			l	ROTGSGEDLQQTPTDLQLRVLT
					ŀ	IRRKTNKOKGHPHONPISSRRO
					ł	EITKIRAELKKIETOKPFKKINES
						RSWFFEKINKIDRLLARLIKKKI
					İ	EKNOIDAIKNDKGNITTNPTEIO
		l				TTIREYYKHLYANKLEHLEEM
						DKFLDIYTLPRLNOEEVESVNR
						PITGSEIEAIINSLPTKKSPGPDRI
		1				TAELYQRYKEELVPFLLKLFQS:
						EKEGILPNSFYEASIILISKPGRD
						TTKKENFRPISLMNIDAKILNKI
						LANQIQQHIKKLIHHHQVGFIPO
		1				MQGWFNILKSINVIHHINRTKD
1		1				KNHMIISIEAEKAFDKIQQPFML
1		1				KTLNKLGIDGTYLTYLKIIRAIY
İ		1			1	DKPTANIILNGQKLEAFPFKTGT
1		1				RQGCPLSPLLFNIVLEALARAIR
		1			ł	QEKEIKGIQLGKEDVKLSLFAD
ł						DMIVYLENPIVSAQNLLKLISNF
		1			ŀ	SEVSGYKINVQKSQAFLYTNNR
		1				QTESQIMSELPFTIASKRIKYLGI
					1	QLTRDVKDLFKENYKPLLNEIK
		1				EDTNKWKNIPCSWIGRINIVKM
						AILPKTLNQKFSYWFRVNKHYI
				[		HQRTFPLKETEFNTIATLYNGA
	İ					SP/CTAPKSTGTNGHQASGLPRF
			1			*RIAFCSALVKSKRKLYQGYLP
		L				GQTDRREEGVSWCPGGP
6263	36631	Α	6313	1	3018	
6264	36632	Α	6314	1	2016	
6265	36633	В	6315	I	1215	

SEQ ID	SEQ ID NO:			Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	bod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
İ	sequence		09/540,217	sequence	or pepude sequence	deletion, (-possible intelegrine insertion)
				Sequence		
6266	36634	Α	6316	1	2268	MAGYPSETKPPEERSDSNICSSA
				İ		IFTVLHPPLLIPRQTAFGMDLQC
				l		MPTDLQLRVLTVKRKTNKQKG
				ŀ		HPHQNPIRTSPSSKTEDFQPTKI
					1	KRDKEGHYIMVKGSIQQEELTI
				ŀ	1	LNIYAPNTGAPRFIKEVLRDLQ
					İ	RDLDSHTIIMGEFNTRLSTLDRS
						MRQKVNKDIQELNSALHQADL
						IDISRNLHPKSTEYTFFSAPHRT
						YSKIDHIVGSKALLSKCKRTEII
						TKCLSDHSAIKLELRIKNLTQNO
						STTWKLNNLLLNDYWVHNEM
	ļ.					KAEIKMFFETSENKDTTYQNL
	ľ					WDTFKAVCRGKFIALNAHKRK
						QERSKTDTLTSQLKELEKQEQT
						HSKASRRQEITKIRAELQEIETQ
				ł		RTLQKISESRSWFFEKINKIDRS
						LARLIKKKREKNQIEAIKNDKG
				ł		DITTNPTETQTTIKEYYKHLYK
				İ		NKLENLEEMDKFLNTYTLPRLN
						QEEVESLNRPITGSEIVAIINSLP
		1				TKKSPGPDGFTAEFYQRCKEEL
				İ		VTFLLKLFQSIEKEGILPNSFYE
				ŀ		ASINLIPKPGRDTTKKENFRPISL
-		i				MNIDAKILNKILANRI/WGN*AE
				ŀ		ERNKEYSIRKRGSQIVPVCR*H
						DCVSRKPHHLSPQSP*ADKQLQ
	1			l		QSLRIQNQCTKITSILIHQ*QTNR
				l		EPNHE*TPIHNCFKENKIPRNPT
				l	l	YKGCEGPLQGELQTTAQ*NKR
				l		GHKQMEEHSMLMDRKNQHRE
						NRHTAQGNL*IQCHSHQATNDF
6267	36635	Α	6317	1	1797	
6268	36636	Α	6318	2	2063	
6269	36637	Α	6319	I	1212	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6270	36638	A	6320	1	2718	MALFRYGMTTRRLGHANKFTR
02/0	30030	^	0320	l¹		DLLVKRLLLYEFVVEIIPGLRTK
						TILVGPLETGYTSSDSVNSPHF
1						MLDIALSHNVKSTOLLLRPWR
		l				NIDCSRNHKNAKKEEOMGDDE
i		l				INROOECSSSPAMEOSWTENDF
		1				DELREEVFRRSNYSELQEEIRTN
						GKEVKSFEKKLDEWITRITNAE
						KSLKHLTELKTKARELQLEKQE
						LTHSKASRROEITKIRAELKEIE
						TOKTLOKINESRSWFFEKINKID
}						
						RPLARLIKKKREKNQTDTIKND
		1				KGDIITDPTEIQTTIREYYKHLY TNKLENLEEMDKFLDTYVLPRL
		l				
						NQEEVESLNRPITGSEIEAIINSL
		l				PTKKSPGPDGFTAEFYQRYKEE
		1				LVPFLLKLSQSIEKERILPNSSYE
						ASIILIPKPGRDTTKKENFRPISL
						MNIDAKILNKILANRTQQHIKK
		l				LIHHEQVGCIPGMQGWFNIRKS
		l		l		INVIQHINRTKDKNHMIISIDAE
1						KLISKFSKVSGHKINVQKSQAF
	1	1				LYTDNRQTESQIMSELPFTIASK
		1				RIKYLGIQLTRDVKDLFKENYK
				1		PLLNEIKEDTNKWKNIPCSWVG
		1		l		RINIVKMALLP\RFSAIPIKLPMT
		l				FFTELEKTTLKFIWNQKEP/CIA
						KSFLSQKNKAGGITLPDFKLYY
				l		KATVPKTAWYCYQNRDIDQW
						NRTEPSEIMLLIYNYLIFDKPDK
						KKEWGKDSLFNKWCWENWLA
L		L				ICRKLKLDPFLTPYTKMNSRWI
6271	36639	Α	6321	I	2307	
6272	36640	Α	6322	I	1989	
6273	36641	A	6323	I	3285	
6274	36642	Α	6324	3	4732	
6275	36643	В	6325	1	2693	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible oucleotide insertion)
				sequence		
6276	36644	Α	6326	603	2976	DNTARGTIRQQHLLFTNIRCSA
						ASAADTQANRVWSGPPANSNR
		1			ŀ	PAA\RVLTVRRKTNKQKGHPH
		1		l		QNPICTSPSSKTKETQTTIREYY
		l		I		KHLYANRLENLEEMDKFLDTY
				1		TLPRLNQEEVESLNRRITESDIE
		1		l		AIINSLPTKKSPGPDGFTAEFYQ
İ						RYKEELVPFLLKLFQSIEKEGIL
1						PNSFYEASIILIPKLGRDTTKKE
l						NFRPISLMNIDAKILNKILANRI
l						QQHIKKLIHHDQVGFIPGMQG
				l		WFNICKSINVIHHMKRTKDKNH
						MIISIDAEKAFDKIQQPFMLKTL
						NKLGIDGTYLKIIRAIYDKPTAN
						IILNGQKLEAFPLKTGTRQGCPL
						SPLLFNIVLEVLARAIRQEKEIK
						GFQLGKEEVKLSLFVDEMILSL
1						ENPMVSAKNLLKLISNFSKVSG
						YKINVQKSQAFLYTSNRQTESQ
						IMSELPFTIASKRIKYLGIQLTGD
						VKDFFKENYKPLLNEIKEDTDK
				i		WKNIPCSRVGRINIMKMAILPK
						VIYRFNAIPIKLPMTFFTELEKTT
						LKFIWNQKRARIAKSILSQKNK
						AGGITLPDFKLYYKATVTKTAC
						HRVGRAQQHSISKWKWYIHDW
						SQVGPEGTNDSARYPDTTQKW
						TAAALQPLSRTSLKDSHEGKSS
						QWAELRAVHLVLRFAWKEKW
						PDVQLYTDSWAVASGLAGWS
1						GTWKKHDWKIGDKEIWGRATP
						VIAQWAHEQRGHGGRDGDYA
6277	36645	Α	6327	3193	6107	SMKTGLEKKMKRNEQSLQEIW
				l		DYVKRPNLPLIGVPESDGDNAT
		l				KLENTLQDIIQENCPNLARQANI
						QIQEIQRTPQRYSSRRATPRHIIV
						RFTKVEMKEKMLRAAREKGRV
						THKGKPIRLTAALSAETLQARR
		l		l		DRRPIFNILKEKNFQPRISYPAK
				l		LSFVSEGEIEYFTDKQMLRDFL
1		1	1	l		MTRPALKELLKEALNMETTGA
				l		PRFIKQVLRELQRDLDTHTIITG
		1		1		DFNTPLSTSDRSTRQKVNKDIQ
		_				ELNSALHQADL
6278	36646	Α	6328	I	1808	
6279	36647	Α	6329	I	4695	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	İ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6280	36648	A	6330	<u> </u>	2915	MIMGDENTPLSTLDRSTROKVN
0200	30048	<u> </u> ^	0330	ľ	2,713	KDTWELNSALHQADLIDIYRTP
						HPKSTEYTFFLAPHHTYSKIDHI
						AGNKALLSKCERTEIITNCLSDF
		ļ				SAIKLQLRIKKLTQNHSTTWKL
						NNLLLNDYWVHNEMKAEIKIF
						FETNKNKDTTYQNLWDTFKAV
						CRGKFIALNAHKRKQERSKTDT
		l				RTSQLKHLENQEQTHSKASRRS
						WFFEKINKIHRPLARLIKKKREK
		l				NQIDAIKNDKGDITTNPTEIQTT
6001	26640	l .	(22)	1	6730	REYYKHLYTN
6281 6282	36649 36650	B A	6331	1	378	
6283	36651	Ä	6333	3	1700	
6284	36652	A	6334	1	1759	
6285	36653	Α	6335	2	409	
6286	36654	Α	6336	1	2051	MFGRSRSWVGGGHGKTSRNIH
		1				SLDHLKYLYHVLTKNTTVTEQ
		1	i i			NRNLLVETIRSITEILIWGDOND
		ı				SSVFDFFLEKNMFVFFLNILROK
		1				SGRYVCVQLLQTLNILFENISHE
		1				TSLYYLLSNNYVNSIIVHKFDFS
						DEEIMAYYISFLKTLSLKLNNH
						TVHFFYNEHTNDFALYTEAIKF
				l		FNHPESMVRIAVRTITLNVYKV
						DNQAMLHYIRDKTAVPYFSNL
						VWFIGSHVIELDDCVQTDEEHR
			ŀ	1		NRGKLSDLVAEHLDHLHYLND
						ILIINCEFLNDVLTDHLLNRLFLF
						LYVYSLENODKVFLIIHHAPLV
						NSLAEVILNGDLSEMYAKTEOD
						IORSSVLPTLSSLWOGSHLSLNC
İ			ŀ			LOSGLHKCSSHLCGAOAAADS
		ı				VTGEIPAIRSLEWLISAGSKART
						FFFLKMLIGFWEKVDCEYORR
		1				OVLSTRLOEALPSNRLTDVAAV
						HSSCMLGFGSTAPRGSWIGDPA
						AVHLPLPGELAEHLGSKGTTTV
			l	1		TKHOPOAKPSIRCFIKPTETLER
			l			SLEMNKHKGKRRVOKRPNYK
			1	1		NVGEEEDEEKGPTEDAQEDAE
				1		KAKGTEGGSKGIKTSGESEEIE
			İ			MVIMERSKLSELAASTSVQEQN
			l	1		TTDEEKSAAATCSESTQWSRPF
						LDMVYHALDSPDDDYHALFVL
			ŀ	1		CLLYAMSHNK/GKSPEKEEGLS
			İ			GTQSHPGKAGTFGKEGAEERK
6287	36655	Α	6337	2	2753	
6288	36656	Α	6338	I	577	
6289	36657	IA	6339	1	849	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide inscrtion)
				sequence		
6290	36658	А	6340	1	1293	
6291	36659	A	6341	1	861	
6292	36660	A	6342	154	6208	RRAPGKIPGQASAFLGRTWSRP
						CLRTQLCVIVSCLAKAGVQGYI
						VGSPGGAKRFLFSERTGSFSKL
	1					AAMSSWLGGLGSGLGQSLGQV
				1		GGSLASLTGQISNFTKDMLMEG
						TEEVEAELPDSRTKEIEAIHAIL
		1				RSENERLKKLCTDLEEKHEASE
	1	ļ		l		IQIKQQSTSYRNQLQQKEVEISH
		l				LKARQIALQDQFLKLQSAAQS\
						PSGAGVPATTASSSFAYGISHHI
						SAFHDDDMDFGDIISSQQEINRI
		1				SNEVSRLESE
6293	36661	Α	6343	3810	5310	SQGTCVPDRPCNVSG*RI\SIEEI
		l				EAGRIPNPHLGPVEERLALHVL
		ı				QQQGLVPEHVESRPLYSPLQPD
		1				IEQAFPSFGRKSRWIRVIPFPRFF
	i i					LRCIIWNTRDVILDDLSLTGEK
		1				MSDIYVKGWMIGFEEHKQKTD
1				1		VHYRSLGGEGNFNWRFIFPFDY
						LPAEQVCTIAKKDAFWRLDKT
				1		ESKIPARVVFQIWDNDKFSFDD
1	1			-		FLDPYAIVSFLHQSQKTVVVKN
					l	TLNPTWDQTLIFYEIEIFGEPAT
	1					VAEQPPSIVVELYDHDTYGADE
	1	1				FMGRCICQPSLERMPRLAWFPL
	1	1				TRGSQPSGELLASFELIQREKPA
		1				IHHIPGFESEDTDLPYPPPQREA
		1				NIYMVPQNIKPALQRTAIEILA
		l				WGLRNMKSYQLANISSPSLVVI
		l				CGGQTVQSCVIRNLRKNPNFDI
		l				CTLFMEVMLPREELYCPPITVK
		1				VIDNRQFGRRPVVGQCTIRSLES
į		1				FLCDPYSAESPSPQGGPDDVSL
						LSPGEDVLIDIDDKEPLIPIQNYA
6294	36662	Α	6344	1	527	
6295	36663	Α	6345	5251	5711	PPQRGPPSSSCYSRSQRSVSRCP
						SRHRPSAASPRPGRPSGRSGLLA
		1				GLRLWAGAGCFQCPPCLQRGL
		1		1	1	FSPEALRPQAPAHKGLFSGSLW
				1	1	PQQRSHQGLRAAATS*DRRAG
		ı				ALCKWCPRPSGTPRGEHLS*EN
		$\perp$				ESLPP**RWAHQTAPQESQTS
6296	36664	Α	6346	I	924	
6297	36665	Α	6347	1	894	
6298	36666	A	6348	1	525	
6299	36667	A	6349	6	343	
6300	36668	A	6350	1	2693	
6301	36669	A	6351	26	353	
6302	36670	A_	6352	1	9182	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, ^=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6303	36671	A	6353		8655	EAAKDLADIAAFFRSGFRKNDE MKAMDVLPILKEKVAYLSGGR DKRGGPILTPARSNHDRIRQE DLRRLISYLACIPSEEVCKRGFT VIVDMRGSKWDSIKPLLKILQE SPFCCHVALIIKPDNFWQKQRT NFGSSKFFFETMWYSLEGLTKV VDPSQLTPEFDGCLEYNHEWI EIRVAFEDYISNATHMLSRLEEL QDILAKKELPQDLEGARNMIEE HSQLKKKVIKAPIEDLDLEGQK LLQRIQSSESF
6304	36672	A	6354	1	1338	
6305	36673	С	6355	152	404	
6306	36674	A	6356	137	1278	MDSOPNSTROGSGRR/MEIKGI QLGKEEVKLSLFADDMIVYLEN AITSQPKISLS**ATSAKSQDTKS MCKNHKHSYTPITOKQRAKS* VNSHSQLLQRE*NT*ESNL*GT* RTSSRKITTNICSMK* KRIQTING RTHAHAFGESIS* KWPYCPR*F IDSMPSPSSYQ*LSSQNWKKRL SSSYGTIKKEPASPSQS* AKRTKL AEASILLPDFKLYYKATVTKTAW DMDEAGNHHSQQTITRITKNQT PHVLTHRWELNNENTWTQGE HHTPGLVVRRSPDPEQNFKAVR CLDLPDFSSSFLAVLTHFKPA FLQSLR**DKPRSISPALGTWHKP *KITPKKQ/HQAITKPNTEYRTA VKPSVVGALPDINSFLKLGGLH RITNGCLLD

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	**Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6307	36675	Α	6357	l .	2569	MRTKTQHTRISWDAFKAVCRG
						KFIALNAHKRKQERSKIDTLTS
						QLKELEKQEQTHSKASRRQEIT
						KIRAELKEIETQKSLQKINESRS
1						WFFERINNIDRPLARLIKKKREK
		1				NQIDTIKNDKGDITTDPTEIQTT
		I				REYYKHLYANKLKNLEEMDKI
l		I				LDTYTLPRLNQEEVESLNRPITC
l						SEIVTIINSLPTKKSPGPDGFTAE
						FYQRYKEELVPFLLKLFQSIEKE
ļ						GILPNSFYEASIILIPKPGRDTTK
						KENFRPISLMNIDAKILNKILAN
		l				RIQQHIKKLIHHDQVGFIPGMQ
		1			1	GWFNIRKSINVIQHVNRAKDKN
		l			1	HMIISIDAEKDFDKIQQPFMLKT
		1				LNKLGIDGTYLKIIRAIYDKPTA
		1				NIILNGQKLEAFPLKTGTRQGCF
	1	1				LSPLLFNIVVEVLASAIRQEKEI
					i	KAQNLLKLISNFSKVSGYKINV
						QKSQAFLYTNNRQTESQIMSEL
	l	ļ			1	PFIIASKRIKYLGIQLTRDVKDLF
						KENYKPLIKEIKEDTNKRKNIPC
						SRVGRINIVKMAILPKVIYRFNA
		l				IPIKLPMTFFTELEKTTLKFIWN
1					1	QKRAHIAKSILSQKNKAGGITLE
		l				DFKLYYKATVTKTAWYSYQNR
					1	DIDQWNRTEPSEITPHIYNYLIF
	1					DKPEKNKQWGKDSLFNKWGW
		1				ENWLAIWRKLKLDPFLTPYTKI
		1				NSRWIKDLNVRPKTIKTLEENL
		1				GITIQDIGMGKDFMSKTP/TSNG
		1				NKRQN*QMGSNETKELLHSKR
6308	36676	A	6358	1702	2252	FLSLFFFISLASSLSILLIHIMNSW
				ļ		IPHSPIFTDLNVESSRLCPLGDIM
	l	1				M*IPLTWYLIVTCTHLSREITTV
		1				PRGLARLWSFTRICPRTHCKPIP
		l				A\VLLRAGCPPSCWWDQDTHS
		l				QLPSKRSSYTLFFCTVTEYPFLD
1		1				*WP*NHGTPC*TAPLWSMF/PCS
						CWYPVTGPGVSCSPSCVQVFSL
1		l				FISHL*VRTCGVWFFVLAIVC*E
l		l				*WFPASSMSQAVLVTVAL*YSL
						KSGSVMPPA\FSFGLGLTWRCR
1	1					LFFGSIRTLK*IFPIL*RKSLVA*
	1				I	WGWH*IYKLRWAVWPFSRY*F
1	1				l	FLPMSM/VMFFHLFVSSFISLSS
					1	GL*FSLKRSFMSLVSWIPKYFIL
	1				1	FEAIVNGSSLMIWLSVCLLLLH
						KNACDFCTLILYPETFLKLLISL
1						RRFWAETMGFSRYTIMSSANR
1		1	1			DNLTSSFPN

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6309	36677	A	6359	207	1209	IPRHIHPPKTKPGRS*/TP*IDO*O
						ALKLRQ/CINSLPTKKSPGPDGF
						TAKFYOSPSLTGKNDKEPEILPY
l						FHADFLVVPGTHQASPVLMVL
		İ				GHKSFPHRNSPPSVCMANFFTQ
	l .					KPPSQSIHNAVNTHTDPPLFLVL
		1				LKDRGLLVIWCHESQGDELWH
	I .					LVLLDSKCCFGSMTHRMEWSG
		1				PSAAGLLEFAGGPLQTLFAWVS
	1	1		1		AVEAAEQRILLNSKCCCLIIPLE
	1	1				ALSQRGIWPWQGSPVPRPWTT1
		1		1		TLWPVRNQATQQETSLMPCQL
	1					EGKEPLALPTKEAEIEGRRTGEI
		1				KKVERDSNTNKEELLLDLAFK
1	1	1				VSSLFDKLEEVVELLVIGELQL
						YPSK
6310	36678	Α	6360	544	678	AFFHVSFGCINVFF*EVSVHML
						CPLFDGVVFFLVNLFEFFVDSG
6311	36679	Α	6361	7	94	VRTSGVWFFVLAIVC*E*WFPA
						SSMSLIY
6312	36680	A	6362	381	431	ATKODSVSKKKEEEEEEEEE
						EEEEEEEEEEEEKEK/GNK
						ERKK/DKGKARQVQARQIYLLS
		_				LHLGRIRKVPNNNKA*SSCP
6313	36681	В	6363	1	603	
6314	36682	Α	6364	1	987	
6315	36683	В	6365	1	444	
6316	36684	A	6366	977	1177	RTSISSPVSSTCSPLVMPTLLPQP
		l				TVPWRMWRPCTQ*RNAGTFSP
		ļ.				AVAMGLPVEAVICLSV*DSPA
6317	36685	A	6367	1148	1395	Will a constitution of the
6318	36686	A	6368	33	663	VHVLCGDTDETGNHHSQQTIA
		ı				RTKNQTPHVLTHRERLSLRRGL
1						HSCAYSLHRWLGARHAQKGSR
		1			1	NTKGCGGQGPRTSERGPASGEF
		1				SENCTSLLGQRGVFSPGRRALL
		1				HSPSDG\SVPLGAVDSSP\PASTR
		l				RDWSHWAVGKPSPEREPAGKV
						T*TTRQLQPASP*REHPLLNSQH
						GHCLKISLPLLPTVLSPSPPLSLC SNVTFSTRPLT
6319	36687	Α	6369	1	1314	
6320	36688	A	6370	120	410	
6321	36689	A	6371	1	492	
			<u> </u>			

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in IJSSN 09/540,217	Nucleotide location of first cudun for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=\$top codun, /=possible nucleotide deletion, \=possible nucleotide insertion)
6322	36690	A	6372	3	945	EEVPRSMSKKKKRKRSRSKER EEEEEEEEEEEEEEEEEEEEEEEEE
6323	3669I	В	6373	I	792	
6324	36692	С	6374	348	884	
6325	36693	A	6375	I	588	
6326	36694	В	6376	I	5339	
6327	36695	В	6377	520	3146	
6328	36696	Α	6378	1	2044	
6329	36697	A	6379	I	585	
6330	36698	A	6380	l	2433	
6331	36699	В	6381	53	441	
6332	36700	A	6382	2	425	
6333	36701	A	6383	1386	2569	FLRKHRESGNDEMTALCSFRO VAGEBELGVIOPEKSVSVAAGE SATLRCAMTSLIPVGPIMWFRG AGAGRELIYNQKEGHFPRVTTV SELTKRNNLDFSIISNITPADAG TTYYCVKFRKGSPDDVEFKSGA TPEHTVSFTCESHGFSPRDITLK WFKNGNELSDFQTINVDPAGDS VSYSIHSTARVULTRGDVHSQV ICEIAHTUQDPLRGTANLSEAI RVPPTLEVTSQPIRAENQANVT WQVSNFYPRGLQLTWLENGNV SKTETASTLIENKDGTYNWMS SKTETASTLIENKDGTYNWMS WILVNTCAHRIDDVVLTCQVEH GQQAVSKSYALEISAHQKEH GSDITHEPALAPTLAPLLVALLLG PKLLLLVVQVSAIYICWKQKA

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6334	36702	A	6384	1	2453	MEPAGPAPGRLGPVLCLLLAAS
0334	30702	l^	0304	l'	2433	CAWSASRQLPAVQVLRGDVTC
				l		GSDHVFLLAYIKHLAVAGRRA
				1		
						LKATVHVHQRTLLRPGGCGSV
					1	PGKRAVTLISKCSDGQPAFPGA
						PAGNTNTFLVCSCGFPDLQSSR
						GPERALCAFIQCLMVRPEEQRE
						KNWPGPRGRSMARPGWNAKPE
						VVQAKAFKNWAVLELSTVSAR
						NLTGSRIPRENTKVILIGTIWVL
		1	1			CFLGSALGVCDPGGTHSHLAM
					į.	HVVIFGPVGSNNPSIVIIIIIRPIL
ı						QIKSQRSRVGETFPGVSWVAEL
						ESKSKHTFSQCQALLQPWGRK
		1				LSSCSQRTYNLLLVCIQSMNVI
						DKHLRKHRGSRVAGEEELQVI
						QPDKSVLVAAGETATLRCTATS
ı						LIPVGPIQWFRGAGPGRELIYNQ
ı						KEGHFPRVTTVSDLTKRNNMD
		1				FSIRIGNITPADAGTYYCVKFRK
						GSPDDVEFKSGAGTELSVRAKP
						SAPVVSGPAARATPQHTVSFTC
						ESHGFSPRDITLKWFKNGNELS
						DFQTNVDPVG\ESVSYSIH\STA
						KVVL\TREDVNSQSFW*GPTVT
						LOGDPLRGTANLSETIRVPPTLE
						VIQQPVRAENQVNVTCQVRKF
						YPORLOLTWLENGNVSRTETA
		i				STVTENKDGTYNWMSWLLVN
						VSAHRDDVKLTCQVEHDGQPA
		1				VSKSHDLKVSAHPKEQGSNTA
		1				AENTGSNERNIYIVVGVVCTLL
6335	36703	A	6385	I	405	
6336	36704	Α	6386	91	2926	PACPSPRLPFTNTDTHIDTSSPA
1						SRSTRCLCISTHGVLAQSGGSSG
						GPAVPTVQRGIIKMVLSGCAIIV
						RGOPRGGPPPEROINLSNIRAGN
						LARRAAATOPDAKDTPDEPWA
		1				FPAREFLRKKLIGKEVCFTIENK
						TPOGREYGMIYLGKDTNGENIA
						ESLVAEGLATRREGMRANNPE
		1			İ	QNRLSECEEQAKAAKKGMWSE
						GNGSHTIRDLKYTIENPRHFVD
		1				SHHQKPVNAIIEHVRDGSVVRA
						LLLPDYYLVTV
6337	36705	Α	6387	2	448	
6338	36706	Α	6388	1	645	
6339	36707	Α	6389	i -	294	
	1				·	·

SEQ ID NO:	SEQ ID NO; of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6340	36708	A	6390	23	321	RGREHTQGIPGAGKRWH*FKV LLTQ/CW*SEFSVIRQFKAGPGG LDQFRDRSK/RWLRDLRGRLLG SLNASLVLRALFSGNWGLTAN QL*LAVGAKGDPEA
6341	36709	Α	6391	1	1599	
6342	36710	Α	6392	1	561	
6343	36711	A	6393		1833	STLASSEQGGFWRGPRAILLL LELECHARSHDGKYSREKN QPKPSPKRESGEEFRMEKLNQL WEKAQRQERYPCRRRRRVKQO WEKAQRQERYPCRRRRRVKQO AGTTRYPELKTFEMGVPELCRP SGPHYLISNAGVRLDLLNSPVL SIPESLRGKVNDLQNKKELLER KGRGETGLARPMHDLTAAQGG YGCALVHGAQVEGAGAQGWA GTVHATCRGCTGTACQEALVT ATACSSCQRGGTRAPQGQHTL ESMGLNCLPQGAASGSDHHCG PRISDLPGSAARTSRWPASSELH LPPVRLAELHADLKIQERDELA WKKLKLDGLDEGGEKEARLIR NLNGHWRAEDAHQDGGVNK WDIPTVVOVGVAAILAVAKKL FLIPNIRGVLSESPATLHSLQV ASVLWSLEFLPYGSRSPVVIQET ULAKYGLDGKKDARQVTSNS LSGTQEDGLDDPRLEKLWHKA KTSGKPSGEELDKLWRELHHK KTSGKPSGEELDKLWRELHHK KKSKHENYLLETLSTEVHPG PQDGVASTGREHSPMETLEQEE LKHFEAKIEKHNHYQKIQLEIA HEKLRHAESVGDRRS*ASPR ESTPCLEGRTKGAGHRPR*KKHLIG
6344	36712	Α	6394	1	185	DFFDNSAQVTIAGIPCDIRHVSP RKIECTTRAPGK\V*GSPPLSQAI EGFFLKLEMLLRDWN
6345	36713	A	6395	1	1512	
6346	36714	A	6396	117	268	QSLLLEYLHLYLHLCYLHLANK QELTLTWYKE*CTFFLPSV*NPF HQNLA
6347	36715	Α	6397	1	500	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
6348	36716	A	6398	1301	2565	TLLTILPFYLFKNRTSI.TGYLRI
05.10	30110	1	0370	1.50.	2505	WILSTKLFCLSTLWLAPTLFLIP/
						LPDPHDCISLIHLAFTPFPHTSFF
		l				PIPHPDHTWFIDGSSTWPNRHSP
						AKVGYAIVVSSTSILEATALPPS
						TTSQQAELIALTRALALAKGLH
		l				VNIYTDSKYAFHILHHNAVIWA
			1			ERGFLSTQRSSIIIASLIKTLLKA
						ALLPKEAGVIHCKGHQKASDPI
		l				AQGNAYADKTKFLDLAFPPLR
				1		LSFTCQITQAVSQALGIQWNLH
						TPYRPOSSGKDWTVFLPLALHR
						IRARPREATGYSPFELLYGRTFL
					ł	LSPNLVPDTSPLGDYLPVLWOA
						ROEIHOAANLLLSTPDSOLYED
						TLAGRSVLIKNLTPOTLOPRWT
						GPYLVIYSTPTAVRLODPPHWV
	ļ					HRSRIKLCPSDNOPNLSSSSWKS
						QVLPTTSLKVTLISEEQ
6349	36717	Α	6399	581	2517	LFLGYSHTSLLPFPPVQSLLHLL
						PLYLHTLTHKYGIPLLPPWRPIM
		l				HPLPSH*NLITLTLLNANIPSCST
						L*KD*SLLSLTCYSMAF*/QPINS
						PYNSPILSVQKPDKPYSSFRYVY
1		l				SLFVESPTITIVPGPDFNLASHIIP
						DTTPDPYDCISLIHLTFTPFPHVS
						FFPVPHPFHTWFIDGSSTRPNCH
		l				TPAKAGYAIVSSTSIIEVTTLPHS
		1				TTSQQAELIALTRTLTLAKGLC
						VNIYTDPISCTTMLFYGLKCFLT
				l		MQGSSIINASLIKTLLKAALLPK
						EAGVIHCKGPQKASDPIAQDNT
						YADKVAKKAASVPTSIPHSSFS
						PSHLVTPTYSPTETSTYQSLPTQ
						GKWFLDQGKYLLPASQAHSILS
						SFCNLFHVGYKPLARLSELLISF
		l				PSWKSILKEITSQCSICYSATPQ
						GLFRPPPFPKHQAWGFVPTQD
				l		WQIDFTHMPQVGKLKYLLVW
						VDTFTGWVEAFPTGSEKATVVI
						SSLLSDVIPRFCLPTSIQSNNGLA
				1		MISQITQAVSQALGIQWKLCTP
						YHPQSSGKVKWANGLLKTHLT
						KLSLQLKKDWTVLLPLALLRIR
						ACLRNATGYSPFELLYRCSFLL
						GPSLIPDTRPTWTAPPKTWHPY
	1					YLLSSHTPIHRSQLLIHALLLFTL
						PVYTVSPSHHS

SEQ ID   SEQ ID NO:   Net   SEQ ID NO:   Notecotide	nucleotide oilde insertion)  EGNICKIQE DPESLLLPPL 1SVAKAELL LGEEEVDH LKLSVLREA LGEEVEANL LILFVGDLDK RVENALNSI KKQQLTGQL
6350 36718 A 6400 281 1095 DCSKRNRHSQVIAI VRRKEDTQGGEKL LAPGPTEYSTYN NKLKDQPEMAEIG ELAQKKIQLIESISS QRGLLEDINANSAI KAVCKSNEFEKYH VVNLLLSLSGRI.AH DSEANQEKLVLIEK ADAKELKEHVDRR SRYLPQDQLQDVQ	EGNICKIQE DPESLLLPPL ISVAKAELL LGEEEVDH IKLSVLREA LGEEVEANL ILFVGDLDK RVENALNSI KKQQLTGQL
6350 36718 A 6400 281 1095 DCSKRNRHSQVIAI VRRKEDTQGGEKD LAPOPTEYSTYYN NKKLDQPEMAEIG ELAQKKIQLEISIS QRGLLEDINANSAI KAVCKSNEFEKYH VVNLLLSLSGRLAF DSEANQEKLVLIEK ADAKELKEHVDRN SRYLPQDQLQDVQ	DPESLLPPL ISVAKAELL ISVAKAELL LGEEEVDH IKLSVLREA LGEEVEANL ILFVGDLDK RVENALNSI KKQQLTGQL
VRRKEDTQGGEKE LAPGPTEYSTYYN NKLKDQPEMAEIG ELAQKKIQLIESISR QRGLLEDINANSAI KAVCKSNEFEKYM VVNLLLSLSGRLAF DSEANQEKLVLIER ADAKELKEHVDRR SRYLPQDQLQDYQ	DPESLLPPL ISVAKAELL ISVAKAELL LGEEEVDH IKLSVLREA LGEEVEANL ILFVGDLDK RVENALNSI KKQQLTGQL
VRRKEDTQGGEKE LAPGPTEYSTYYN NKLKDQPEMAEIG ELAQKKIQLIESISR QRGLLEDINANSAI KAVCKSNEFEKYM VVNLLLSLSGRLAF DSEANQEKLVLIER ADAKELKEHVDRR SRYLPQDQLQDYQ	DPESLLIPPL ISVAKAELL LGEEEVDH IKLSVLREA LGEEVEANL ILFVGDLDK RVENALNSI KKQQLTGQL
LAPGPTE/VSTYYN NKLKDQPEMAEIG ELAQKKIQLESISR ORGLLEDINANSAI KAVCKSNEFEKYH VVNLLLSLSGRLAR DSEANQEKLVLIEK ADAKELKEHVDRR SRYLPODQLQDYQ	ISVAKAELL LGEEEVDH KKLSVLREA LGEEVEANL ILFVGDLDK RVENALNSI KKQQLTGQL
NKLKOPEMAEIG ELAQKKIQLIESISS QRGLLEDINANSAI RAVCKSNEFEKYH VVNLLLSLSGRI-A DSEANQEKLVLIEK ADAKELKEHVDRR SRYLPODQLODYQ	LGEEEVDH KKLSVLREA LGEEVEANL ILFVGDLDK RVENALNSI KKQQLTGQL
ELAQKKIQLIESISR QRGLLEDINANSAL KAVCKSNEFEKYH VVNLLLSLSGRLAF DSEANQEKLVLIEK ADAKELKEHVDRR SRYLPODQLODYQ	KLSVLREA LGEEVEANL ILFVGDLDK RVENALNSI KKQQLTGQL
QRGLLEDINANSAL KAVCKSNEFEKYH VVNLLLSLSGRLAF DSEANQEKLVLIEK ADAKELKEHVDRR SRYLPODQLODYQ	LGEEVEANL ILFVGDLDK RVENALNSI KKQQLTGQL
KAVCKSNEFEKYH VVNLLLSLSGRLAF DSEANQEKLVLIEK ADAKELKEHVDRR SRYLPQDQLQDYQ	ILFVGDLDK RVENALNSI KKQQLTGQL
VVNLLLSLSGRLAF DSEANQEKLVLIEK ADAKELKEHVDRR SRYLPODOLODYO	RVENALNSI KKQQLTGQL
DSEANGEKLVLIEK ADAKELKEHVDRR SRYLPODQLODYQ	KKQQLTGQL
ADAKELKEHVDRR SRYLPQDQLQDYQ	
SRYLPQDQLQDYQ	
ESLLLGPSNF	EEQLACER
6351 36719 A 6401 1 972	
6352 36720 A 6402 514 736	
6353 36721 B 6403 446 991	
6354 36722 A 6404 521 903 NIKPASQISPG*I*VI	HEEDTODI C
APPSAA/GRLLSLSL	
TARCIPAGRLEPLC	
LHLSLKSKGSGGRS	
NOSVCIQAEKPPLK	
MNVLRCRAYSWVI	
6355 36723 A 6405 11 545	IDWD
6356 36724 A 6406 3 2920	
6357 36725 A 6407 1 2388	
6358 36726 A 6408 275 479	
6359 36727 A 6409 1 3810	
6360 36728 A 6410 7 1047	
6361 36729 A 6411 1 705	
6362 36730 C 6412 304 638	
6363 36731 A 6413 99 759 WAYLDFWM*HIPH	LGVLL/SAH
LLSDLNSCQF*MGS	SRTEGSATG
PGSCSAALPLGPYD	PADPMVLE
VSMADRDASPHDP	LAKFLFPVP
MTLHSALLEVLVPI	<b>EGGTLPPGD</b>
TTTIPLNW/IVKIAT	*TLWVPPTF
KFTGCRLNTMWKI	PRLGASTL
*SNSLRCTLTSFSHI	DWSGWDAG
HOVIRPHGFAGYN*	TCGCFHRL
MLSACGFSRQMVQ	
GSGG	
6364 36732 A 6414 I 685	
6365 36733 A 6415 I 1359	
6366 36734 A 6416 3 7714	
6367 36735 A 6417 I 723	
6368 36736 A 6418 I 528	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6369	36737	A	6419	38	530	HSPRRSAASLLSQRDHEPHOKE
0309	30737	<u> </u> ^	0717	100	330	ETPNTSEHOKEKTPDTPPLRTV
		1		l		TLTVRVHGFILEVSETKNPPIPD
		1				TKLRG/ERLOGFGLAGFRSE/GC
	1	1	1	1		RPSP*VLQLIKAVWTQRPLGGR
		1			l	WDWAPWSRRWCSSGRLRPHR
		1		1		NOWSGWEAOAWGLOVPEPCP
		ı				AGRQLRPGEKSSTAP
6370	36738	A	6420	1	649	AGRGERI GERESTAI
6371	36739	A	6421	1	987	
6372	36740	A	6422	1	924	
6373	36741	A	6423	i i	435	
6374	36742	A	6424	1	147	
6375	36743	Α	6425	11	1107	
6376	36744	Α	6426	3	913	
6377	36745	Α	6427	1	159	
6378	36746	Α	6428	313	1083	
6379	36747	Α	6429	1	1245	MAQELRDTCTSFSSRFDQVEER
		1				VMVIEDQINEMKQEEKFREKR
						VKRNKQSLQEIWDYVKRPNLR
		1				LIGVPEKNLEETDKFLDTYTLPR
		1		1		LNQEEVESLNRPITDSEIEAIINS
l		1	l	1	i	LPTKKSSGPDGFTAEFYQRYKE
		1				ELP/RQRHNKKREF*TNIPDEHR
1		1		ł		CKSPQ*NTGKPNPAAHQKAYPP
		1		i		*SSGLHPWDARLVQHTQINKRN
		1		1		PAYKQNQGQKPHDYLSRCRKG
		1		1		L*QNSAALHAKNSQ*IRY*WDI
		1		1		SQNNKSYL*QTHSQYHTEWAK
		1				AGSIFFENWHKRGMPSLTTPIQ
		ł				HSVGSSGQGNQAGERNKGYSI
		1		1		RKRGSQIVPVYR*HNCISRKPH
		1				HLSPKSP*AGKQ/SSAKSQD/DKI
		1		ŀ		NVQKSQAFLHTNNRQTESQIMS
		1		:		E/APIHNCYKENKISRNPTYKGC
		1_				EGPLQGELQTTAQRSKKGHKQI
6380	36748	Α	6430	39	314	KSECLIYTKGSQRLASNGTKLD
		1			I	GE*L**VDRIRLQKIGNDKLLPA
		1				KGGCSNPSQRS*KPRKKIRQMA
				1		N*NKQHRGDLK*PDGAENHGT
		_				RTT
6381	36749	Α	6431	213	843	VDRSRLQKVSNNKLL*AKGECS
		1				NPLQGS*KP*KKIRRMAN*NKH
		1				CREDLK*PDGVENNGTRTS*FM
						HKLQ*PI*SSGRKGISD*R*N**N
						KIHQG*NEGKSVKGSQRERSSY
		1				PQRKAHQTNSGSLSRNPTSQKK
				1		VGANIQHS*RKEFSTQNFISSQT
		1		1		KLHK*RRNKIFYRQADAERFCH
						HQACVTRAPEGSTKHGKKQPV
	1	$\perp$		L		PAPAKTGQIV

SEQ ID NO:	of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6382	36750	A	6432	1	2112	MRAFVVLMDVSKLPSERGOFG LRSNQOHMRHETSYDRGSVS LLADAVAAATPQGTYSQPRGPS NLAADLRVAEESSGMENLFLK MSFDSIRPAQDGQCTPEISMVTP SPGWSVHTGDLDGHPLPRMVS AHRRSRWSPPPQDGQCTPEISM VIPSPGCSVHTGDLDGHPLPRM LSHARRSRWSPPPQDAQCTPEIS MVTPSPGWSVHTGDLDGHPLPRM LSHARRSRWSPPPQDAQCTPEISM MYTPSPGWSVHTGDLDGHPLPRM LSHARRSRWSPPPQDAQCT PEISMVTPSPGSVHTG
6383	36751	A	6433	1	648	TEIDIN'T TEI GESTING
6384	36752	A	6434		1539	MILVSFVSLGSLCLQPGSQTILE KNETVKPHVSFTLLPALSHVSE KNEAESMNSLIPPPPNLHTPAQ APFPLPTKEQDRSSPATEQSW TENDFDELTEVGFRSSVITNSSK LKEDVRTHCKEAKNLEKRLHE/ SAN*NQCGREDL**PASEIGNET RTS*HMHKLQ*PI*SSGRKGVSD *GSNQ*NK*WGEWNQVCKHSS GYYPGELPGYSKAGQHSNSGNT ENTTKILLEKSNPKTHNCQHQ GYPGELPGYSKAGQHSNSGNT ENTTKILLEKSNPKTHNCQHQ GYNEGKSVKOSQGERTREARA NKFKS*QKARYN*DQCRTERD RNTENPSKN**IQEPVF*KDQQN **NASKTNKEKEREESNRNKK **KNRTVKPHVSFTLLPALSHVS ENNEAESMNSLIPPPNLHTPAQ APFPLPTKEQDRSSSPATEQSW TENDFTEKTERSTREPQVEERVS LEDVRTHCKEAKNLEKRIHE WLTRINSVEKTLNDLKLKSMA RELHDTCTSFNSRFDQVEERVS AIEDOTNEINNGENGTKLENTL QDIIQENFPNLA RQANIQQEIRR RCHOTTSFNSRFDQVEERVS AIEDOTNEINNGENGTKLENTL QDIIQENFPNLA RQANIQQEIRR TORNSVEKTRINDELTEVGREERECT KASKRKQRITKISAELKEIETQK TURKINEFRSFFFKKINKIDKTL ARLIKKKREKNQTDAIKNDKR KLENLEEMDKFLDTYTLPFLYNLY
6385	36753	В	6435	137	586	
6386	36754	Α	6436	129	506	
6387	36755	Α	6437	1	237	
6388	36756	Α	6438	182	1034	

SEQ ID	SEQ ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6389	36757	A	6439	203	650	SAIVCGSPLRLRMOAVSSRINSA
						HSRGAIYSQASSSAACPSVSIAF
						LRR*IEANVS/WIRTLLSTLCTPK
						CGPGFKHRIVLCKSSDLSKTFPA
						AQCPEESKPPVRIRCSLGRCPPP
	ŀ					RWVTGDWGQ/CDSRDPRPGRR
			1			RRDFCRNGRAGAGH
6390	36758	Α	6440	207	426	AECTRCAIPK/HSCYPVLLIVVS
						P*KKQ\NCSLGELSCWRRESCRS
	Ì					SWSNKALPSLTRCLRGFVCGLS
						CYKGSS
6391	36759	A	6441	524	783	TAVLAARISNQWILSCWS/AVG
						CTPKCGPGFKHRIVLCKSSDLS
				•		KTFPAAQCPEESKPPVRIRCSLG
						RCPPPRWVTGDWGQLSPTREK
6392	36760	A	6442	1	1524	
6393	36761	A	6443	1	8738	
6394	36762	A	6444	1	642	
6395	36763	A	6445	1	549	
6396	36764	A	6446	8	434	
6397	36765	A	6447	1	2922 1158	PL DEDODVCC A LUTCI DENU DIV
6398	36766	Α	6448	18	1138	FLDFDCPYGSAHITGLRFWLPW YRKRQRYWGSHGNCMPPPSLR
	l					VPERCPSHTEPRNLTGA*ELLLL
						GLSEDPELQPILAGLSLSMYLVT
			1			VLRNLLISLAVSSDSHLHTPMC
						FFLSNLCWADIGFTSAMVPKMI
	ŀ		l			VDMOSHSRVISYAGCLTOMSLF
						AIFGGMEE\NMLLSVMAYDWF
			İ			VAICHPLHYPVIMNPHLGVFLD
						LGAFFLSLLDSQLHSWIVLQFTF
1			ĺ			FKNVEISNFV*DPSQLLNLACSD
	ļ.	l				SVINSIFIYLDSIMFGFLPISGILW
						SYANNVPSILRISSSDRKSKAFS
		l				TCRSHLAVVCLFYGTGIGVYLT
						SAVAPPLRNGVVASVTYAVVT
						PMLNPFIYSQRNRDIQSALRRLR
						SRTVESHOLLHPFSCVGKKGQA
6399	36767	A	6449	2	1535	
6400	36768	Α	6450	1	635	
6401	36769	Α	6451	222	1040	
6402	36770	Α	6452	2	1135	
6403	36771	Α	6453	1	576	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
			ŀ	sequence		
6404	36772	A	6454	2	694	QCGGIQRSHGSWSQEASDSVW
						QLQSMWMLDKLTGVFAPRPST
						GPHKLR\ECLSRIIF\LRNRLKYA
						LTGDEVKKI\CMQRFIKI\DGKV
1			!		}	RT\DITYPVG\FMDVI\SIDKTGR
						EFPVLIYDTKG/RAFAVHRITP\E
			l			EAQVPSCAKVRRDLCGAQKGIP
						HLVTH\DARTIPLPR\$PSSKVND\
	1					TIQI\DLEDWARFT*FSSKFDNW
						*TCCMGDWEGA*P*GRNWVLI
						HQQRRRAPWDLF
6405	36773	A	6455	1	243	
6406	36774	A	6456	3	766	
6407	36775	A	6457	1	741	
6408	36776	В	6458	500	8643	
6409	36777	A	6459	1	7863	MKPRTLTVRVTALKVARLESV
		l				PSDVQMCSEFLPSDSAAQLASP
						SGSRTGAAGGAAYQSCAVLPH
						SSALWVVDGTRCRGAGGSAHQ
				1		GGSATQEPTERVEGSGMAGCR
						SRVLPHWKAANVLGMSVESAP
				1		AVEEEKGEELEQKEKEKEEDTS
						GNTTHSLGAEDTASSQLGFGVL
						ELSQSQDVEENTVPYEVDKEQL
	ŀ					QSVTTNSGYTRLSDVDANTAIK
						HEEQSNEDIPIAEQSSKDIPVTA
						QPSKDVHVVKEQNPPPA
6410	36778	A	6460	2	669	ERRRKLTIPCPPPHPAPPTGGQ
						ACRENAEGIL*AANTSEPGKDA
						EK*KIKV*LAP/CSHSGSSLQSDP
1				!		HFGCSLGPS/DPALGLSGCILPPC
	İ	ļ				SGSYLAPAPNSRIPKPGLKPW/H
						/ESYLPSAVRPHGTQAPGLWPE
						RGL*PAGFLLRPEPVRAASER/Q
i				1		EAVSPER*VPRPPKAQQLHGQS
						PDPSSLCTALRQDHTHWLDARS
						VYPDWRGQPWPPLHQDCGHG
		_			200	GWR
6411	36779	В	6461	241	369	
6412	36780	A	6462	1	510	
6413	36781	В	6463	1	630	COD CAND A LL ELINGON COOLIG
6414	36782	Α	6464	229	561	SCRGYSRILLLFHKSSWCSQVIS
1				1		IFRYNIICSRLPRSWKWRLPVY
						MNWL*YHWFKQYHSSINFISFR
1						SMWFIIIINFKRSPAFILSGSWSIS
L		L		L	L	IARWQIFVFFTTFGSRTKV

SEQ ID	ISEO ID NO.	Mat	SEQ ID NO:	Nucleatide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6415	36783	Α	6465	1271	1710	TEGLGHRSSETPGGAALDALTC ERPRVACFPAARGRGLRPRPRL
						MIGPFETGGGQRLLTLRPRRRR QRRRP/WQGLERPHVRNWGIEL
						ETLRDAFRPQPSVWRTARGEA GKRKGRLVECLGSQRKVLEGV
6416	36784	В	6466		772	LLYAVTRGSFPNLFTPRD
6417	36785	A	6467	1	1272	
6418	36786		6468	3	236	
6419	36787	A C	6469	1	457	
6420	36788	_	6470	148	324	
6421	36789	B A	6471	148	1407	
			6472	1		
6422	36790	Α			651	
6423	36791	Α	6473	619	835	
6424	36792 36793	Α	6474	319	535	L COUNTY OF THE
6425	36/93	Α	6475	1319	647	LCRRIYMYFCVMKNWMQSLW KLCTNKR*RIDKPTLHOVVVRK
		l				*LTPLGMKNQVDSLELLETRSL
		1				KKDPVELGSKSLRRCCCQTEPV
					1	NLLPHVSIGTLKI*SRILRLQRP
6426	36794	A	6476	39	515	
6427	36795	В	6477	1	807	
6428	36796	Α	6478	3	247	GANICCW*GLQE/VFHSW*KTQ
	1					EPSWLHLVDPTTGLQVELPASP
	1					APFARIPQPLGGRWDWAPWSR
						GWCSSGRLGQHRSPWSG
6429	36797	Α	6479	27	363	
6430	36798	В	6480	1132	1268	
6431	36799	A	6481	1628	2008	
6432	36800	Α	6482	953	1087	
6433	36801	Α	6483	2	443	QLAGRCGGRGMSGNRGC\WGA
		l			l	CGPAGVPGG/CWAWCALHSEE
						PASPALRSISRRALAAFPRGRAR
					l	DLQPAMPEPPTPSVGSCAAQAS
		l				PTSAAPCSMAPSPIDHPRAEECV
		1				ARRGTGRHDELIVALPFMMIPW
						HSSIQPFTIHPFNWNFG
6434	36802	С	6484	175	423	
6435	36803	В	6485	122	608	
6436	36804	Α	6486	644	1149	KTMHWKAPLMSWHMHRASSQ
	1	1				KQTRTGTQT/MEAQLQQLQRY
	1	1			1	QEALLQVLRKGEKKAFNMGNI
				1	I	SEVLQRADESCSQFYERLYEAF
				1		QLCSPFDPEATENQCMVNAVF
				1		VGQTQGDIRRKLQKLECFTGM
					1	NVTQVLEVATKVYTNCEEETQ
				1	1	GKGQFAGGSTYGKGGECPKTK
6437	36805	Α	6487	1	2847	
6438	36806	В	6488	329	742	
6439	36807	A	6489	1	1035	
- 102	- 0001	1:	1	1		L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop cadon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6440	36808	A	6490	13	630	INPPPPPFRPEPPSSSNSPKMTDF
	1					KGERGEATRYMFSRPF\RK\HG
	1					VVPLGPHICRI\YRKGDIVD\IKG
						MGYCSKKGIAPTKCY\HGONLE
	1	ı				GVLPMLPQHACWPFVVNQPVL
	1					GQSFFPRELMCRIEHI*ALLRAR
	1					DKLPETVLKENDSEKERSPNEK
						GTWGSNLKRHPGSTPEEAHFV
						RTQWGRSLELAGTLFPMNFMG
1		1				IIGVKEIK
6441	36809	Α	6491	I	1020	
6442	36810	A	6492	I	330	
6443	36811	С	6493	250	372	
6444	36812	Α	6494	1	345	
6445	36813	A	6495	2	335	TVRAYNVPQHAVGIVVNRQVK
ŀ						GKIPAKRINVGIKHFKHSTS*EN
ļ	1					FLKRMKENDQKKKEAKEKVT
	1					WIQLKHQSAPPRE/AQCERTNG
				l		KEPELLEPLPYEFMHNTYIHIYV
				l		CVH
6446	36814	A	6496	2	490	
6447	36815	Α	6497	150	536	NCKISFLHFCYIFVKALKRISAL
	İ	1		l		SRGKILAKRINVRIEHIKHSKSR
	1	1			\	DSFLKRVKENDQKKKEAKEKG
						TWVQ/RKAPGKNLVYISLVLRA
	1				1	L*G*DLTHHIIILFPFFFL**PAPP
						REAHFVRTNGKEPELL
6448	36816	Α	6498	54	553	
6449	36817	A	6499	131	803	TMFCQTGSSVRRVGPGPWAEN
						RTAMLRPCGGTFARKTRLSRLG
						NSPKMNEQQRGKRRGTPIIMFS
	1	1		i	1	KGLLRKHG\VVPLAHIFMR\IYK
		1		1	1	\KGDIVRHPRGMGYLVPKRELP
	1				ĺ	PQSCYPWPKPGRSLTNVTPAML
		l				VGHLL*NKQV*GQRFLPKRNL
		1		1		MWRI*APFRHFLRSPRLASLKT
	1	1		1		CGRENGSRKKERKPKGGKVTW
		l				GFQLKRRHLGFPPQEEATFLLK
		L				EPIGGREP
6450	36818	A	6500	I	489	

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6451	36819	A	6501	29	2028	ENEEEGEKMASTDYSTYSOAA
						AQQGYSA\YTAQPTQGYAQTT
	1					OOAYGOOSYGTYGOPTDVSYT
						QAOTTATYGQTAYATSYGOPP
	1					TGYTTPTAPQAY\SQPVQG\YGT
						GAYDTTTATVT\TTQASYAAQS
	1					AYGTQPAYPAYGQQPAATCPT
	1					RTED*\NKPTETSQPQSSTGGYN
	İ	1				QPSLGYGQSNYSYPQVPGSYP
1						MQPVTAPPSYPPTSYSSTQPTSY
						DQSSYSQQNTYGQPSSYGQQSS
	l .					YGQQSSYGQQPPTSYPPQTGSY
		1		1		SQAPSQYSQQSSSYGQQSSFRQ
l	1					DHPSSMGVYGQESGGFSGPGE
	i				i	NRSMSGPDNRGRGRGGFDRGG
						MSRGGRGGGRGGMGSAGERG
	ŀ					GFNKPGGPMDEGPDLDLGPPV
	l		İ			DPDEDSDNSAIYVQGLNDSVTL
						DDLADFFKQCGVVKMNKRTG
	İ	l				QPMIHIYLDKETGKPKGDATVS
		l				YEDPPTAKAAVEWFDGKDFQG
						SKLKVSLARKKPPMNSMRGGL
						PPREGRGMPPPLRGGPGGPGGP
						GGPMGRMGGRGGDRGGFPPRG
						PRGSRGNPSGGGNVQHRAGDW
						QCPNPGCGNQNFAWRTECNQC
						KAPKPEGFLPPPFPPPGGDRGRG
						GPGGMRGGRGGLMDRGGPGG
		19			i	MFRGGRGGDRGGFRGGRGMD
		l				RGGFGGRRGGPGGPPGPLME
		<u></u>				QMGGRRGGRGGPGKMDKGEH
6452	36820	Α	6502	1	693	
6453	36821	A	6503	3	657	
6454	36822	Α	6504	1	434	
6455	36823	A	6505	208	443	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6456	36824	Α	6506	3	2650	LLPAFLLLCSDSHFLQFCSQFAP
0.150	5002	1		ľ		RKTOGSGSVNNIQANIIAKKSN
						NHLMKKNDQKFKDLPQMAGH
ŀ						PIHHOAOGPPGAKNPQEOORRP
						MGOTTLPAEQEESRVKCKNCG
					ļ	AFGHSARNKTCPIKRWSGALPL
ŀ						QVLGSHKEKENLKPAKAQLPFT
					i	TPGPFTTNDREKERSPSSTMNPS
						EMQRKASPRRWKHHNQTPSIH
ł						KVNKMVMSEEOMKLPSTKKA
1						EPPTWAQLKKLTQLPKKSLEN\
						TKVTQTPENTLLAALMIVST/A
		l				GAAAANYTYWAYVPFPPLIRA
		1				VTWMDNPIEVYVNNSAWVPGP
İ					1	TDDRCPDKPEEEGMMINISTGY
				1		RYPPICLGRAPACLMPAIONWL
	}		ì			VEVPTVGTTSRFTYHTGLLTFR
1						DVAIEFSOEEWKCLDPALEDSY
						TRRKANSCGKPYKCNECGKAF
ŀ						TQNSNLTSHRRIHSGEKPYKCS
						ECGKTFTVRSNLTIHQVIHTGE
	į					KPYKCHECGKVFRHNSYLATH
				1		RRIHTGEKPYKCNECGKAFRGH
						SNLTTHQLIHTGEKPFKCNECG
i						KLFTQNSHLISHWRIHTGEKPY
1						KCNECGKAFSVRSSLAIHQTIHT
1						GEKPYKCNECGKVFRVGRGVSI
1		1				GTTCLLSVFQVITVSSRKSRASP
						ENRATQSILILAPPTSRGSGPGP
						ASVLRRLAQTRKRMAWTESCT
		1				AACAFPSCLVLLYRGRGVPTDL
	1					QVPAPLFSTQSKLKRPGSRTKSS
6457	36825	A	6507	54	360	CSTMNPSEMORIAPPRRORHRS
0437	36823	l <sup>A</sup>	0307	34	300	RAPSAHKMNRMVMSEEOMKL
						PSTKKAEPPTWAQLKKLTQLA
				1		
						KKK\LENTKVTQTPENMLLAAL
6458	26926	L-	6508	525	3656	KTVSTVSAGVPSSSEESD SSTMNPSEMORKAPPRRRRHR
0458	36826	A	6508	323	3030	
1		1	1			NRAPLTHKMNKMVTSEEQMK
	1					LPSTKKAEPPTWAQLKKLTQLA
						TKYLEN\TKVTQTPENTLLAAL
			İ			MIVSMVVSLPMPAGAAAANYT
1			İ			YWAYVPFPPLIRAVTWMDNPIE
1			l		1	VYVNNSA WVPGPTDDHCP\AK
			1			PEEEGMMINISTGYRYPPICLGR
		1	l		i	APACLMPAIQNWLVEVPTVGT
						TSRFTYHTIDLMTEKWVVLASV
			l		1	EVLLRFPLKPGEDPTARYVSNK
		L.		Ļ		KCQPSVDWPTTISQRRGY
6459	36827	A	6509	!	246	
6460	36828	Λ	6510	1	246	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6461	36829	A	6511	1	279	
6462	36830	A	6512	1	363	
6463	36831	c	6513	109	245	
6464	36832	A	6514	2	429	LMTFCWDTPRQSGVPRERMPH
1						TGTWRTVGIRCPKKKLRSANSS
		1				MMRGKVQPFRP/DIQAYGAAPF
l						EDLOVDFREMPKCGGNKYVLV
1	i					LGRTYSGWVEAYPTRTEKTRE
						VTPVLLRDLIRRFRPPLWIGSDN
	1	1				GPAFLAALVQKTAK
6465	36833	c	6515	31	895	
6466	36834	Ā	6516	2	4735	
6467	36835	ÍÀ.	6517	263	418	
6468	36836	A	6518	120	295	YDPLPTWILGKISQRGAEEPAQ
0.00	30030	Ι.,	05.0	.20		HPGCQL*LPPP/SPPRTSSSPSCA
		i				GLTSVSPRPRFPR
6469	36837	A	6519	ir -	1758	MKIRRRFPSSLQLSADLQVPVR
0.05	30037	Ι΄.	0517	ľ	1	KAPROGVSQEKRTKPSLELMIS
	1	1				GTISOEDIRNNVTRGCTPPAIOR
	1	1				VISSSPLLAIRNNVTEGVYTPCD
	1	1				TGGRVHLPVILLLISRDGGHDIS
		ł				FNIAVDVHSPCDTDPNIQGVEY
		1		1		DMTPNIAMNVQPPGTISQKRCT
1	1					LPAILGLISYASSVNIRSNITGWL
	1	l .				YIDRYVGSHVILYPLGIRMGVT
1	1					GEMKGERRRGLHAATKWLEE
						HAPADYONPOEYGRTOLPGTO
	1	1				POLDPHEREDMORLNRDREAL
		1				LEGFKRGAQKATNVNKVSEVI
	l	1				QGKEESPAQFHQRLCEACAKQ
		1				VLVNGDAVSREEKRKENERQA
	ŀ	1				RRNADLLVSCSNOSGPPKEARE
		1				ELWTKDYRPGQDLRLLSQATL
		1				TFHPTVPSPSTLLGLLPAEDSWF
		1		1		TCLDLKDAFFPIRSAPESOKLFA
		1				FQWEDPESALAKTVRQRCVSC
		1				RQHHA\GKVQPFRP/DIQAYGA
		1		1		
1		1		1	1	AAFEDLQVDFTEMPECGGNKY LPVLGRTYSGWVETYPTRAEK
		1			1	
		1			I	AREVTRVLLRDLIPRLELPFRIG
		1		1	1	SDNGPAFVADLLQKTATVLGIT
		1				RKLHAASRPQSSGKGIQNNRTG
	10000	١	1500	ļ	1242	GVYTPCDIESHVILFRSGY
6470	36838	A	6520	1111	1342	MFVPHIGFQNTAALCLLRLGVL
					1	FP*PVGFPAGSCLLI*WNRHWH
		1			1	VPDFSCVTTPQEWCGGVSDVC
L		1		L	L	CGHPHAEPFHLQ

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide Idention of last	Amino neid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codna far last amino acid	
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
6471	36839	A	6521	1	1144	MRGAQKATNVNKLSEDIQGKE
		1				ESPTQFYERLWEAYRMYTPFDP
	1	İ	l			DSPENQRMIPMALVRQSAEDM
		l				RRKLQKQAGLAGMNPSQLLEI
				ł		ASQVFVNRDAVSRKENGKENG
ŀ			l			GQARRYADLFSRTKNYQPVQD
			l			LRLLHQAKLTFHPTVPNPSTLL
1		1			ŀ	GFPPAEDSWFTCLDLKDAFFPIR
l		1				LAPERQKLFAFQWEDPESGWPP
		l				CWRALAATALLVQEANKLTLG
		l				OKLNIKASRAVVTLMNTKGHH
						WLTNATLTDYOTLLCENPRITIE
1						VCNTLHPATLLPVSKSPVKPGC
1						VEVLDSIDSSRPDLWDOPWASV
l						DWELYLDGSSFFNPQGEVEG\S
1						RGDTSELPPCWVCGIPALTORL
		1				EKQHLPPSGHQGSLKHLIWDLL
		1				LLTKKRTFSSMI
6472	36840	A	6522	1	554	LLTRRETT 35MI
6473	36841	В	6523	63	620	
6474	36842	Ā	6524	1	796	SRTKNYOPVODLRLLHOAKLT
0474	30042	l^	0.524	ľ	1,70	FHPTVPNPSTLLGFPPAEDSWFT
						CLDLKDAFFPIRLAPERQKLFAF
						OWEDPESGWPPCWRALAATAL
		ľ				LVQEANKLTLGQKLNIKASRA
		ľ				VVTLMNTKGHHWLTNATLTD
ł	İ	ļ.		1		YOTLLCENPRITIEVCNTLHPAT
		1		i		LLPVSKSPVKPGCVEVLDSIDSS
ŀ			l			
	1	l				RPDLWDQPWASVDWELYLDG
ļ		ŀ				SSFFNPQGEVEG\SRGDTSELPP
1					ĺ	CWVCGIPALTQRLEKQHLPPSG
	0.0040	ļ			2640	HQGSLKHLIWDLLLLTKKRTFS
6475	36843	A	6525	3	2640	
6476	36844	Α	6526	2745	3732	IRIGKNYFKVHMEPKKSPHRQV
		ł				NPKPKEQSWRHHTT*LQTILQG
l		1				YSNQNSMPGPTPQ\PSTPAPGG
						NLRNPQSSDLLQVTKQQGQAL
		l		l		AIQREAPLHRIPAPEAIPWYFQP
1	1	1		1		QPATQLGSPPVDPPSSAMM/SR
ŀ						RAHRSRGPDRQGYPLQGD*PGE
	1	1				PRPQEH*RGHSQERLPSSEKQTP
		1				ICPPAQATQHPEEPDAHQPYKH
	1	l				LFQVCAHQGHPVAQRRN*PGY
		1	1			WERYHSAEDPELQPILAGLSLS
						MYLVTVLRNLLIS
6477					10/0	
	36845	A	6527	1	1860	
6478 6479	36845 36846 36847	A A	6527 6528 6529	1	1458	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hođ	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6480	36848	Α	6530	3	515	TISOKRCTLPAILGLISYASSVNI
						RSNITGWLYIDRYVGSHVILYP
		ŀ				LGIRMGVTGEMKGERRRGLHA
		1				ATKWLEEHAPADYQNPQEYGR
		l			ľ	TQLPGTQPQLDPHEREDMQRL
			i		ŀ	NRDREALLEGFKRGAQKATNV
						NKVSEVIQGKEESPAQFHQRLC
		1				EAYRMYTPLDHDSPENQRMIH
		ŀ			ŀ	MALVRQSAEDMRRKLQKQAG
						LAGMNPSQLLEIASQVFVNRDA
		1				VSPKENSKENGGQARRHDDLF
						SPVEPDCVEVLDSIHSSRPDLRD
						QPWPSGDW/RTICGWEQLLQPP
						RRERCRVCSDNPGH/WLLKPHR
		1	ì			CPRPLQARKLNSLLSLGP*NSTR
		_				DCVRPIVCILPLITIALKISA
6481	36849	В	6531	96	2524	
6482	36850	В	6532	61	2025	
6483	36851	Α	6533	674	2913	
6484	36852	В	6534	120	1849	
6485	36853	A	6535	1	426	
6486	36854	A	6536	2	475	
6487	36855	A	6537	1	501	
6488	36856	Α	6538	15	593	SMWWNSAREPCPWRIVDDCGG
	ļ	l				AFTMGVIGGGVFQAIKGFRNAP
		l				VCRLLSEAPLFIYSCSRSVSPTV
		l		i		NVSSERAESRPTLFMAVSLHMA WCLAHIGIRHRLRGSANAVRIR
		l				
	l	1				APQIGGSFAVWGGLFSTIDCGL VRLRGKEDPWNSITSGA\LTGA
		l				VL\AARSAPLAM\VGSAMMGGI
		l				LL/ALIEGVSILL/TR*TATV
6489	36857	A	6539	2	557	RRFRASAMEEYAREPCPWRIVE
6489	36857	I <sup>A</sup>	0239	2	337	DCGGAFTMGVIGGGVFQAIKG
		1				FRNAPVGIRHRLRGSANAVRIR
		l		ł		APQIGGSFAVWGGLFSTIDCGL
		l			i	VRLR\GKEDPWNSIT\SGA\LTG
	ŀ	l				
						AVL\AAR\SGPLAMGGLQQ*WG
1						GILFAPHLRAFGILLTRYTAQ\Q
						FRNAPPFLEDP\SQ\LPPKDGTPA
	25050	<del>  -</del>	6540	222	2274	\TGYP\SYQQYH
6490	36858	A	6540	223	2274	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion. \=possible nucleotide insertion)
		l		sequence		
6491	36859	Α	6541	2795	3762	FLHFHLRNAVPHQQWNKAGW
						RMTLRS*EKKASDDQITLSYGR
		l l				TFKPK/DKEVENFEQNLEECITR
		ŀ				ITNTEKCLKELMELKTKARELR
						EECRSLRSRCDQLEERISVMED
						EMNEMKREGKFREKRIKRNEQ
		1				SLQEIWDYVKRPNLRLIGVPES
						DGENGTKLENTLQHIIQENFPN
	1	l				LARQANVQIQEIQRTPQRYSSRI
		l				AIPRHIIVRFTKVEMKEKMLRA
	1					AREKGRVTLKGKPIRLTADLSA
		1				ETLQARREWGPIFNILKENNFQ
ł		1	l			PRISYPAKLSFISEEEIKYLTDKQ
ł	i	1				MVRDFVTTRPALKELLKEALN
ŀ						MERNNRYQLLQNHAKF
6492	36860	Α	6542	245	1293	TGAVPIRPSWQRWGKNRTEKL
1		1				ETLKRRAPLLLQRNAVPHQQQ
1		l				NKAGWRMILTS*EKKASDDQIT
l		l			ŀ	LSYGRTFKPK/DKEVENFEKNL
l	1	l				EECITRITNTEKCLKELMELKTK
l	1	1				APELREECRSLRSRCDQLEERV
l						SAMEDEMNEMKREGKFREKRI
	1					KRNEQSLQEIWDYVKRPNLHLI
1	1					GVPESDVENGTKLENTLQDIIQ
		1				ENFPNLARQANVQIQEIQRTPQ
						RYSSRRATPRHIIVRFTKVEMK
		l				EKMLRAAREKGRVTLKGKPIR
ŀ					l .	LTADLSAETLQARREWGPIFNIL
	i					KEKNFQPRISYPAKLSFISEGEIK
	l	1				YFIDKQMLRDFVTTRPALKELL
						KEALNMERNNRYQPLQNHAK
6493	36861	С	6543	116	283	
6494	36862	Α	6544	51	281	KSQNQLLSSKGEYADGQQDQV
		1				SIPAPSPYTLSGPQTQSCPVRPE
		1				LGL*GASSAVQAPAVRYLTRFL
		<u> </u>				LFVMSNLHSP
6495	36863	В	6545	1	897	
6496	36864	В	6546	91	8030	
6497	36865	Α	6547	126	362	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6498	36866	A	6548	936	2064	ERADCLFKRKTNNQKGHLHRK
	1					PICTSPSSKTKSR*NHKDGEKTE
	ļ					OKNWKL*NAERLSSS/IRNAVP
1	1					HQQQNKAGWRMILTS*EKKAS
	1					DDQITLSYGRTFKPK/DKEVENF
	1					EKNLEECITRITNTEKCLKELME
						LKTKARELHEECRSLRSRCDQL
l	1	1				EERVSAMEDEMNEMKREGKFR
		1				EKRIKRNEQSLQEIWDYVKRPN
						LRLIGVPESDVENGTKLENTLO
					İ	DIIQENFPNLARQANVQIQEIQR
						TPORYSSRRATPRHIIVRFTKVE
						MKEKMLRAAREKGQVTLKGK
						PIRLTADLSAETLOARREWGPIF
1						NILKEKNFQPKISYPAKLSFISEC
						EIKYFIDKOMLRDFVTTRPALK
						ELLKEELNMERNNRYQPLQNH
6499	36867	A	6549	I	767	MAGAPPPASLPPCSLILDCCASN
						QRDSVGVGPSEPGVGYSLVVR
					1	RFLSRSEKRNIRVGVTRFSSEM
						NPVPQMEMQKSPSSASLTLGA
						VDRSCSYSAILAPPLGFCFYPLY
					i	ENSTLQSAKKRDAELANGALGI
						IELNNDYTLKKVMKPLITSNTV
	1					TDEIERANVFKMNGKWYLFTD
						SRGSKMTIDGINSNDIYMLGY/D
	1					IKLFNRPLQAAEQNRACAANGS
						*SKRCDIHLLSLRSAASQRQQC
						GYHKLHDKQRLLRG
6500	36868	В	6550	50	327	
650I	36869	Α	6551	333	1301	FLHFHLRNAVPHQQWNKAGW
						RMTLRS*EKKASDDQITLSYGR
		1	i			TFKPK/DKEVENFEQNLEECITR
					İ	ITNTEKCLKELMELKTKARELR
		1			1	EECRSLRSRCDQLEERISVMED
						EMNEMKREGKFREKRIKRNEQ
					1	SLQEIWDYVKRPNLRLIGVPES
						DGENGTKLENTLQHIIQENFPN
					1	LARQANVQIQEIQRTPQRYSSRI
1		1		l	l	AIPRHIIVRFTKVEMKEKMLRA
						AREKGRVTLKGKPIRLTADLSA
	1		1	İ		ETLQARREWGPIFNILKENNFQ
l	1	1	l	i		PRISYPAKLSFISEEEIKYLTDKQ
l			l			MVRDFVTTRPALKELLKEALN
			1			MERNNRYQLLQNHAKF
6502	36870	Α	6552	352	2304	
6503	36871	A	6553	1	1617	

SEO ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hnd	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	l '	l		sequence		
		ᆜ				
6504	36872	A	6554	I	257	MGPIHKISHYVYANISKSEKVL
		l				KSEHFRSQAFQPGQQSETVSEK
	ŀ	l				KKKTRKKRKKRKKKKK
		l		ŀ		KKKKKKKKKKKKKKKKK
		1				SE*DRLGKKEEDEEEEEEEEE
	ŀ				i	EEEEEEEEEEEEEEE
						EEEEEEEEEEEEEE
6505	36873	A	6555	5	156	RKKGGG/EREEEGEGEEEEEE
		l				EEEEEEEEEEEEEEEEVVL
		1				LTPGTGAEDFKKH
6506	36874	A	6556	1	279	
6507	36875	Α	6557	3	120	TEEEEEEEEEEEEEEEE
		1				EEEEEEEEEEEEGEEE\EEEE
6508	36876	A	6558	3	123	
6509	36877	Α	6559	239	432	CLWLFQEEEEEEEEEED*EEE
		l				EEE/EEEEEEEEEEEEEE
		1				EEEEEEEKIFLGHRVGI
6510	36878	A	6560	1	588	
6511	36879	A	6561	ti	204	
6512	36880	A	6562	75	234	
6513	36881	В	6563	100	2510	
6514	36882	A	6564	47	4976	
6515	36883	A	6565	3	4755	SCRCRRRRRGPAPAMAQILPVR
0313	30883	<u> </u> ^	0303	ľ	4733	FOEHFOLONLGINPANIGFSTLT
i		[				MESDKFICIREKVGEOAOVTIID
		1				
İ		1				MSDPMAPIRRPISAESAIMNPAS
		l				KVIALKAGKTLQIFNIEMKSKM
		1				KAHTMAEEVIFWKWVSVNTV
		1				ALVTETAVYHWSMEGDSQPM
		ı				KMFDRHTSLVGCQVIHYRTDE
		1		i		YQKWLLLVGISAQQNRVVGA
		1				MQLYSVDRKVSQPIEGHAAAF
1		1				AEFKMEGNAKPATLFCFAVRN
L						PTGGKLHIIEVGQPAAGNQ
6516	36884	В	6566	47	482	
6517	36885	Α	6567	1	555	MNARPHKVD/GRVVEPKRAV*
		1				EDSQRP\AFVAGIKEDTEEHHLR
		l			l .	DYFQQYGKMEVIEIMTDRGSG
	ı					KKRGFAFVTFDNHDSVDKTVV
		l		1		OKYHTANDHNCEGRKALSKOE
	i	1	İ		l	MASASSSORGHSSSGNFRGGHG
		1	١.	1	1	GGFGGNDIFGYGENFSGHGGFS
		1				GSCGGGGYGSSGGGYNEFGND
		1				GSNTGGGGSYNDFGN
6518	36886	A	6568	1	645	SS.T. SUGGOT TIDE OF
0219	120000	10	0308	<u>                                     </u>	1045	l

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6519	36887	A	6569	2	944	GRGLRKLFIGGLSF*FIDESLKS
0517	50007	1	0507	_		QVGEWGTLTDCVVMRDPNTK
						RSRGFGFVTYAT\VEEVDAAMN
				I	•	ARPHKVDGRVVEPKRAVSRED
				l		SORPGAHI/TLVKKIFVGGIKED
				1		TEEHHLRDYFEOYGKIEVIEIMT
						DRGSGKKRGFA\FVTFDDHDSV
						DKIVIOKYHTVNGHNCEVRKA
				i		LSKQEMASASSSQRGRSGSGNF
						GGGRGGGGGNDNFGRGGNFS
						GRGGFGGSRGGGGYGGSGDGY
						NGFGNDGSNFGGGGSYNDFGN
1						YNNQASNFGPMKGGNFGGRSS
		1				GPYG\GGGQYF\AKPR\NQGGY
		1				GGSSSSSSYGSGRRF
6520	36888	A	6570	1	1512	
6521	36889	Α	6571	2864	3677	RCQLDHLPCHLCCCCHR/CIPSL
						RDPQQAPGSTRLSRAPHIESRV
						GRKPPEEPANPTMNSLTLRDKQ
						/HDASTC/DWKRAL*VPESGLPR
		l				ALLKYIRCPNMSSAQKPRELSK
				İ		RRN*K*PCVKRTPFRPT*E/DLP
				f		YSGKKTGVKGLICPVPGTAVK
				ŀ		APQRPPGPQQPHPAPQSASETA
l		ŀ				WFPVADRRVFSENPGWTAAKT
				,		LGTLSSPCQAGAGVGRQDGDP
						GQELTSQEKPWVGRKIPEHAV
	1					ADKGYRQQCGAGEARGGPVF
						WAAAPRTSWQQASYT
6522	36890	Α	6572	1	666	
6523	36891	Α	6573	2926	3304	EYSLGHRHYNWKC*ALGQKDQ
						VTFATKFAPTSHRTRKQPELWR
	ŀ		ł		1	/QDPGSYGEKQPAWCSVPPGRF
						SGGLVGLGFLDGGIVVQPLRRP
						CCQDCVCGFPTLRSSTKTSTEL
		<u></u>				GPSFLPCERQGKETISVT
6524	36892	A	6574	1	665	

NO:         of peptide sequence         hod models of peptide sequence         action of first code for peptide sequence         addon for last amino actid "Stop coden," possible nucleotide insertion) acquerate           6525         36893         A         6575         3         1121         SSTFPRMPWRLVTSWTAVIPEL EGSTSDPSPAVAQKGEKPVK GNSLWGHTEPVPRRGTGPRP SFVHRLPTMDPHKVNALRAFV KMCKQLSVLHTKEMFIFLER WVESMGKLSPATQKVKSEP TKEKPDSKKVEEDLKADERS TKEKPDSKKVEEDLKADERS TKEKPDSKKVEEDLKADERS TKEKPDSKKVEEDLKADERS TKEKPDSKKVEEDLKADERS GESNLLIDNEDVIEPDPDAPQER GDENALTEEMMDQANHKKV.           6526         36894         A         6576         3         1351         PEAGGEREREAQREEEARGQSVAQY GNFKVM           6526         36894         A         6576         3         1351         PEAGGEREREAQREEDRGMPGNFPG GMPGMPG GMPGMPG GMPGMPG GMPGMPG GMPGMPG GMPGMPG GMPGMPG GMPG GMPGMPGMPGMPG GMPGMPGMPGMPG GMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPG	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
Sequence   Sequence   STPPRMPWRLVTSWTAYIPEL	NO:						
	1	sequence	1	09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
EGSTSDDSPAVAQKGEKPVK.			1		sequence		
EGSTSDDSPAVAQKGEKPVK.	6525	126802	1.	6575	[2	11121	CCTEDDA/DWDI V/TCW/TA VIDE!
GNSL WGSHTEPVPRPGTGPRPI   SFVHRLPTMDPHKVNALRAFV   KMCKQDLSVLHTKEMHELRE   WVESMGGKLSPATQKVYKSEE   TKEKPPDSKKVEEDLKADPES   EESNLLIDNEDVIEPDPDAPQE   GDENAEITEEMMDQANHKKV.   AIEALNGGLQKAIDLFTDAIK   NPQLAILYAKRASVFIKLQKPN   AAIRDCDRAVEITYSAQPYKWE   GKYEQKREEREIKERIERVKA   REEQERAQREERARGQSVAQY   GSFPDGLPGGMLEMRGGMPGI   POITGLNEIFSDPEVLAAVQDPI   VMV/AFFQDVAQNPANMSQY   GNPKVM   PEAGGERERERAQREEDSTRQ;   RAQYGSFTGGFPGGMPGNFPG   GMPGMGGPSARSRAQRISLE   PDRSPPSYAHILPTMDPRRVN)   LEAFEKMCKQDPSVLHTEEMR   FLIRECVESMGGKVPPATHKAN   SEENTTEEKPDSEKAEEDLQAL   EPSSEESDLRKLIKEGVIEPDTD   APQEMGDENAEIPEEMMDQA   NDKKVAAIEALNDGELQKAID   FTDAIKLNPRLAILYAKRASVY   VKLQKPNAAIRALNGGLQKAID   FTDAIKLNPRLAILYAKRASVY   VKLQKPNAAIRALNGGELQKAID   FTDAIKLNPRLAILYAKRASVY   VKLQKPNAAIRALNGGELQKAID   FTDAIKLNPRLAILYAKRASVY   VKLQKPNAAIRALLOHWEE   AAHDLALACKLDVDEDASAM   KEVQPRAQKIAEHRRKYYERK   EEREIKERIERVKKAEEHERA   QREEEARRQSGAQYGSPPGGFI   GGMFONFFGGMPOMGGGMPC   MAGMPGLNEILSDEPVLAAMC   DPEVMVARQPVAQNPANMSK   YQSNRVMNILSKLSAKFGGG   GGMFONFFGGMPOMGGGMPC   MAGMPGLNEILSDEPVLAAMC   DPEVMVARQPVAQNPANMSK   YQSNRVMNILSKLSAKFGGG   GFMFONFFGGMPOMGGGMPC   MAGMPGLNEILSDEPVLAAMC   DPEVMVARQPVAQNPANMSK   YQSNRVMNILSKLSAKFGGG   GFMFONFFGGMPOMGGGMPC   MAGMPGLNEILSDEPVLAAMC   DPEVMVARQPVAQNPANMSK   YQSNRVMNILSKLSAKFGGG   GMFONFFGGMPCMGGGMPC   MAGMPGLNEILSDEPVLAAMC   DPEVMVARQPOVAQNPANMSK   YQSNRVMNILSKLSAKFGGG   GMFONFFGGMPCMGGGMPC   MAGMPGLNEILSDEPVLAAMC   DPEVMVARQPOVAQNPANMSK   YQSNRVMNILSKLSAKFGGG   GMFONFFGGMPCMGGGMPC   MAGMPGLNEILSGKRPQN   QSALQQHMEVARQVSSYCISC   CNRTFSHTALKRHLRSHTGDI   PYECEPCGSCTRDE   PYECEPCGSCTRDE	6523	30893	A	63/3	3	1121	
SSEVHRLPTMOPHIKVNALRAFY KMCKQDLSVLHTKEMHFLRE WYESMGKLSPATQKYKSEEP TKEEKPDSKKVEEDLKADFES EESNLLIDNEDVIEPPDPAPQEP GOENALITEEMMDQANHKKV AIEALNDGELQKAIDLFTDAIK NPQLAILYAKRASVFIKLQKFW AAIRDCDRAVEIYSAQPYKWE GKYEQKREEREIKERIERVKKK REEQERAQREEEARGQSVAQV GSFPPGLPGGMEMERGGMFG PGITGLNEIFSDPEVLAAVQDPI VWVIAFFQDVQNPANNSQYY GNPKVM  6526 3 1351 PEAGGEREERAQREEDSTRQ: RAQYSSTTGGFGGMFGNFG GMFGMGGPSARSRAQRLSLE PDRSPSYAHHLPTMDPRR.VNI LRAFEKMCKQDFSVLHTEEME FLIRECVESMGGKVPPATHKAN SEENITEEKPDSEKAEEDLQAG EFSSESDLRKLIKEGVIEPDD APQEMGENAEREEMDQA APDEMGENAEREEMDQA NDKKVAAIEALNDGELQKAID FTDAIKLNPRLAILYAKRASVF VKLQKPNAAIRDCDRALEINPE SAQPYKWRGKAHRLLGHWEE AAHDLALCKLDVDEDASAM KEVQPRAQKIAEHRRKYERKR EEREIKERIERVKKAREEHERA QREEGARROSGAQYGSPFGGFI GGMFGNFFGGMFGMFGGGMFC MAGMGELSHEIDSDFEVLAMW DPEWMVARQDVAQNPANMSK YQSNPKVMNLISKLSAKFGGQ GGMFGNFFGGMFGMGGGMFC MAGMGCLSEILSDFEVLAMW DPEWMVARQDVAQNPANMSK YQSNPKVMNLISKLSAKFGGQ GFHINLSSPRGGILKTYGGELG KRFLDSLRRMHLLAHSAGAK AFVCQQCGAGFSKEDALETHR QTHITGTDMAVFCLLCGKRFQA QSSALQHMEVHAGVRSVICSE CNRTFPSHTALKRHLRSHTGDI PYECEFCGSCFRDE	1						
KMCKQDLSVLHTKEMHELRE		ł	1				
### WYESMGGKLSPATQKVKSEE TKEEKPDSKKVEEDLKADEPS: EESNLLIDNEDVIEPPPDAPQEP GDENAEITEEMMDQANHKKV. AIEALNIDGELQKAIDL-FTDAIK NPQLAILYAKRASVFIKLQKPN AAIROCDRAVEITYSAQPY KW# GKYEQKREEREKERIERVKKA REEQERAQREEEARGQSVAQY GSPFDGLPGGMERMGGMGI POITGLNEISDPEVLAAVQDPI VMV/AFPQDVAQNPANMSQYG GNPKVM  6526 36894 A 6576 3 1351 PFAGGERERERAQREEDSTRQI RAQYGSTTGGFGGMFGNFGG GMFGMGGPSARSRRAQRLSLE PDRSPSYAHHLPTIDPRRKVI) LRAFEKMCKQDPSVLHTEEMR FLIRECVESMCGKVPPATHKAN SEENTTEEKPDSEKAEDLQAG EPSSESDLRKLIKEGVIEPDTD APQEMGDENAEIPEEMMDQA NDKKVA AIEALNDGELQKAID FTDAIKNPRLAILYAKRASVF VKLQKPNAAIRDCDRAIEINFT SAQPYKWRGKAHRLLGHWEE AAHDLALACKLDVTEDASAM KEVQPRAQKIAEHRIKYSPKR EEREIKERIERVKKAREEHERA QREEEARRGSGQYGSFPGGFI GGMGNTGNFFGGMPGMGGGMPC MAGMGELNEILSDPEVLAMM DPEMVARGDVAQNPANMSK YQSNRVMNLISKLSAKFGGQ GGMGTGNFFGGMPGMGGGMPC MAGMGELSDEPVLAMM DPEMVARGDVAQNPANMSK YQSNRVMNLISKLSAKFGGG GGMFGNFFGGMPGMGGGMPC MGGMCHAEILSDPEVLAMM DPEMVARGDVAQNPANMSK YQSNRVMNLISKLSAKFGGG GTHTOTTDMAVFCLLCGKRFQA QSVALQHMEVHAGVRSVICSC CNRTFPSHTALKRHLRSHTGDI PPECEPCGSCTRDE			1				
### TREEKPPSKKVEEDI.KA.DFESS  ### EESNLLIDNEDVIEPDPDAPQES  GOENAEITEEMMDQANHKKV. AIEALNIGGELQKAIDL-TIDAIK  NPQLAIL-YAKRASYPIKLQKFW AAIROCDRAVEIYSAQPYKWE  GKYECKREEREIKERIIERVKA  REEQERAQREEBERGQSVAQV  GSFPDGLPGGMLEMRGGMFGI  PGITGILNEIRSDEVLAAVQPDI  VMV/AFFQDVAQNPANMSQYG  GMPKVM  ### GRYECKREREIKERIIERVKA  ### AAYOSFTGGFPGGMFGFG  GMPKGMGSPASRRAQRISLE  PDRSPPSYAHHLPTMDPRRVNI  LRAFEKMCKQDPSVLHTEEME  FLRECVESMGGKNPPATHKAN  SEENITTEEKPDSEKAEEDLQAE  PSSESESLIRKLIKGOVIEPDTD  APQEMGDENAEIPEEMMDQA  NDKKVAAIEALNDGELQKAID  FTDAIKLNPRLAIL/AKRASYP  VKLQKPNIAAIROCDRAIEINPE  SAQPYKWRGKAHLLGHWEE  AAHDLALACKLDYDEDASAM  KEVQPRAQKIAEHRRKYBER  EEREIKERIERVKKAEEHERA  QEEEARRQSGAQYGSPFGGFI  GGMPONFPGGMPGMGGMPC  MAGMGLISDFEVLAAMQ  DPEVMVARQDVAQNPANMSK  YQSNRVMNISKLSAKFGGQ  GMRGMCGAGRAG  GS27 36895 A 6577 2 433 GPPLNLSSPRGGILKTYGGELCK  KRFLDSLRLRMHLLAHSAGAK  AFVCDQCGAGFSKEDALETIR  QTHITGTDMAVFCLLCGKRPQA  QSSALQHMEVHAGVRSYCSE  CNRTFPSHTALKRHLRSHTGDI  PYECEPCGSCFRDE		t	1				
EESNLLIDMEDVIEPDPDAPOER GDENAEITEEMMDQANHKKV. AIEALNOGELQKAIDLITDAIK NPQLAILYAKRASVPIKLQKPN AAIRDCDRAVEITSAQPYKWE GKYEQKREEREIKERIERVKKA REEQERAQREERARGQSVAQY GSFPDGLPGGMLEMRGGMFGI POITGLNEIFSDPEVLAAVQDPI VMV/AFFQDVAQNPANMSQYY GNPKVM  6526 36894 A 6576 3 1351 PEAGGERERRAQREDSTRQI RAQYGSTTGGFPGGMPGNFPG GMFGMGGPSARSRAQRISLE PDRSPPSYAHILPTMDPRKVN) LRAFEKMCKQDPSVLHTEEMR FLIRECVESMGGKVPPATHKAN SEENTTEEKPDSEKAEEDLQAL EPSSEESDLRKLIKEGVIEPDTD APQEMGDENAEIPEEMMDQA NDKKVAAIEALNDGELQKAID FTDAIKLNPRLAILYAKRASVY VKLQKPNAAIRDLODRAIENPE SAQPYKWRGKAHRLLGHWEE AAHDLALACKLDVDEDASAM KEVQPRAQKIAEHRRKYERKR EEREIKERIERVKKAEEHERA QREEEARRQSGAQYGSPPGGFI GGMGNFGFFGGMPGMFGGGMPC MAGMPGLNEILSDPEVLAAMC DPEVMVARQDVAQNPANMSK YQSNRVMNLISKLSAKFGGG 6527 36895 A 6577 2 433 GPPLNLSSPRGGILKTYGCELCC KRFLDSLRRMHLLAHSAGAK AFVCDQCGAGPSKEDALETHR QTHTGTTDMAVFCLLCGKRPQA QSVALQHMEVHAGVRSVICSS CNRTFPSHTALKRHLRSHTGDI PYECEPCGSCTRDE		ŀ	ı				
GDENAEITEEMMDQANHKKV		l	1				
AIEALNOGELQKAIDLFTDAIK   NPQLAILYAKRASYFIKLQKPN   AAIRDCDRAVEITYSAQPY KW   GKYYEQKREREIKERILERVKKA   REEQERAQREERAGQSVAQV   GSFPDGLPGGMLEMRGGMFGI   PGITGLNEIFSDPEVLAAVQDPI   VMV/AFPQDVAQNPANMSQY   GMPKVM   GMPKVM   GMPKVM   GMPKVM   PEAGGERERERAQREDSTRQ: GMPKVM   GMPKVM   GMPKVM   GMPKVM   GMPKVM   GMPKVM   GMPKVM   LEAFEKMCKQDPSVLATEEMR   FLRECVESMGGKVPATHKAN   EENTTEEKPDSEKAEEDLQAI   EPSEESDLRLIKEGVIEPDTD   APQEMGDENAEIPEELMMDQA   NDKKVAAIEALNDGELQKAID   FTDAIKLNPRLAILVAKRASVF   VKLQKPNIAAIROCDRAIEINPE   SAQPYKWRGKAHRLIGHWEE   AAHDLALACKLDVDEDASAM   KEVQPRAQKIAEHRRKYERKR   EEREIKERIERVKKAEEHEREA   QREEEARRQSGAQYGSPFGGFI   GGMPGNFPGGMPGMGGGMPC   MAGMPGLNEILSDPEVLAAMC   DPEVMVARQPVAQNPANMSK   YQSNPKVMNLISKLSAKFGGG   GGMPGNFPGGMPGMGGGMPC   MAGMPGLNEILSDPEVLAAMC   DPEVMVARQPVAQNPANMSK   YQSNPKVMNLISKLSAKFGGG   GFINTANTIC   GFINTANTIC   GRAND   GMPLINISPRGGILKTYGCELCC   KRFLDSLRIRMIHLAHSAGAK   AFVCDQCGAGFSKEDALETHR   QTHTGTDMAVECLLCGKRPQA   QSIALQHMEVHAGVRSVICS   CNRTFPSHTALKRHLRSHTGDI   PVECEPCGSCTRDE   PVECEPCGSCTRDE   CSSZ		İ	1				
NPQLAILYAKRASVFIKLQKPN			1				
AAIRDCDRAVEITYSAQPYKWE   GKYPQKREERBIKERIERVKKA     REEQERAQREERBIRGSVAQY     GSFPDGLPGGMLEMRGGMFGI     PGITGLNEIRSDEVLAAVQDP     VMV/AFPQDVAQNPANMSQYG     GNPKVM     PFAGGERERERAQREEDSTRQ!     RAQYGSTTGGFPGGMPGNFG     GMPMGPSSRSRAQRISLE     PDRSPPSYAHHLPTMDPRRVNI     LRAFEKNCKQDPSVLHTEEMR     FILRECVESMGGKVPPATHKAN     SEENITTEEKPDSEKAEEDLQAL     EPSSEEDLRKLIKGVIEPDTD     APQEMGDENAEIPEEMMDQA     NDKKVAAIEALNDGELQKAID     FTDAIKLNPRLAIL/AKRASY     VKLQKPNIAAIRODGRAEINPE     SAQPYKWEGKAHLLGHWEE     AAHDLALACKLDYDEDASAM     KEVQPRAQKIAEHRRKYERK     EEREIKERIERVKKAEEHERA     QREEARRQSGAQYGSPGGF     GGMPGNFPGGMPGMGGMPC     MAGMPGLNEILSDEVLAAMG     DPEWMVARQDVAQNPANMSK     YQSNKVMBLISLSAKFGGG     GGPLNLSSPRGGILKTYGGELCK     KRILDSLRIKHLLAHSAGAK     AFVCDQCGAGFSKEDALETHR     QTHITOTDMAVECLLGGKRPQ     QSIALQHMEVELAGVRSYCSC     CNRTFPSHTALKRHLRSHTGD     PPECEPCGSCTRDE     1 687			1				
GKYEQKREEREIKERIERVKAR REEQERAQREERARGQSVAQY GSFPDGLPGGMLEMRGGMPGI PGITGLNEIFSDPEVLAAVQDPI VMY/AFFQDVAQPANMSQYY GNPKVM  6526 36894 A 6576 3 1351 PEAGGEREERAQREEDSTRQ: RAQYGSFTGGFPGGMPGNFPG GMPGMGGPSARSRRAQRISLE PDRSPPSYAHILPTMDPRKVN) LRAFEKMCKQDPSVLHTEEMR FL'RECVESMCGKVPPATHKAN SEENTTEEKPDSEKAEEDLQAL EPSSEESDLRKLIKEGVIEPDTD APQEMGDENAEIPEEMMDQA NDKKVAAIEALNDGELQKAID FTDAIKLNPRLAILVAKRASVY VKLQKPNAAIRDCDRAIENPE SAQPYKWRGKAHRLLGHWEE AAHDLALACKLDVTEEDASM KEVOPRAQKIAEHRRKYERKR EEREIKERIERVKKAEEHERA QREEEARRQSGAQYGSPPGGFI GGMGNFFGGMPGMGGGMPC MAGMPGLNEILSDPEVLAAMG DPEVMVARQDVAQNPANMSK YQSNPKVMNLISKLSAKFGGG 6527 36895 A 6577 2 433 GPPLNLSSPRGGILKTYGCELCC KRFLDSLRRMHLLAHSAGAK AFVCDQCGAGPSKEDALETHR QTHTGTTDMAVFCLLCGKRFQA QSSALQQHMEVHAGVRSYCSC CNRTFPSHTALKRHLRSHTGDI PYECEPCGSCTRDE							
REEQER AQREELARGGSV AQY GSFPDGLPGGMLEMRGGMPGI PGITGLNEIISPEVLAAVQpDI VMV/AFFQDVAQNPANMSQY( GNPKVM  6526 36894 A 6576 3 1351 PEAGGERERERAQREEDSTRQ: RAQYGSFTGGFPGGMPGNFPG GMPGMGGPSARSRAQRISLE PDRSPPSYAHHLPTMDPRRVNI LRAFEKMCKQDPSYLHTEEMR FLNECVESMCGKVPPATHKAN SEENITEEKPDSEKAEEDLQAL EPSSEESDLRKLIEGVIEPDTD APQEMGDENAEIPEEMMDQA NDKKVAAIEALNDGELQKAID FTDAIKLNPRLAILVAKRASVY VKLQKPNIAAIRODGRAEINPE SAQPYKWRGKAHRLIGHWEE AAHDLALACKLDVDEDASAM KEVQPRAQKIAEHRRKYERKR EEREIKERIERVKKAREEHERA QREEEARRQSGAQYGSPPGGFI GGMPONFPGGMPGMGGGMP MGGMPGFGGMPGMGGMP MGGMPGMGGMP MGGMPGMGGMP MGGMP MGMPGMGGMP MGGMP MGMPGMGGMP MGGMP MGMGMGMG		l	1				
GSFPDGLPGGMLEMRGGMFGI		ı	ı				
PGITGLNEIFSDEVLAA VQDPP		l	1				
VMV/AFPQDVAQNPANMSQY(			ļ				
6526 36894 A 6576 3 1351 PEAGGEREERAQREEDSTRQ: RAQYGSTTGGFPGGMPGNFPG GMPGMGGPSARSRRAQRISLE PDRSPPSYAHILPTMDPRRVN) LRAFEKMCKQDPSVLHTEEMR FL\RECVESMCGKVPPATHKAN SEENTTEEKPDSEKAEEDLQAL EPSSEESDLRKLIKEGVIEPDTD APQEMGDENAEIPEEMMDQA NDKKVAAIEALNDGELQKAID FTDAIKLNPRLAILVAKRASVY VKLQKPNIAAIRDCDRAIEINPE SAQPYKWRGKAHRLLGHWEE AAHDLALACKLDVTEEDASAM KEVOPRAQKIAEHRRKVYERKR EEREIKERIERVEKKAEEHERA QREEEARRQSGAQVGSFPGGFI GGMFONFFGGMPGMGGGMPC MAGMPGLNEELSDEPEVLAAM DPEVMVARQDVAQNPANMSK YQSNPKVMNLISKLSAKFGGG 6527 36895 A 6577 2 433 GPPLNLSSPRGGILKTYGCELCC KRFLDSLRRMHLLAHSSGAK AFVCDQCGAGPSKEDALETHR QTHTGTTDMAVFCLLCGKRFQA QSSALQQHMEVHAGVRSYCSC CNRTFPSHTALKRHLRSHTGDI PYECEPCGSCFRDE				ŀ			
		ļ	l				
RAQYGSFTGGFPGGMPGNFPG GMPGMGGPSARSRAQRLSLE PDRSPPSYAHHLPTMDFRRVN) LRAFEKMCKQDPSVLHTEEM FLRECVESMGGVPPATHKAN SEENTTEEKPDSEKAEEDLQAL EPSSESDLRALIKGVIPPDTD APQEMGDENAEIPEEMMDQA NDKKVAAIEALNDGELQKAID FTDAIKLNPRLAILVAKRASVY VLLQKPNIAAIRDCDRAIEINPE SAQPYKWRGKAHRLLGHWEE AAHDLALACKLDVDEDASAM KEVQPRAQKIAEHRRKYERKR EEREIKERIERVKAEEHERA QEEEARRQSGAQYGSPFGGFI GGMPGNFPGGMPGMGGGMPC MAGMPGLNEILSDPEVLAAMC DPEVMVAFQDVAQNPANMSK YQSNPKVMNLISKLSAKFGGG 6527 36895 A 6577 2 433 GPPLNLSSPRGGILKTYGCELCG KRFLDSLRIRMIHLAHASGAK AFVCDQCGAGPSKEDALETHR QTHTGTDMAVFCLLCGKRFQA QSSALQQHMEVHAGVRSYCSS CNRTFPSHTALKRHLRSHTGDI PYECEPCGSCTRDE			┖				
GMPGMGGPSARSRRAQRI.SLE   PDRSPPSYAHHLPTMDPRR.VNI     LRAFEKMCKQDPSVLHTEHRM     FIJRECVESMGGKVPPATHKAN     SEENITEEKPDSEKAEEDLQAG     EPSSESDLRKLIKEGVIEPDTD     APQEMGDENAEIPEEMMDQA     NDKKVAAIEALNDGELQKAID     FTDAIKLNPRLAILVAKRASVF     VKLQKPNAAIRDCDRAEIMPF     SAQPYKWRGKAHRLLGHWEE     AAHDLALACKLDVEDGASAM     KEVQPRAQKIAEHRRKYERKR     EEREIKERIERVKKAREEHERA     QREEAAROSGAQYGSPPGGF     GGMPGNFPGGMPGMGGGMPC     MAGMPGLNEILSDPEVLAAM     DPEMVARQPOVAQNPANMSK     YQSNPKVMNLISKLSAKFGGQ     G6527   36895   A   6577   2   433   GPPLNLSSPRGGILKTYGCELC     KKFLDSLRRMHLLAHSAGAK     AFVCDQCGAGPSKEDALETHR     QTHIGTDMAVFCLLGGKRFQA     QSNLQHMEVHAGVRSVICS     CNRTFPSHTALKRHLRSHTGDI     PVECEPCGSCFRDE     6528   36896   A   6578   1   687	6526	36894	Α	6576	3	1351	
PDRSPPSYAHHLPTMDPRRVNI		i					
LRAFEKMCKQDPSVLHTEEMR FL\RECVESMCGKVPPATHEAMR FL\RECVESMCGKVPPATHKAN SEENTTEEKPDSEKAEEDLQAL EPSSEESDLRKLIKEGVIEPDTD APQEMGDENAEIPEEMMDQA NDKKVAAIEALNDGELQKAID FTDAIKLNPRLAILVAKRASVF VKLQKPNAAIEALNDGELQKAID FTDAIKLNPRLAILVAKRASVF VKLQKPNAAIRDCDRAIEINPT SAQPYKWRGKAHRLLGHWEE AAHDLALACKLDVTEEDASAM KEVOPRAQKIAEHRRKVYERKR EEREIKERIERVKKAEEHIERA QREEEARRQSGAQVGSFPGGFI GGMFÖNFFGGMPGMGGGMPC MAGMPGLNEILSDEPVLAAMM DPEVMVARQDVAQNPANMSK YQSNFKVMNLISKLSAKFGGG FTDAINSKLSAKFGGG GFTTTTTTMAVFCLLCGKRFQA QSVALQHMEVHAGVRSVICSS CNRTFPSHTALKRHLRSHTGDI PYECEPCGSCFRDE		!	1				
FIJRECVESMGGKVPPATHKAN SENTTESKPDSEKAEEDLQAL EPSSESDLRKLIKEGVIEPDTD APQEMGDENAEIPEEMMDQA NDKKVA AIBALNDGELQKAID FTDAIKLNPRLAILYAKRASVF VKLQKPNIAAIRDCDRAIEINPI SAQPYKWBGKAHRLLGHWEE AAHDLALACKLDVDEDASAM KEVQPRAQKIAEHRRKYERKR EEREIKERIERVKKAREEHERA QREELARRQSGAQYGSPPGGFI GGMPNFFGGMPGMGGGMP MAGMPGLNEILSDPEVLAAMQ DPEVMVAFQDVAQNPANMSK YQSNPKVMNLISKLSAKFGGG KRFLDSLRIKHLAHSAGAK AFVCDQCGAGFSKEDALETHR QTHTGTTDMAVFCLLCGKRFQA QSIALQQHMEVHAGVRSVICS CNRTFPSHTALKRHLRSHTGDF PYECEFCGSCFRDE							
SEENTTEEKPOSEKAEEDLQAT							
EPSSEESDLRKLIKEGVIEPOTD		l					
APQEMGENAEIPEEMMDQA NDKKVAAIEALNDGELQKAID FTDAIKLNPRLAILVAKRASVY VKLQKPNIAAIRODGRAEINPE SAQPYKWRGKAHRLICHWEE AAHDLALACKLDVDEDASAM KEVPRAQKIAEHRKYERKR EEREIKERIERVKKAREEHERA QREEEARRQSGAQYGSPPGGFI GGMPNFFGGMPGGGMP MAGMPGLNEILSDPEVLAAMQ DPEVMVAFQDVAQNPANMSK YQSNPKVMNLISKLSAKFGGO KRFLDSLRIKHLICHWEE AHDLALACKLDVDEDASAM KEVPRAQKIAEHRAGAGK AGGEGARQSGAQYGSPGGFI GGMPNFFGGMIKTYGGELCK KRFLDSLRIKHHLLAHSAGAK AFVCDQCGAGFSKEDALETHR QTHTGTTDMAVFCLLCGKRFQA QSIALQQHMEVHAGVRSYICSE CNRTFPSHTALKRHLRSHTGDF PVECEFCGSCFRDE		1					
NDKKVA AIEALNOGELQKAID   FTDAIKLNPRLAILYAKRASVF							
FTDAIKLNPRLAIL VAKRASVF		l	1				
VVLQKPNIAAIROCDRAIEINPT   SAQPYKWRKARHLIGHWEE   AAHDLALACKLDYDEDASAM   KEVQPRAQKIAEHRRKYPERK   EEREIKERIERVKKAEEHERA   QREEEARRQSGAQYGSPFGGFI   GGMPGNFPGGMPGMGGMPC   MAGMPGLNEILSDFEVLAAMC   DPEVMVAFQDVAQNPANMSK   YQSNFKVMNLISKLSAKFGGG   SASSPKVMNLISKLSAKFGGG   A 6577 2 433 GPPLNLSSPRGGILKTYGCELCC   KRFLDSLR.RMHLLAHSAGAK   AFVCDQCGAGFSKEDALETHR   QTHTGTDMAVFCLLCGKRFQA   QSGAQQHMEVHAGVRSYICS   CNRTFPSHTALKRHLRSHTGDF   PVECEPCGSCFRDE   C528   36896   A 6578   1 687							
SAQPYKWRGKAHRLLGHWEE			1				
AAHDLALACKLDYDEDASAM		i	1				
KEVOPRAQKIAEHRRKYERKR   EEREIKERIERVKKAREEHERA     QREEEARROSGAQYGSPFGGF    GGMPÖNFPGGMPÖMGGGMPC     MAGMPGLNEILSDPEVLAAM     DPEVMVARODVAQNPANMSK     YQSNRKVMNLISKLSAKFGGO     KRFLDSLRRMHLLAHSAGAK     AFVCDQCGAGPSKEDALETHR     QTHTGTDMAVFCLLCGKRFQA     QSALQQHMEVHAGVRSYCIS     CNRTFPSHTALKRHLRSHTGD-     PYECEFCGSCFRDE     6528   36896   A   6578   1   687		ı	1				
EEREIKERIERVKKAREEHERA		l	1				
QREEEARRQSGAQYGSPFGGF    GGMPGNFPGGMPGMGGGMPC    MAGMPGLNEILSDFEVLAMMC    DPEVMVAFQDVAQNPANMSK    YQSNPKVMNLISKLSAKFGGO    6527   36895   A 6577   2   433   GPPLNLSSPRGGILKTYGCELCC    KRFLDSLRLRMHLLAHSAGAK    AFVCDQCGAGFSKEDALETHR    QTHTGTDMAVFCLLCGKRFQA    QSSALQQHMEVHAGVRSYICSE    CNRTFPSHTALKRHLRSHTGDI    PYECEFCGSCFRDE    6528   36896   A 6578   1   687	1	ł	l	1			
GGMPGNFPCGMPGMGGMPC    MAGMPGLNEILSDPEVLAAMC    DPEVMVAFQDVQNPANMSK    YQSNPKVMNLISKLSAKPGQQ    6527   36895   A   6577   2   433   GPPLNLSSPRGGILKTYGCELCI   KRFLDSLRIZMHLLAHSAGAK    AFVCDQCGAGPSKEDALETHR   QTHTGTDMAVFCLLCGKRFQA    QSSALQQHMEVHAGVRSYICSE    CRFFPSHTALKRHLRSHTGDH    PYECEFCGSCFRDE    6528   36896   A   6578   1   687	ŀ						
MAGMPGLNEILSDEVLAAMC   DPEWMVARQDVAQNPANMSK   YQSNPKVMNLISKLSAKFGQG			1				
DPEVMVAFQDVAQNPANMSK YQSNPKVMNLISKLSAKFGGQ 6527 36895 A 6577 2 433 GPPILNLSSPRGIGILKTYGGELG KRFLDSLRLRMHLLAHSAGAK AFVCDQGAQFSKEDALETHR QTHTGTDMAVFCLLGGKRFQA QSIALQQHMEVHAGVRSYICSE CNRTFPSHTALKRHLRSHTGDH PYECEFCGSCFRDE	l		l				
YQSNPKVMNLISKLSAKFGGQ    6527   36895   A   6577   2   433   GPPLNLSSPRGGILKTYGGELCK   KPRLDSLRIZMHLLAHSAGAK   A   A   A   A   A   A   A   A   A   A	l		l				MAGMPGLNEILSDPEVLAAMQ
		l	l		1		
KRFLDSLRLRMHLLAHSAGAK APVCDQCGAQFSKEDALETHR QTHTGTDMAVPCLLGGKRPQA QSIALQQHMEVHAGVRSYICSE CNRTFPSHTALKRHLRSHTGDH PYECEFCGSCFRDE			L				
AFVCDQCGAQFSKEDALETHR QTHTGTTDMAYELLLGGKRFQA QSSALQQHMEVHAGVRSYICSE CNRTFPSHTALKRHLRSHTGDH PYECEFCGSCFRDE 6528 36896 A 6578 1 687	6527	36895	Α -	6577	2	433	
QTHTGTDMAVFCLLCGKRFQA   QSIALQQHMEVHAGVRSYICSE   CNRTFPSHTALKRHLRSHTGDH   PYECEFCGSCFRDE   6528   36896   A   6578   1   687	l		ı		1		KRFLDSLRLRMHLLAHSAGAK
QSIALQQHMEVHAGVRSYICSE   CRITFPSHTALKRHLRSHTGDH   PYECEFCGSCFRDE   1   687   6528   1   687			ı				AFVCDQCGAQFSKEDALETHR
CNRTFPSHTALKRHLRSHTGDH PYECEFCGSCFRDE 6528 36896 A 6578 1 687			1	1	I		QTHTGTDMAVFCLLCGKRFQA
PYECEFCGSCFRDE			1	1	1		QS\ALQQHMEVHAGVRSYICSE
6528 36896 A 6578 I 687			1				CNRTFPSHTALKRHLRSHTGDH
							PYECEFCGSCFRDE
6529   36897   A   6579   2   449	6528						
	6529	36897	Α	6579	2	449	

SEQ ID NO:	SEQ ID NO: of peptide	Mct hod	SEQ ID NO:	Nucleotide location of first	Nucleotide location of last	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6530	36898	A	6580	852	1084	TDAGCYYAARQCGTAVPSRDV HIRHQGTPVPQF*TAPLRARS/E VSPARRRARMLSSSASFASANIT TSSAWSDTLQP
6531	36899	A	6581	1	681	
6532	36900	Α	6582	1	483	
6533	36901	А	6583	I	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG\SLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS
6534	36902	A	6584	1	678	DKING
6535	36903	A	6585	3	634	
6536	36904	A	6586	4	479	CSAKTAIRGVSECLIHHHGIPHS TASDQGTHFTAKEVWQWAYA HGIHWSYHVLHHPEEA/GKER WNGLLKSQLQCQLGDNTLQG* GKVLQQAVYVLN*HPIYGTVSP IARIH/GSRNQG/VETELTPLTITP SDPLAKFLLPVPPTLHSAGLEIL VPEGEIR
6537	36905	A	6587		1539	MVGKAKWKPLELPLPRKMVSQ KQYRILGGTAEISVTIKULKDA RVVIPSTSPFYSPIWPVQKIDGS WRMTEDYRKLNQVYTPTAAA PVPVYSLLEQINTSPGTRYAAID LTNAFSIPFIKAHQKLFAFSW QGQQYTFTVLPWGDINSPALCH NLIRRDPDCFSLPQDITLYHHID DIMLTGSREQEVADTADFLVKD KLHLAPPTTKQAQHLVGLF GFWRQHIPLLGYLLQPIYRVTQ KVASFEWSQEQKTALQQVQAA VQAVLPLQPYNPADPMVLEVS VADRDAVCSLWQAPIGGSQWR PLGFWSKALVESADNVSPFERQ LLA/CHKVGHAQQHSISKWK*Y HIDRAQADYHPWTQACLIHCQ GIPHSIASDKDAHFTTREVWQW THAHEIHWCYHVLHPEAAGL TERWNRLLKSQLQRDLGDNTL CREWNRLLKSQLQRDLGDNTL QGSGKVLQKAMYALNQHPYG TISPIARIHGSSNQGVEVAPLTIT PSDPLAKFLLCYPTTLRSAGLD VLYPEGGMTQQFH

SEO ID	SEO ID NO:	IALat	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				L	L	
6538	36906	Α	6588	I	566	MGRNQSRKAENSKNWSASSPP
		1				KDHSSLPAMEQSWMENDFDEF
					1	TEVGFRRSVITNFSELKEHVLTY
	l	l				CKEAKNVEKRIYRSRNQGMEV
i	1	ı				KVAPLTITPSDPLANFFASVPAT
		l				LHSAGLEVLVPEGGTLPLGDTT
1	1	l			i e	MIPLNWKLRLRTGYFGLLLRLS
1		l				QQAKKGAMVLA/GVVDPDYQ
						NEISLLLHN*GKTHDH
6539	36907	Α	6589	221	357	
6540	36908	С	6590	228	342	
6541	36909	A	659 I	745	849	
6542	36910	Α	6592	1	240	
6543	36911	A	6593	2	495	FVRLVGRGDCDPLLSVCLTTMP
					Į.	LYEGLGSGG\EKTAVVIDLGEA
				l .		FTKCGFAGETGPRCIIPSGIKRA
İ		ı		l	ŀ	GMPKPVRVVQYNINTEELYSYL
		l				KEFIHILYFRHL\LVNPRDRRV\V
1				i		IIES\VLCPS\HFREDTHSCFFFKY
				i		FE\VPSVLLA\PS\HLMALLTLGI
		l			İ	NSWHGPRL
6544	36912	A	6594	I	579	
6545	36913	A	6595	I	621	
6546	36914	A	6596	ı	35I	
6547	36915	Α	6597	I	447	
6548	36916	Α	6598	114	880	
6549	36917	Α	6599	1	2625	
6550	36918	Α	6600	1	1674	
655I	36919	Α	6601	1035	2235	QTHSQYHTEWAKTGSIPFENW
		l				HKTGIPSLTTPIQHSVGSSGQGN
		l				OAGEGNKGYSIRKRGSOIVPVC
				l	i	RRHD/VYI*KTPLSQPEISLS**A
		1				TSAKS/LGYKINVQKSQAFLYT
		l				NNROTESQIMSELPFTIASKRIK
		l				YLGIOLTRDVKDLFKENYKPLL
		l		ł		KEIKEDTNKWKNIPCSWVGRIN
		1				IVKMAILPKVIYRFNAIPIKLPM
	Ì	1				PFFTELEKTTLKFIWNQKRARIT
				l	ŀ	KSILSOKNKAGGITLPDFKLYY
		1				KATVTKTAWYWYQNRDIDQW
	1			1		NRTEPSEITPHIYNYLIFDKPEK
		l				NKQWGKDSLFNKWCWENWLA
1				1	1	ICRKLKLDPFLTPYTKMNSRWI
						KDLNVRPKTIKTLEENLGITIQD
	1	1				IGMGKDFMSKTPKAMATKAKI
		1				DKWDLIKLKSFCTAKETTIRVN
						ROPTK
	J		L		L	NOLIV

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of lirst codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop coden, /=possible nucleotide deletion, \=possible nucleotide insertion)
6552	36920	Α	6602	369	1917	AGEGNKGYSIRKRGSQIVPVCR RHDIVYI'KTPLSQPKISLS**AT SAKS/LGYKINVQKSQTFLYTN NRQTESQIMSELPFTIASKKIKY LGIQHTRDVKDLFKENYRHL EIKEDTNK WKNIPCSWVGRINI VKMALIPKVIYRFNAIPIKLPMT FTELEKTISKFIWNQKRARITK SLSQKNKAGGITL-PDFKLYYK ATVIKTAWYLLYQNRDIDQWN RTEPSEMTPHTYNYLIFDKPEK NKQWGKDSLFNKWCWENWLA ICRKLKLDPELPTYKINSRWIK DLNVRPKTIKTLEENLGITIQDI GMGKDEMSKTPKAMATKOKID KWDLIKLKSECTAKETTIRVNR QPKKWEKIFATYSSOKGLISRIY NELKQIVKKKTNPIKKWAK DNNRHFSKEDIYAAKKHMKKCS SSLAIREMQIKTTMRYHLTPVR MAIIQKSGNNRCWRGGGEIGTI. LHCWWDCKLKQHILTHRWEL NNEITWTQEGEYHTLGTVVGW
6553	36921	Α	6603	1	2781	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
6554	36922	Α	6604	1320	2403	LQTILQVYSNQNSMVLVPKOR
						YRSMEONRALRNNATYLOLSD
						L*QT*EKQAMGKGFPI**MVLG
			i			KLASHM*KAETGSLPYTLYKN
						QFKMD*RLKR*T*NSKKQSPSP
						PPKERSSSPATEQSWTENDFDE
		l				LREEGFRRSNYPELREDIQTKG
		İ				KEEIQTTIREYYKHLYANKLEN
						LEEMDKFLNTYTLPRLNQEEVE
						SLNRPITGSEIVAVINSLPTKKSP
						GPDGFTAEFHQRYKVELVPFLL
			i			KLFQSIEKEGILPNSFYEASIILIP
ŀ						KPGRDTIKKENFRPISLTNIDAKI
						LNKILANRIQQHIKKLIHYDQV
						GFIPGMQDWFNIRKSINVIQHIN
						RTKVKNHMIISIDAEKAFDKIQ
						QRFMLKTLNKLAQNLLKLISNF
						SKVSGYKINVQKSQAFLYTNNR
						QTESQIMSELPFTIASKRIKYLGI
						QLTRDVKDLFKENYKPLLKEIK
						EDTNKWKNIPCSWVGRLNIVK
						MAILPKVIYRFNAIPIKLPMTFF
						TELEKTTVKFIWNQKRACITKSI
İ						LSQKNKAGGITLPDFKLYYKST
						VTKTAWYWYQNRDIDQWNRT
				l		EPSEIMPHIYNYLIFDKPEKNKQ
						WGKDSLFNKWCWENWLAICR
				l		KLKLDPFLTPYTKINSRWIKDL
						NVRPKTIKTLEENLGITIQDIGV
						DKDFMTKTPKAMATKPKIDKW
						DLIKLKSFCTAKETTIRAFDELD
						DVHPHEEIEACRVWQNYGTHP
6555	36923	Α	6605	2202	2515	KSLQCEHSSHIQDLPLACLGLR
						KHYMVAQYL*HSHS/ASGGGSR
						YDVLKISVSCSSTIDI*LAFVSLG
				İ		*DKRTS**TNLAESSPNFFHWV
		_				WIFLASKKFCSVPAR
6556	36924	Α	6606	1934	2077	AIPFRIQA WARTSCPKHKKQWQ
						QKPKLTNGI*FN*RASAQQKKL
L		L_				PSE
6557	36925	В	6607	1	2325	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6558	36926	A	6608	1524	2877	IRKRGSQIVPVCRRHD/VFV*KT
0550	50,20	· ·				PSSQPKISLS**ATSAKS/LGYKI
l						NVOKSQAFLYTNNRQTESQIMS
l		ŀ				ELPFTIASKRIKYLGIQLTRDVK
1						DLFKENYKPLLKEIKEDTNKW
					1	KNIPCSWVGRINIVKMAILPKVI
1		į.				YRFNAIPIKLPMTFFTELEKTIL
						KFIWNOKRARIAKSILSOKNKA
					1	GGITLPDFKLYYKATVTKTAW
						YWYONRDIDOCNRTEPSEIMPH
					1	IYNYLIFDKPERNKQWGKDSLF
						NKWCWENWLAICRKLKLDPFL
					1	TPYTKINSRWIKDLNVRPKTIKT
		l				LEENLGITIQDIGVGKDFMSKTP
		l				KAMATKDKIDKWDLIKLKSFC
l		l				TAKETTIRVNRQPTTWEKIFAT
		1			ŀ	YSSDKGLISRIYNELKQIYKKKT
		1			1	NNPIKKWAKDMNRHFSKEDIY
		1				AAKKHMKKCSSSLAIRERQIKT
		1			ľ	
		1				TMRYHLTPVRMAIIKKSGNNR
6559	36927	-	6609	1	2226	DMDEIGNHHSQ
6560	36928	A	6610	1	674	MGKKONRKTGNSKTOSASPPP
0300	30926	l^	0010	l'	0,4	KERSSSPATEQSWMENDFDELR
		1				EEGFRRSNYSELREDIOTKGKE
		ļ				VONFEKNLEECITRITNTEKCLK
		1				ELMELKTKARELREECRSLRSR
						CDOLEERVSAMEDEMNEMKRE
						GKFREKRIKRNEQSLQEIWDYV
		1				KRPNLRLIGVPESDVENGTKLE
						NTLQDIQEN/CPQSSKAGQRSD
						SGNTENATKILLEKSNSKTHNC
		l			l	OIHOS
6561	36929	В	6611	t-	5175	QINQS
6562	36930	A	6612	1666	2032	LOTILOGYSNONSMVLVPKOR
0502	150750	1	0012	1000	2002	YRSMEQNRALRNNATYLQLSD
						L*QT*EKQAMGKGFPI**MVLG
		1				KLASHM*KAETGSLPYTLYKN
		1	i			QFKMD*RLKH*T*NHKNPRRKP
		l				RHYHSGHRHGQGLHV
6563	36931	A	6613	1596	2169	AGEGNKGYSIRKRGSQIVPVCR
0303	20931	l^`	10013	1370	2107	*HD/VYI*KTPLSOPKISLS**ATS
			l			AKS/LGYKINVQKSQAFLYTNN
		1				ROTESQIMSELPFTIASKRIKYL
				i		
		1	l			GIQLTRDVKDLFKENYKPLLKE
			l			IKEDTNK WKNIPCS WVGRINIM
		1	l			KMAILPKVIYRFNAIPIKLPMTF
			l			FTELEKTKVHMEPKKCPHHQG
	L			l		NPKPKEQSWRHHTT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	deletion, \=possible nucleotide insertion)
6564	36932	A	6614	1667	3103	AGEGNKGYSIRKRGSOIVPVCR +HDVYI+KTLSOPKISLS-*ATS AKS/LGYKINVQKSQAFLYTNN KQTEKQIMSELPITASKRIKYL GIQLTRDVKDLFKENYKPLLQE IKEDTSKWKNVPCSWVGRINIV KMALIPKVIYRFNAIPIKLJPMPF FTELEKTILKFIWDQKRARIAKS ILRQKNRAGGITLPDFKLYVKA TVTKTAWYWYQNRDIDQCM TEPSEITPHIYNYLIFDKPEKN WOGKDSLFRKWCWENVLAIC RKLKLDPFLTPYTKINSRWIKD LLNIRPKTIKTLEENLGTIQDIGM KOFFMSKTPKAMATNAKIDK WDLIKLKSFRTAKETTIRVNRQ PTIKWQKIPATYSSDKGLINSRIY NELKQIYKKKTNINIKWAED MNRHFSKEDIYAAKHMKKCS SLAIREMQIKTTMKYHLTPVR MAIIKKSGNNRLTLLNNHNNPQ PLISIKEPREKELINLOV
6565	36933	Α	6615	3134	3288	
6566	36934	Α	6616	1	2630	
6567	36935	В	6617	877	7936	
6568	36936	Α	6618	2	1589	
6569	36937	Α	6619	1	240	
6570	36938	Α	6620	200	486	
6571	36939	Α	6621	1	558	
6572	36940	Α	6622	1	3885	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6573	36941	Ā	6623	1	2302	KLPVTNRAAHGLCASLGPDFM
				l		TFKVPSSWRHSDSICREWFTLA
	1					GAPSRDVLLVSAIITVSLSVTVV
		i				LCGLCHWCQRKLGKRYKNSLE
				ŀ		TVGTPDSGRGRSEKKAIKVSRP
	1				ļ	CPPPAKASATHPTCKSPRSQEK
						VESPGDLDRDFWNNNESTVQQ
						KWSSYPPKEFILNISPYAPYGDF
						RLSLNGTLLSGAKVAAAAGLA
						VEREGRLGEKPAPVPPPGEDAL
						RSGGAAPSEPGSGGKAGRGRW
				1		RTVQSHLAAGKLNLSNFEDSTL
					l	STATTLESIPSSTGEPKCORPRT
						LMRQQSLQQPLSQHQRGRQPS
				1		QPTTSQSLGQLQAHMASAPGP
						NPRAYGRGQARQGTSAGSKYR
						AAGGRSRSNPGSWDHVVGQIR
						NRGLDMKSFLTTSSRAAK WNF
						TNSETVPALDLDSAVVLIPWISS
	İ					KEDTGDSHYGRVAIYHKGLSFS
						SDGLVYPGAKGREGRMVVLSL
						VLGLSEQDDFANIPDLQNPGTQ
				l		QNQNAQGDKRLPAGGKAVNT
					-	APVPGOTPHDESDRRTEPRSSV
						SDLVNSLTSEMLMEDWPPAVF
				1	l	SSGWAIATAHPASLHSPLIGYSF
	ļ					LAARGGLLLFEADFCWCKRSG
	İ					STFPDCDGVANLAATEMALSO
		1				LRFSKETAMRESLVMLSPGSEE
		l				DEAHEGCSRENLGRIQFSVGYN
		l				FQESTLTLKIMKAQELPAKDFS
						GTSDPFVKIYLLPDKKHKLKTK
6574	36942	Α	6624	1	576	
6575	36943	Α	6625	1	155	
6576	36944	Α	6626	4746	5258	DAGAQPSLPRYLIYHQPSRFFRI
						TSTVTPFSKPISSLLWLV*/GLHC
						DILL/RLLQS*RC*CRSHPEYHSO
						PPGRWQGPSPAPQKCSRTTSRS
		l				RSSR*HPPPPRPGGSAPSSPASYS
		ĺ		1		WTPPRTVPGSWARRWRRHLSR
			l	l		PSWATOPSWTATLWSOPLWRL
				l		KWEDCLSPGRSRLQ
6577	36945	A	6627	1	588	

SEQ ID	SEQ ID NO:	Mct	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hođ	in USSN	location of first		*=Stop codon, /=possible nuclcotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6578	36946	Α	6628	444	1056	GPLLREPHQLCHFPVAGFVLDA
			l			GLPEAAAAPHDRGPELAGPQA
		1				AGQHPAQVAHQPRAAAQQRQ
		1				GRRAREEAGAQAQEEPRGPQE
						RRRRLAEGLRRQCGHPAGRDG
						RGGYRRAAQGPARGGRTPEWQ
		l				QSGGARRTPSVGHPRRARAD\W
	ŀ	1				CLTGANDALSCSSPTCGKFLKT
			l			VSKVPVCRRGLAVNRKEAEGR
	1	1			ŀ	SSESPTSSATFQSPALSWMLVS
		1				QRLLLPHMIGAQSSPGPKRPGN
		1				TLRKWLTSPVRRLSSGKADGH
		1				VKKLAHKHKKSREVRKSADAG
		l				SQKDSDDSAATPQDETVEEDTV
		1				AQPRGRREGAGRQSGSRAAGP
		1				GGRRASAIRGGHARTDVGKRN
						GTRTRKELMPLHGKRKDAAEH
						DEPTSASRPAGERPELTLAAVQ
						TEYNCSFPS
6579	36947	Α	6629	128	1103	
6580	36948	A	6630	1	602	
6581	36949	Α	6631	3	1618	
6582	36950	Α	6632	1	602	
6583	36951	Α	6633	3	1618	
6584	36952	Α	6634	1	912	
6585	36953	Α	6635	195	396	VLPLHRQI**LLH*SKKHNHYK
		1				GKQQDLR/CSSTVPRRPQGILPII
l						SFSNVPVGSRRLKAPLVFIGPG

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6586	36954	A	6636	2	1813	FNTPLSTLDRSSRQKVNKDIQD
		l		l		VISALHEAGLIDIYRTLHPKSTE
	ļ.	1				YTFFSAPHHTYYKIDHIVGSKA
		l				LLSKCKRTEITINGLSDDRAIKL
	1	1				ELRIKKLTONYTTTWKLNNLLI
	ľ				1	SDYWVNNEMKAEIKMFFETNE
	ŀ	1				NKDTMYONLWDTFKAVCRGK
	į.	1				FIAVNAYKRKQERSKIHTLTSO
		l				LKEPEKOEOTHSKASRROEITK
	l .					RAELKEIDTOKTLOKISVSRSW
1		1				FSERINKIDRLIARLMKKKREK
	1					NOIDAIKNDKGDITIDPTEMOTT
		1				IREYYKNLYANKLENLEEMDK
		l				FLDTYILPRLNQEEVELPNRPIT
						GSENEAUNSLP/TKKSPGPDEFT
						AKFYORYKG\LARAIROEKERE
						DTOLGKEEVKLLLFAEDMIVYL
		ı				ENPIVSAONLLKLINNFSKVSGY
	1					KINVOKSOAFLHTNNROTESOI
				l		MSECPLTIASKRIKYLGIQLTRD
	,			l		VKDLFKENYKPLLNKIKEDT\N
						KWKNIPRSWLGRNNIVKMTILP
	ŀ	1				KVI/YKKTTLNFIWNOERARIAK
						TILSKKNKAGGITLPDFKLYYK
	1				i	ATVTKTARYWTLTIKKGSVWP
	ŀ			i	i	SLKSEKRGHRTRPLWKLCHND
			ļ		1	VOGELLKTIOFLFGSPLGHSSLD
6587	36955	A	6637	1	2988	MPPHSEQPHSPSTRQKRKVPLF
						VROCPSFVIQAPKAKMDTFDGF
						KKOFTRFLFLFSMDOLGOGRFS
		1				MOTLSFALAVYRKDSPLVACO
	1	l				VOALGNLEPSSVEAHVSSHGIA
		1				DRKGWHVSLFSIOPGDCFPKAL
		1				VEDSPRDRARROOSSKEEGWC
	ì					RDRRRLKFHSKKGAAAIVVKS
	1	1		I		KKYESPSFGVCFESLLNPPRLTS
	1	1				RREKTISSSKRCROCHAEETTV
		1			I	VFWAKESQTGEQTGRGAGQRR
						MGMIICKACSMLPAE
6588	36956	В	6638	362	1463	
6589	36957	A	6639	1	1061	
6590	36958	A	6640	1	1581	
0390	30738	<u></u>	0040	l'	11361	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, ^=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6591	36959	A	6641	46	862	AAFPARTLEFLSRPLAPTACAA FRPEFWRLNMKLPARVFTLGS RLPCGLAPRRFSYGTKILYQN TEALQSKFSPLQKAMLPPNSF QGKVAFITGGGTGLGKGMTTL LSSLGAQCVIASRKMDVLKAT AEQISSQTGNKVHAIQCNVKYP DMVQNTVSELIKVQGPPSTVIT N*STERSSISSLLPTIYA*DWFRF CSTQVLLPKQVWKPMSKSLAA
6592	36960	A	6642	1	2902	EWGKIWNAIQC WYKGSLQQEELTILNIYAPNTE APRFIKQVLRDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKINKD TQELNSALYQADLIDIYGTH KSTREYTFPSAPHHTYSQNWTT IVGSKALLSEHKRTEITNYLSD WISAMKLELRIKKLTQNIRSATW KLNNLLLNDYWYHNDMKAEI KMFEFTKENKUTTYQNLWT FKAVCRGKFIAKINAHNRKQE RSKIDTLTSQUKELEKKEQTYL KASRROETT
6593	36961	Α	6643	1	5127	
6594	36962	В	6644	1	3570	
6595	36963	Α	6645	1	3663	
6596	36964	В	6646	143	3122	
6597	36965	Α	6647	ī	3235	
6598	36966	Α	6648	1	3249	
6599	36967	A	6649	1	3297	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuelcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eudon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6600	36968	A	6650	n	2563	MKAEIKMFFETNENKDTTNON
	150500	ľ`	1	1		LWDAFKAEEVESLNRPITGAEI
						GAIINSLPTKKSPGPDGFTAEFY
		1				ORYKEELVPFLLKLFQSIEKEEI
						LPNSFYEASIILIPKPGRDTTKKE
						NFRPISLMNIDAKILNKILANRI
						OOHIKKLIHHDOVGFFPGMOG
						WENIRKSINVIOHINRAKDKNH
						MIISIDAEKAFDKIQQPFMLKTL
						NKLGIDGTYFKIIRAIYDKPTAN
				ŀ		IILNGOKLEAFPLKTGTROGCPL
						SPLLFNILLEVLARAIROEKEIK
				ł		GIQLGKEEVKLSLFADDMIVYL
	Ì					ENPIVSAONLLKLISNFSKVSGY
ĺ						KINVQKSQAFLYTSNRQTESQI
					İ	MSELPFTIASKRIKYLGIQLTRD
				1		VKDLFKENYKPLLKEIKEDTNK
				1		WKNIPCSWVGRINIVKMAILPK
						VIYRFNAIPIKLPMTFFTELEKTT
						LKFIWNQKRAHITKSILSQKNK
						AGGITLPDFKLYYKATVTKTA
				İ		WYCYONRDIDOWNRTEPSEITP
						HTYNYLIFDKPEKNKOWGKDS
	1			Į.		LFNKWCWENWLAIWRKLKLD
						PFLTPYTKINSRWIKDLNVRPKT
l						IKTLEENLGITIQDIGMGKDFMS
				ĺ		RTPKAMATKAKIDKWDLIKLK
				ł		SFCTAKETTIRVNRQPTTWEKIF
						ATYSSDKGLISRIYNELKQIYKK
.				I		KTNNPIKKWEKDMNRHFSKED
l						IYAAKKHMKKCSSSLAIREMQI
						KTTMRYHLTPVRMAIIKKSGNN
660I	36969	Α	6651	1	3402	
6602	36970	Α	6652	I	3288	
6603	3697I	Α	6653	I	3168	
6604	36972	Α	6654	1	3516	
6605	36973	Α	6655	1	3693	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6606	36974	IA	6656	11577	3354	TEPKTKTT*LSO*MOKRPLTKF
		1				NNLSC*KLSIN/IVLEVLARAIRC
1						EKEIKGIOLGKEEVKLSLFADD
		1		1		MIVYLENPIVSAQNLLKLISNFS
				1	1	KVSGYKINVQKSQAFLYTNNR
		1		1		QTESQIMSELPFTIASKRIKYLGI
İ		1		1		QLTRDVKDLFKENYKPLLKEIK
		1		1	ł	EDTNKWKNIPCSWVGRINIVK
		1		1		MAILPKVIYRFNAIPIKLPMTFF
		1		l		TELGKTALKFIWNQKRARITKS
1		1				LSOKNKAGGITLPDFQLYCKAT
1	ł					VTKTAWFPSGDVGLEADFSPSF
		1				TLKTQFFSCLAEFAAASCFFQR
		-				MNGFGMAMTTTYSTGAAESPL
		1				PSCSIDQGDDTKLHRARSPGRT
		1				FPAAAGIPAAAAPDGPPLSLLH
		1				KLWFPVELGGRALPRAEESHGI
	ļ	1				VAALGVMVVAQGGKNQGEEA
		l				RSTPWLRPTSHLPPCSSSSAWW
		1				TEQTDAHPLLFLLCLGIYLLNA
		1				LSNLSMVALVRSDGALRSPMY
		į .				YFLGHLSLVDVCFTTVTVPRLL
		1				AGLLHPGQAISFQACFAEMYFF
						VALGITESYLPAAMSYDRATAA
	1	ı		i		CRPLRYGALVTPWALRLAARY
						DRLASVVYAVITPTLNPFINSLR
						NKEVKGALKRGLRWRAAPQE
6607	36975	Α	6657	1	3514	MELKTKARELREECRSLRSRCD
						QLEERVSAMEDEMNEMKREG
						KFREKRIKRNEQSLQEIWDYVK
					1	RPNLRLIGVPESDVENGTKLEN
				ŀ		TLQDIIQENFPNLARQANIQIQEI
					İ	QRTPQRYSLRRATPRHIIVRFTK
	1					VEMKEKMLRAAREKDRSTRQK
	l				ŀ	VNKDTQELNSALHQADLIDIYR
	1					TLHPKSTEYTFFSAPHHTYSKT
						DHIVGSKALLSKCKRTEIITNYL
			i	1		SDHSAIKLELRIKNLTKSRSTTW
						KLNNLLLNDYW
6608	36976	Α	6658	3	3316	
6609	36977	Α	6659	1	4794	
6610	36978	Α	6660	1	3570	
6611	36979	В	6661	1	3384	
6612	36980	Α	6662	1	3429	
6613	36981	Α	6663	1	3780	
6614	36982	Α	6664	1	3894	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6615	36983	A	6665	1	3335	MVKGSIQQEELTILNIYAPNTG
						APRFIKOVLSDLQRDLDSHTLI
						MGDFNTPLSTLDRSTROKVNK
						DTOELNSALHQADLIDIYRTLH
						PKSTEYTFFSAPHHTYSKIDHIV
						GSKALLSKCKRTEIITNYLSDHS
						AIKLELRIKNLTQSRSTTWKLN
						NLLLNDYWVHNEMKAEIKMFF
						ETNENKDTTYONLWDAFKAVO
						RGKFIALNVYKRKOERSKIDTL
						TSOLKELEKOEOTHSKASRROE
i						ITKIRAELKEIETO
6616	36984	В	6666	1	3145	
6617	36985	A	6667	1	4398	
6618	36986	Α	6668	523	3852	
6619	36987	Α	6669	1	3934	MGKKQNRKTGNSKTQSASPPP
		l				KERSSSPATEOSWMENDFDELR
						EEGFRRSNYSELWEDIQTKGKE
		1				VENFEKNLEECITRITNTEKCLK
l		l				ELMELKTKARELHEECRSLRSR
		l				CDOLEERVSAMEDEMNEMKRE
		l		1		GKFREKRIKRNEQSLQEIWDYV
l		l				KRPNLRLIGVPESDVENGTKLE
		1		-		NTLODIIOENFPNLAROANVOI
		1				<b>QEIQRMPQRYSSRRATPRHIIVR</b>
		1				FTKVEMKEKMLRAAROKAPH
		l		-		HTYSKIDHIVGSKAL
6620	36988	В	6670	1	5215	
6621	36989	Α	6671	1	7171	
6622	36990	Α	6672	3	493	
6623	36991	Α	6673	1	729	
6624	36992	Α	6674	3	800	
6625	36993	Α	6675	1	327	
6626	36994	Α	6676	2	462	KSSWLEEDDDPVVARVNRRMQ
						HITGLTVKTAELLQVANYGVG
1	1	l				GQYEPHFDFSRRPFDSGLKTEG
l	1		1	1		NRLATFLNYMSDVEAGGAT\VF
	1			I		PDLGAAIWPKKGTAVFWYNLL
l			l			RTGEGDYR\TRHAACPVLVGCK
						WVSNKW\FHES\GQEFLRPCGST
l		1	1	1	l	EVD

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleatide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop endon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6627	36995	A	6677	3	717	RHRLRNRLKDVGGEAFYPLLE
						DDQSNLPHSNSNNELSAAATLP
		l				LIIREKDTEYQLNRIILFDRLLKA
						YPYKKNOIWREARVDIPPLIRG
						LTWAALLGVEGAIHAKYDAID
						KDTPIPTDRT/QLKWDIPRCHSV
						R*TVIHAPEGHAKFRRVLK\AW
						VVSHPDLVYWQGLDSLCAPFL
			į			YLNFNNEALVYACMSAFIPKYL
						YNFFLKDNSHVIQEYLTVFSQM
		ł				IAFHDPELSNHLNEIGFIPD
6628	36996	A	6678	1	508	IAT TIDI EESITIETEIGI II D
6629	36997	Α	6679	I	888	
6630	36998	Α	6680	2	584	
6631	36999	Α	6681	2	152	QVAKGMDALLQHLEDCGYR/S
		1		l		SKKKAQICRQQVTKWGDGSAL
				ŀ		MGTSTTASL
6632	37000	Α	6682	733	894	
6633	37001	В	6683	1	1626	
6634	37002	Α	6684	I	1971	MAQVWANDNPPGLAVNQAPV
						LIDVKPGAQPIRQKQYPVPREA
l	İ					LKGIQPGTKDYQPVQDLRLVN
				l	-	QATVTLHPTVPNPYTLLGLLLA
		1				EDSWFTCLDLKDAFFSIRLAPES
						QKLFAFQWEDPQSDLGCILLLY
1						VDDLLLGHSTAVECAKGMDVL
		l				LQHLEDCRYKMSKKKAHICRQ
1		[				QVRYLGFTIRKGERS\WEREKM
		1				AVGVLTQTVGPWPRPVAYLSK
						QLD/EVSKGWPLCLRTLAATAL
						LAQEADKLTLGQNLNIKAPHA
						VVTLMTTEGHHWLTNARLTKY
						QSLPCENPHITIEVCNTLNPTTL
1						LPVSESPGEHNCVEVLDSVYSS
		1				RPDLRDQPWASSVDWELYMD
	1	1				GSSFINSQGERCAGYAVVTLDA
			1			VIKAKLWLOGTSAOKAELIALT
	1	l				RAVELSEGQESLEELLGRYFYV
	1	1				SHLPAFAKAVAQLCITCROHNA
		1				ROSPTVSPHIOAYGAAPFEDLO
	1			I	1	VDFTEMPKCGGNKYLLVLTCT
	l			l	İ	YSGWVEAYPTRTEKPYKKGKN
						DPSCTKGQCNPLELVITNPLNP
	1			1		HWKKGERVTLGIDRARLDPRV
						NILVRGGEVYERSPEPVFOTFY
						DELNVPVPEIPGKTRNLFLOLA
	1			l		ECVAOPLNVTSCYVCGGTVTG
	1	1	1	1		YOWPWKARELYPVDPVPDEFL
						AQKNYPDNFWVLKPSITGQYCI
6635	37003	A	6685	1	1461	,
6636	37004	A	6686	î	1005	
سنتنب	1					

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6637	37005	Α	6687	1	174	
6638	37006	Α	6688	519	588	
6639	37007	Α	6689	2	4527	GRAGLGWSSGGRGSRACSEGP
						AEARGREGDKGSAALSPPLPLT
		1				LGEEMAAERGARRLLSTPSFWL
		1				YCLLLLGRRAPGAAAARSGSAF
		1				QSPGASIRTFTPFYFLVEPVDTL
		1				SVRGSSVILNCSAYSEPSPKIEW
		1				KKDGTFLNLVSDDRRQLLPDGS
		1				LFISNVVHSKHNKPDEGYYOCV
		1				ATVESLGTIISRTAKLIVAGLPR
		1				FTSQPEPSSVYAGNNAILNCEV
		1				NADLVPFVRWEQNRQPLLLDD
l		1				RVIKLPSGMLVI
6640	37008	A	6690	1	879	
6641	37009	Α	6691	407	594	
6642	37010	A	6692	1	3621	
6643	37011	В	6693	1	609	
6644	37012	В	6694	1335	1599	
6645	37013	Α	6695	i i	354	
6646	37014	Ä	6696	181	683	SRYFILLRKPTFPAMALLPVLFL
						VTVLLPSLPAEGKDPAFTALLT
		ı				TOLOVOREIVNKHNELRKAVSF
		1				PASNMLKMEWSREVTTNAOR
		1				WANK/CTLOHSDPEDRKTSTRC
		1				GENLYMSSDPTSWSSAIQSWY
		1				DEILDFVYGVGPKS/PQYCPAG
		1				NNMNRKNTPYOOGTPCPG
6647	37015	A	6697	199	969	
6648	37016	Α	6698	1	564	
6649	37017	A	6699	153	427	
6650	37018	Α	6700	1	978	
6651	37019	Α	6701	3	419	
6652	37020	Α	6702	9	255	VRAPAQGPDLAGGRRRCGSGA
		1				SCTPSPRGPASWSRSAAQVPRS
1		1				SRWRAGSASS*N/GRQPAPPTSQ
		1				PPRAQPFAQPPGPWPLS
6653	37021	В	6703	96	283	
6654	37022	Α	6704	172	365	PTYHLYPCHFWYQHRTRRIPRK
		1	1			SERLFPTPPPQLSWKGTWDY*I
		1				CLLCCNDSEGRDFLVLRVLK
6655	37023	Α	6705	3	1171	
6656	37024	Α	6706	2	740	
6657	37025	A	6707	256	461	
6658	37026	Α	6708	1	414	
6659	37027	Α	6709	1330	1386	YIDSILPK*NHDTLQSYCRYM\H
		1			1	SRQRAAS*PLSTGKLQQCLGLD
		1	1		1	LVLC

	SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
	NO:	of peptide	hod		location of first		
		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
NDMEDWYKSIRRVIGOLSG    IFGQKLEDTVRYEKRYGNRL   MI.VEQCVDFIRQRGLKEEG    LPGQANLVKIELQDAFDCGE   SFDSNTDVHITVASLLKLYLR    EPGVIPYAKYEDFLSCAKLLS   EEAGVKELAKQVKSLPVVN					sequence		
NDMEDWYKSIRRVIGOLSG    IFGQKLEDTVRYEKRYGNRL   MI.VEQCVDFIRQRGLKEEG    LPGQANLVKIELQDAFDCGE   SFDSNTDVHITVASLLKLYLR    EPGVIPYAKYEDFLSCAKLLS   EEAGVKELAKQVKSLPVVN	6660	27029	Ι.	6710	207	11173	I I I I I I I I I I I I I I I I I I I
	0000	37028	l^	0,10	207	11173	
MI.VEQCVDFIRQRGLEEGI							
LPGQANLVKIELQDAFPCCE			1				
SFDSNTDVHTVASILKLYLR   PEPVIPYAKYEDFLSCAKILS   EEAGVKELAKQVKSLPVNN   LLXYICRFLDEVQSYSGVNK   VQNLATVFGPNILRPKVEDP  MEGTVVVQQLMSVMISKHD   FPKDAELQSKPQDGVSNNNE KKATMGQLQNKENNNTKDS   RQCSWDKSESPTEKQHEQW   HSSIRQQNQQPKEQWSQAI   173   881   1844   1851   1844   1851   185			1				
PEPVIPYAKYEDELSCAKLLS   EEAGVKELAKQVKSLPVVN							
EEAGVRELAKQVKSLPVNN   LIKYICRIDEVQSYSGVNK   VQNLATVFGPNILRPKVEDP  MEGTVVVQQLMSVMISKHE   FPKDAELQSKQDGVSNNS  KKATMGQLQNKENNTKDS   RQCSWDKSESPTEKQHEQW   HSSIRQQNQQPKEQWSQAI   6661   37029   A 6711   173   881   SSIRQQNQQPKEQWSQAI   6662   37030   A 6712   1605   1844   SSIRQQNQQPKEQWSQAI   6663   37031   B 6713   123   699   SSIRQQNQQPKEQWSQAI   6665   37033   A 6714   1   462   462   4665   37033   A 6715   1   2607   SSIRQQNQQPKEQWSQAI   6665   37034   A 6716   1   918   SSIRQQNQQPKEQWSQAI   6667   37035   A 6718   1   687   SSIRQQNQQPKEQWSQAI   6668   37036   A 6718   1   549   SSIRQQNQQPKEQWSQAI   6670   37038   A 6719   1   258   SSIRQQNQQPKEQWSQAI   6670   37038   A 6720   90   1621   HGLDLRTMNRSRQVTCVAW   RCGVAKETPRKVELSKGGVI   LIAEAEEKLQEGGGSDEEK   SPLEEGINQSARTQARPIREPI   DGDPEDIDRTLDDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDFPDETT   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDFPDETT   KYDEEGDPDETTLDDELAEVD   KYDEEGDPDETTLDDELAEVD   KYDEEGDFPDETT   KYDEEGDPDETTLDDELAEVD   KYDEEGDFPDETT   KYDEEGDPDETTLDDELAEVD   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDPDETTLDDELAEVD   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPDETT   KYDEEGDFPT   KYDEEGDFPT   KYDEEGDFPT   KYDEEGDFPT   KYDEEGDFT   KYDEEGD					ŀ		
LILKYICRFLDEVQSYSGYNK   VQNLATVFGPNILRPK VEDPI   MEGTVVVQQLMSVMISKHD   FPKDAELQSKPQDGVSNNNIK   KKATMGQLQNKENNTKSD   RQCSWDKSESPTEKQHEQW   HSSIRQQNQQPKEQWSQAI   6661   37029   A   6712   1605   1844   6663   37031   B   6713   123   699							
WONLATYGOPNILERY VEDPR   MEGTVVVQLMSVMISKHD							
MEGTVVQQLMSVMISKHD			l				
FPKDAELQSKPQGGVSNNNK KKATMGQLQNKENNTKD6							
RKATMGQLQNKENNTKDE   RQCSWDKSESPITEKQHEQW   HSSIRQQNQQPKEQWSQA1			1				
RQCSWDKSESPTEKQHEQW   HSSIRQQNQQPKEQWSQAI			1				
HSSIRQQNQQPKEQWSQAI			1				
1661   37029   A   6711   173   881	1	-	l				
100   100	6661	27020	<u></u>	6711	172	001	HSSIKQQIQQFKEQWSQAI
6654   37031   B   6713   123   669							
6564   37032   A   6714   1   462							
1			-				
6666   37034   A   6716   I   918							
5667   37035   A   6717   1   549							
6668   37036			_				
100   100							
6670 37038 A 6720 90 1621 HOLDLERTMINESROYTUVAW RCGVAKETPIKVELSKGGVI LIAEAEEKLQEEGGGSDEEK: SPLEEGIMQSARTQARPIREPI DGDPEDIVBRITLDDELAEVD KYDEEGDPDAETLGIESLLGI VYGSNDQDPYVTLKDTEQYI EDFLIKPSDNLIVCGRAEQDG NLEVHVYNQEEDSFYVHHDI SAYPLSVEWLINDFDSFDDSTG YIAVGNMTPVIEVWDLDIVD EPPFTLGSKLSKKKKKKGKK SAEGHTDAVLDLSWYKLIRS LASASADNTVILWDMSLGKF ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALVDCRSPDES RWWRFSGQIERTVTWHFSPG FLASTDDGFVYNLDARSDKF TLNAINDEISGLDLSSQIKGG VTASADKYVKIWDILGDRPS HSRDMKMGVIFCSSCCPDLF YAFGGGKEGLRVWDISTVSS NEAFGRERILVLGSARNSSIS FGSRSSDTPMES					1	258	
LIAEAEEKLQEEGGSDEEK SPLEEGMQSARTQARPREPI DGDPEDDRTL.DDELAEVD KYDEEGDPDAETLGESLLGI VYGSNDQDPYVTI.KDTEQYI EDFLIKPSDNLIVCGRAEQDC NLEVHVYNQEEDSFYVHHDI SAYPLSVEWLNFDPSPDDST YIAVGNMTPVIEVWDLDIVD EPVFTLGSKLSKKKKKKGKK SAEGHTDAVLDLSWNKLIRN LASASADNTVILWDMSLGKE ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALVDCRSPDES RMWRPSQQIERVTWHHPSPC EMSTDDGFVYNLDARSDKE FLASTDDGFVYNLDARSDKE TLNAFNDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HISRDMKMGVLFCSSCCPDLE YAFGGQKEGLRVWDISTVSS NEAFGRREILVLGSARNSSIS FGSRSSDTPMES	6670	37038	Α	6720	90	1621	HGLDLRTMNRSRQVTCVAWV
SPLEGSMOSARTOARPREPI DGDPED\DTDDELAEYD KYDEGDPDAETLGESLIGI VYGSNDQDPYVTLKDTEQYI EDFLIKPSDNLIVCGRAEQDC NLEVHYYNQEDSFYVHHDI SAYPLSVEWLNFDSPTDDSTT YIA VGNMTFVIEVWDLDIVDU EPVFTLGSKLSKKKKKKGKK SAEGHTDAVLDLSWKLLIRR LASASADNTVILWDMSLGKF ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALYDCRSPDES RWWRFSGQJERYTWHNFSPC FLASTDDGFVYNLDARSDKF TLNAHNDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HSRDMKMGVIFCSSCCPDLF YAFGGQKEGLRV WDISTVSS NEAFGRERLVLGSARNSSIS FGSRSSDTPMES							RCGVAKETPDKVELSKGGVKR
GOPEDURITLDOBELAEVD KYDEGDPURITLDOBELAEVD KYDEGDPURITLGIESLLGI VYGSNDQDPVOTI.KDTEQYI EDFLIKFSDNLIVCGAEQDC NLEVHVYNQEEDSFYVHHÜD SAYPLSVEWLNFDFSPDDST YIA VGNNTPULWVDLDIVU EPVFTLGSKLSKKKKKKKGKK SAEGHTDAV.LD.SWRKLIRN LASASADNTULWDMSLGKF ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALYDCRSPDES RMWRFSQQIERVTWNHFSPC FLASTDDGFVYNLDARSDKP TLNAHNDEISCLD.SSQIKGC YTASADKYVKIWDILGDRPS HISRDMKMGVIFCSSCCPULF YAFGGQKEGLRVWDISTVSS NEAFGRERIVLGSARNSSIS FGSRSSDTPMES	l		1				LIAEAEEKLQEEGGGSDEEKTG
KYDEEGPPAETLGISELGI VYGSNDQDPVTILKDTEQYI EDFLIKPSDNLIVCGRAEQDC NLEVHVYNQEEDSFYVHHDI SAYPLSVEWLINFDFSPDDSTI YIAVGNMTPVIEVWDLDIVD EPPYFILGSKLSKKKKKKGKK SAEGHTDAVLDLSVMKLIRN LASASADNTVILWDMSLGKI ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALYDCRSPDES RMWRFSCQIERVTWHHFSPC FLASTDDGFVYNLDARSDKF FLASTDDGFVYNLDARSDKF TLNAINDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HISRDMKMGVLFCSSCCPDLE YAFGGQKEGLRVWDISTVSS NEAFGRREILVLGSARNSSIS FGSRSSDTPMES			1		l		SPLEEG\MQSARTQARP\REPLE\
VYGSNDQDPYVTI.KDTEQYI EDFLIKPSDNLIVCGRAEQDC NLEVHYVNQEEDSFYVHHDI SAYPLSVEWLNFDFSPDDSTT YIA VGNMTPVIEVWDLDIVD EPVFTLGSKLSKLKKKKKGKK SAEGHTDA VLDLSWNKLIRN LASASADNTVILWDMSLGKF ASLA VHTDKVQTLQFHPFEA LISGSYDKSVALYDCKSPDES RMWRFSGQJERVTWNHFSPC FLASTDDGFVYNLDARSDKP TLNAHNDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HISRDMKMGVIFCSSCCPDLE YAFGGQKEGLRV WDISTVSS NEAFGRERLVLGSARNSSIS FGSRSSDTPMES			l		ŀ		DGDPED\DRTLDDDELAEYDLD
EDFLIKPSDNLIVCGRAEQDC NLEVHVYNQEEDSFYVIHDI SAYPLSVEWLNFDPSPDDSTY YIA VGRMTFPVIEWDLDIVD EPVFTLGSKLSKKKKKKGK SAEGHTDAVLDLSWRKLIRR LASASADNTVILWDMSLGKF ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALYDCRSPDES RMWRFSGQIERVTWHHFSPC FLASTDDGFVYNLDARSDKF TLNAHNDEISGLDLSSQIKGC VTASAKYVKIWDLIGDRPS HSRDMKMGVLFCSSCCPDLE YAFGGQKEGLRVWDISTVSS NEAFGRREILVLGSARNSSIS FGSRSSDTPMES	İ		1		i		KYDEEGDPDAETLG\ESLLGLT
NLEVHYYNQEDSFYVHIDI SAYPLSVEWLNFDPSPDDSTO YIA VGNMTPVIEVWDLDIVD EPVFTLGSKLSKKKKKKGKK SAEGHTDAVLDLSWKLLIRN LASASADNTVILWDMSLGKI ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALYDCKSPDES RWWRFSGQIERVT WHIFSPC FLASTDGGFVYNLDARSDKF TLNAHNDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HISRDMKMGVLFCSSCCPDLI YAFGGQKEGLRV WDISTVSS NEAFGRERLVLGSARNSSIS FGSRSSDTPMES			1				VYGSNDQDPYVTLKDTEQYER
SAYPLSVEWLNFDPSPDDSTY YIA VGNMTPVIEV WDLDIVD EPVFTLGSKLSKKKKKKKK SAEGHTDAVLDLSWNKLIRN LASASADNTVILWDMSLGKF ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALYDCRSPDES RMWRFSQQIERVTWNHFSPC FLASTDDGFVYNLDARSDKP TLNAHNDEISGLDLSSQLKGC YTASADKYVKIWDILGDRPS HISRDMKMGVLYCESSCCPDLE YAFGGQKEGLRVWDISTVSS NEAFGRERILVLGSARNSSIS FGSRSSDTPMES			1				EDFLIKPSDNLIVCGRAEQDQC
YIAVGNMTPVIEVWDLDIVD EPVFTLGSKLSKKKKKKGKK SAEGHTDAVLDLSWKLIRK LASASADNTVILWDMSIGKE ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALVTCRSPDES RMWRFSGQIERVTWHHFSPC FLASTDDGFVYNLDARSDRF TLNAFNDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HISRDMKMGVLFCSSCCPDLE YAFGGQKEGLRVWDISTVSS NEAFGRREILVLGSARNSSIS FGSRSSDTPMES			ı				NLEVHVYNQEEDSFYVHHDILL
EPVFTLGSKLSKKKKKKGKK SAEGHTDA VLDLSWNKLIRN LASASADNTVILWDMSLGKF ASLA VHTDKVQTLQFHPFEA LISGSYDKSVALYDCKSPDES RMWRFSGQJERVTWNHFSPC FLASTDDGFVYNLDARSDKP TLNAHNDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HISRDMKMGVLFCSSCCPDLF YAFGGQKEGLRV WDISTVSS NEAFGRERLVLGSARNSSIS FGSRSSDTPMES			ı			}	SAYPLSVEWLNFDPSPDDSTGN
SAEGHTDA VLDLS WNKLIRN LASASADNTVILWDNSLGKF ASLA VHTDKVQTLOFHPFEA LISGS YDKS VALYDCRS PDES RMWRFSG QIERVTWNHFSVC FLASTDDGFVYNLDAR SDLFP TLNAHNDEISGLDLSSQIKGC VTASADK YVK IWDILGDRPS HISRDMKMGVLFCSSCCPDLF YAFGG QKEGLRV WDISTVSS NEAFGRREILV LGS ARNSSIS FGSRSSDTPMES		ļ	i				YIAVGNMTPVIEVWDLDIVDSL
LASASADNTVILWDMSI,GKF ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALYDCRSPDES RMWRFSGQIERVT WHIFSPE FLASTDDGFVYNLDARSDKF TLNAINDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HSRDMKMGVLFCSSCCPDLF YAFGGQKEGLRV WDISTVSS NEAFGRREILVLGSARNSSIS FGSRSSDTPMES		l	l				<b>EPVFTLGSKLSKKKKKKKGKKSS</b>
ASLAVHTDKVQTLQFHPFEA LISGSYDKSVALVDCRSPDES RMWRFSQGJERVTWNHFSGF FLASTDDGFVYNLDARSDKF TLNAHNDEISCLDLSSQIKGC VTASADKYVKIVDILGDRPS HSRDMKMGVLFCSSCCPDLF YAFGGQKEGLRVWDISTVSS NEAFGREELLJGSARNSSIS FGSRSSDTPMES			l				SAEGHTDAVLDLSWNKLIRNV
LISGSYDKSVALYDCRSPDES RMWRFSQQIERVTWNHFSVC FLASTDDGFVYNLDARSDKF FLASTDDGFVYNLDARSDKF TLNAHNDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HISRDMKMGVLFCSSCCPDLF YAFGGQKEGLRVWDISTVSS NEAFGRREILVLGSARNSSIS FGSRSSDTPMES		1	l				LASASADNTVILWDMSLGKPA
RMWRFSGQIERVT WHIFSPC FLASTDDGFVYNLDARSDKP TLNAHNDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HISRDMKMGVIFCSSCCPDLF YAFGGQKEGLRV WDISTVSS NEAFGRERLVLGSARNSSIS FGSRSSDTPMES			ı				ASLAVHTDKVQTLQFHPFEAQT
FLASTDDGFVYNLDARSDKP TLNAHNDEISGLDLSSQIKGG VTASADKYVKIVDILGDRES HSRDMKMGVLFCSSCCPDLF YAFGGQKEGLRVWDISTVSS NEAFGRREBLVLGSARNSSIS FGSRSSDTPMES			ı				LISGSYDKSVALYDCRSPDESH
TLNAHNDEISGLDLSSQIKGC VTASADKYVKIWDILGDRPS HISRDMKMGVIFCSSCCPDLE YAFGGQKEGLRVWDISTVSS NEAFGRREILVLGSARNSSIS FGSRSSDTPMES			l		ŀ		RMWRFSGQIERVTWNHFSPCH
VTASADKYVKIWDILGDRPS HSRDMKMGVLFCSSCCPDLF YAFGGQKEGLRVWDISTVSS NEAFGRREELVLGSARNSSIS FGSRSSDTPMES		1					FLASTDDGFVYNLDARSDKPIF
HSRDMKMGVLFCSSCCPDLF YAFGGQKEGLRVWDISTVSS NEAFGRREALL/GSARNSSIS FGSRSSDTPMES			1				TLNAHNDEISGLDLSSQIKGCL
YAFGGQKEGLRV WDISTVSS NEAFGRERLVLGSARNSSIS FGSRSSDTPMES							VTASADKYVKIWDILGDRPSLV
YAFGGQKEGLRV WDISTVSS NEAFGRERLVLGSARNSSIS FGSRSSDTPMES	1		1			l	HSRDMKMGVLFCSSCCPDLPFI
NEAFGRERLVLGSARNSSIS FGSRSSDTPMES							YAFGGQKEGLRVWDISTVSSV
					1		NEAFGRRERLVLGSARNSSISGP
6671 37030 A 6721 1 540		1			1		FGSRSSDTPMES
10071   37037   A   0721   1   1347	6671	37039	Α	6721	1	549	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	uf peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6672	37040	A	6722	1	1318	AKOOLNLRTHMADENKNEYA
0072	3.0.0	ľ.	0.22	ľ	1.5.10	AQLQNFNGEQHKHFYVVIPQIY
						KOLOEMDERRTIKLSECYRGFA
	l					DSERKVIPIISKCLEGMILAAKS
	i	l				VDERRDSOMVVDSFKSGFEPPG
						DFPFEDYSQHIYRTISDGTISAS
	į.					KOESGKMDAKTTVGKAKGKL
	1					WLFGKKPKPQSPPLTPTSLFTSS
	l	ı				TPNGSOFLTFSIEPVHYCMNEIK
						TGKPRIPSFRSLKRGWSVKMG/
		1				AALEDFSHLPPEORRKKLOORI
	1	1				DELNRELQKESDQKDALNKMK DVYEKNPOMGDPGSLOPKLAE
		1				
						TMNNIDRLRMEIHKNEAWLSE VEGKTGGRGDRRHSSDINHLVT
	i					QGRESPEGSYTDDANQEVRGPP
		1				QQHGHHNEFDDEFEDDDPLPAI
						GHCKAIYPFDGHNEGTLAMKE
						GEVLYIIEEDKGDGWTRARRQ
6672	27041	١.	6723	1	741	NGEEGYVPTSYIDVTLEKNSKG
6673 6674	37041	A	6724	1	1063	MPFYISDLSICGDRILRALCPOD
00/4	37042	^	0724	1	1003	LPTYSLHSRGKMRASCSRKFLD
		l				NNSSRLVSCNMGALISIWGTTT
						PPLHATILDSQPTVHPPLAKDCL
						PCGLOASASDLRARALORLCO
	I					QLPWVGSQPHTRSPSPQRGGKT
						GLFAGLASSVSMRPASPPSPAA
	l					
	l					DSCSACRFFARRPPLRVTWVKP
						SSALALCVSISDSIPGNLKALPA
						ETRAQLHHAEASLSQPPLQLRP
	i					FPKTSQAGDLQDLGPYVCVRK
		l				AVGKGDKQIRAVVKEHSVRSQ
						ERIWHYPGITTANMPGHLGQNT
		l				ESGRDKLPMFGVWFPGCRFWG
l						LWVWRLP*LKLAAPCRPSRSLR
	L	<u> </u>				SSPISRRASTTRCLTVSGCPAAP
6675	37043	Α	6725	25	573	
6676	37044	A	6726	1	483	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
l	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6677	37045	IA	6727	1	996	MVGKAKWKPIELPLLRKIVNO
1	15.015	1.	0,2,	ľ		KOYHIPGGVAKISATIKDLKDV
		1		1		GVVIPTTSPFNSPIWPVQKTDGS
		1		1	i	WRKW\LS*QGQQFT/FTVLPHG
l		1				YINSLALCHNLIRRDLDHFSLPO
						DITLVHYIDDIVLTGSSEOEVAN
						TLDLLTSLDWALVETECLTMG
	1	1				HQVTMQPELTIMNWALSDPSN
				1		YKVGCAQQHSIIKWKWYIRDQ
1		1				ARAGTTCKWTAAALQPLSRTS
		1				LKDSGERKSSQWAELRAVHLI
						MHFAWKEKWPDVQLYTDSWA
					1	VANGSAGWSGTWKNHDWKIA
						TTVIAQWAHEQSSHGSRNGGY
				1		TWAQQHGLPLTKADVATATDE
		_				CPICQQQRPTLSP
6678	37046	Α	6728	2	1380	CLAGLFGFWSPCIPHLGVLLQSI
				1	l '	YLVTQKAA/SSEWGPEQEKALQ
				1		EVQAAVQAALILEPYDPAGPVV
						LEVSLADRDAVWSLWQAPIGE
						SQQRPLGFWSKALPSSA/DHKA
		1				CHAQQHSIIKWKWYIHDRARA
						GPEGTNSSARYAATM*KW\TAS
						ALQPLSRKSLKDSSEGKSSQWA
					ŀ	ELRAVHLAVHVAWKEKWPDV
					1	RLDTDSWAVANGLARWSGTW
						KEHDRKIGDKEVWGRGTRIELS
					ŀ	EWSKTVTIFVSH/VLLPRLPSIRG
						LTECLIHQHGIPHSIASDQGTHF
		1				TAKELQQWAHAHGIHWSYHVP
						HHPG\WGKVLQKAVYALNQRP
						IYEWKEESCLHTGVADALRGN
		1				WAEGHREHKALWLGLWSTWS
						QHPLRSLKTTRHHPGLGVLSED
					l	ICEAGGATEELSRASGFATGYG
					ŀ	KRKEDTKKHKQHSVSDIIEQQH
						SLGLTEKTVKGTPTQGISMRPG
		_				LYHKATEFQE
6679	37047	A	6729	1	2229	and opening work of the
6680	37048	A	6730	1	789	RDLQPFTSVTVHCRKGNDQTF
		ı				GGPLDAGSELTLIPGDPKHHCG
		1	l			PPVKVGAYGGQVINGVLA\HPL
						IWLVQKTDGS/WRMTVDYCKL
		1	l			NQVVIPIAAAVSDVVSLLEQINT
l		1	l	I		SPGTWYAAIDLANAFFSIPVHK
		1				AQQKQFAFSWQGQQYTFTVLP
		1	1	l		QWYINSPALCHNLIRRDLDCFS
1		1	l	I		LPLDITLVHYIDDIMLIGSSEQE
		1	l			VANTLDLFVRHLRARGWEINPT
		1	l			KIQGPSTSVKFLGFQWCGACQA
l				L		IPSKMRDKLLHLVPPTTKKEAQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6681	37049	А	6731	1	553	MTVDYCKLNQVVIPIAAAVSD VVSLLEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKOPAFSWQQ QVTFTVLPQWYINSPALCHNL IRRDLDCFSLPLDITU-HYIDDI HLIGPRQLLACYWALVETEHL TISHQVTMRPELPIMNWVLFDP SSHKVGCAQQHSIIKWKWYVH DWARAGPEGT
6682	37050	Α	6732	3	266	
6683	37051	Α	6733	3	582	
6684	37052	Α	6734	3	403	
6685	37053	Α	6735	1	2712	
6686	37054	A	6736	875	1506	LISIYLYTQKAA/SSEWGFEQEK ALQEVQAA/VQALLIEPYDPA GPVVLEVSLADRDAVWSLWQ APIGESQQRPLGFWSKALPSSA/ DHKACHAQOHSIIKWKWYHID RABAGPEGTNSSARYAATM*K WTASALQPLSRKSLKDSSEGK KWTBYSLADRLAYHLAYHVAWKE KWPDVRLDTDSWAVIANGLAR WSGTWKEHDRKIGDKEVWGR GTRI
6687	37055	A	6737		633	MTVDYRKFRQVVTPMAA/AVP DAVSLLEGINTFPGTWYAAIDL ANAFSIPVHEAHQKQFAFLPQ GVITLVHYIDDILLIGSSEGEV NTLDILLIHKRSKEAEHTAASRIR VSCLPEQKSHEQITLPWQVPSS GDIKEYFPNAFVLLTTASLQQQ DNTSQLQLTWKAPEDIKMSKT DADADEEIEALRG
6688	37056	A	6738	2		DLWPFTRYTLHRGKRNDQTTG GLLDTGSELMIPEDTKHHCOP PWK-VEA YGGQVINGVILAQIQLT VGPVGSGTHPVVIYPVPECIIGI GILSSWQNPHIGSLTSRKTDGS WRMTYHYHKLNQMYTPIAAAI PDVVSLLEGVVNTSPGSWYAL LANAFFIPVHKAHQKQFAFSW QGQQYTFTVLPQWYINSPALCH NLIRRDLDCFSLPLDITLVHYID DIMLIGSSEQEVANTLDLFVRH LERAGWEINFYKIQGFSISWKFL GFQWCGACQAIPSKMRDKLH LVPPTTKKEAQCLQLLACY/W ALVETEHLTISHQVTMRFELPI MNWVLFDFSSHKVGCAQQHSII KWKWYYHDWARAGFEGTI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	ļ.			sequence		
6689	37057	IA	6739	1	2058	
6690	37058	A	6740	2	1173	WEVROYTFTVVPQGHINSLVLO
				1		HDVVRRDLGHFFLPQDITLVHY
						IDDIMLIGSTPPITKKKAQHLVG
		1		ŀ	1	LFGFWROLVPHLGVLLWPIYO
		1				VTQQAASFEWGPEKEKALQQV
		1				OAAVOAALPLGPYDPADPMVL
	1	1				EVSVADRDAVWSLWODPIGES
		1				OWRSLGFWSKALPSSADNYSPI
		1				EROLLACYWVLVETERL\OWV
	1					TPAEEDFNNQVDRMTHSVDTT
						QPLSPATHVITQWAHEQSGHG
		1				GRDGGYTRVQQHGLPLTKADL
		1				ATAGKVFOKAV*ALN*HSIYGT
		1				LSLIARIHRSRNOGVEVEVAPLT
		1			ł	ISPSDPPAKFLLPVPPTLRSAGLE
		1				FLVPEEGMLPSGDTTVPLNWKL
		1			ł	RLPPGHFGLLFPLHQQANKGVT
		1				VLVGVTDLDYODEISLLPHNG
6691	37059	A	6741	823	2487	KELKLWKNRHKLLSYPTVGAA
007.	3,037	ľ.		023	1.07	VTOLONLTAMGVIGSHGARGO
		1			ŀ	VVALNROROGDLOPFTRVTVH
		ł				WGKG/NMOIFGGLLDTGSELTL
		1				IPGDPKHHCGPPVKVGAFGG\Q
		1				VINGALARVQLIVGPVGPWAHI
		1	İ			VVISPVPECIIDIDILSSWONPHIS
		1				SLTGRVRAIMVGKAKWKSLEL
		1		1	i .	PLPRKIVNQKQYHIPGGIVEISA
		1		1		TIKDLKDAGEVIPIPTTFPLNSPI
		ļ				WPVRKTDGCWRMTVDYCELN
		1				QVVTPTAATVPDVVSLLEQINT
		1				SPGTWYADIDLANAVFSIPVHK
		1			1	AHQKQFAFSWQGQQYTFTVLP
		1				OEYINSLGLCHNLIORDLDHFSL
1		i			1	LQDITLVHYIEDIMLIGSTEQEIA
1						NTLDLLFMAKEVWOWAHAHG
						IHWSYHVSHHPEAAGLIEWWK
						GLLKLQLQCQLGDNTLEGWGK
l						VLQKTVYALNQHPIYGTVSPIA
						RIHRSRNKGVEVAPFTITPSDPL
		1			i	POFLLPVPATLCSAGLEVLAPE
l		1	1		1	GGTLPPGDRTTIPLNWKLRLPP
		1				EDFGLLPSLSOOAKKGVTVLAG
		1				VIHPDYQDEISLLLHNGCKEDL
6692	37060	A	6742	3	350	TALL DI QUEISCECHINGCKEDE
6693	37060	A	6743	1	3339	
6694	37062	A	6744	1	2271	
0094	1002	_^_	10/44	<u> </u>	2211	<u> </u>

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codnn for last amino acid	*=Stnp codon, /=possible nuclentide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6695	37063	A	6745	3	1377	AHLAADDFCTK*GWVSG\LPOG
						LDKLTLPGANLEMOPENLKED
	1	1				LVYLKKNHEELSMAIKRNESM
	i	1				AKGLQRALLQQQPEDDSKCFP
						RPODLIRLYDIILOLTLEDREGK
		1				GLSFSFACVDKDVSVKMDTVP
		1				GVNLSCILNEMRDQDKKLVEK
		1				SCKDAQGWFFSLKALLEGSLVE
						TEVCYRTQLAQLOGLIRSMEQQ
		1				LCELCCDAEHODHEHOVLLDV
	1	1				KTOLEGEIATYSRLLEVEDAQL
		1		•		ATQYSLSLASQPTREDLEKAIL
1		1				KFIWNONRAQIAKTILSKKSKA
		1				RGIMLPSFKIYYKTTVTKTAWC
		1				WYKNRHIDOWNRIENPEIRPHT
	ŀ					YNHVIFDKPDKRKOWGKDSLF
						NKWCWENWLAICSKLTLDPFL
						NPYTKVNSRWIKDLNLQPKTIK
	1	l				ILKENLGNAIQDTGKGKDFMTK
	i .	ı				MPKAIATKAKIDKWDLIKLKSF
						CTALRNYQQSKPTTYRMGENF
6696	37064	Α	6746	1	882	ornela i i dona i i i i ande i i
6697	37065	A	6747	13	1402	STGSTHACDLLFSPSPVCLPPAA
						ATMTTSIR\QFTSSS\SIKGSSGL
						GGG\SSRTSCRLSGGLG\AGSCR
1	ŀ					LGSAGGLGSTLGG\SSYSSCYSF
		ĺ				GSGGGYGSSFGGVDGLLA\GGE
						KA\TMONL\ND\RLGSYLDKVPC
		1				PWKEANTELEVKI\RDLVTRGR
l	l					APGPARDYSQYYRTIEELQNKI
	l .					LTATVDNANILLQIDNARLAAD
	į.	l				DFRTKFETEQALRLSVEADING
		[				LRRVLDELTLARADLEMQIENL
		l				KEELAYLKKNHEEEMNALRGO
						VGGEINVEMDAAPGVDLSRILN
	1	1			1	EMRDQYEKMAEKNRKDAEDW
		1				FFSKTEELNREVATNSELVOSG
		1		i		KSEISELRRTMQALEIELQSQLS
		1		l		MKASLEGNLAETENRYCVQLS
		l				QIQGLIGSVEEQLAQLRCEMEQ
		l				QNQEYKILLDVKTRLEQEIATY
1		1		1		RRLLEGEDAHLTOYKKEPVTTR
		l	l	l	1	OVRTIVEEVODGKVISSREOVH
6698	37066	A	6748	2	452	FLLPSSFSCTHSLLSPTITIVPGP
1000	1 7000	l^	1 . 40	Ī~		DFNLASHIIPDTTPDPHDCISMIH
	1		İ		1	LTFTPFPHISFFPVPHPDHA*FID
		ŀ	l			GSSTRPNRHTPAKAGYAIAQAT
	1		l	i		IPPLRTSHFLSIVEIYPQGNNFSV
			l	1		FHVLFYYSSGIIQAPSLPYTLRR
				1		DRRPGTSRA
6699	37067	A	6749	1	1791	DIRTUISRA
0099	19/00/	JA.	0749	L'	1791	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6700	37068	A	6750	1	219	
6701	37069	A	6751	2	528	TLTVESKSIKAYKLSLOFPHFTC
					1	PKTGHALOVSSGFVESPTVTIVP
						GLDINLASHTIPDNTPEPHDCIS
						LIHLTFTPFPHVSFFPVPHPDHT
						WFIDGSSTRPNCHSPAKTGYAI
						VSSTLIIDATALPPSTTSQQAELI
i						ALTRALTLAKGLPINIHTDSKY
-						AFHILHHHAVI*AER
6702	37070	В	6752	1	1744	
6703	37071	Α	6753	1	1376	MCKRMPGLQASQTVCPFYDKN
				i		YLDLKRKGTEIKRRERLKCGTK
				l		IERRKRLRDSERLEKRIKRGCLP
		1			1	DLKLSTEIQINRLRGLYTLLRKE
		1		l		RRFGLQETINYAEVTGIYVKELI EDREHLNSGKYIFNIFDIKVPRV
		1				VFGIIDPYMLWEKKEGTKEGIK
		1				EGMKRESOKRIKWERSFITFIAL
		1				NTADRTLMSSAGCYRKQVKIHI
	1	1				DALPPPNSQTLKKRGGASLIISF
		1				RRQSGPSAAGLWEFARGPFQTL
		1		-		FAWLSPAEAAEQQRLLPASSAE
						SFIAEGDPPDAGQSSPPSSLHAA
		1				AATALMLLEALKITNYAQLTLY
						SSPNFQNLFSSSHLTHILSADWL
İ	1					LOLYSLEVESPTITIVPGPDFNPA
						FHFIPDTTPDPHDCISLIHLTFTP
					1	FPHISFFPVPHPDHTWFIDGSST
	1	1				RPNRHTPAKAGYA/DGRNTSYC
	1	-				VLSPVGNSPLVPNPGSARCTEG
						GLLYARA
6704	37072	В	6754	400	820	
6705	37073	В	6755	1	1190	
6706	37074	A	6756	1	1002 3216	
6707 6708	37075 37076	B	6757 6758	1	4020	
6709	37077	A	6759	1	1155	
6710	37078	A	6760	2	346	SSYLMHILSAPNLLOLYSLEVES
0,10	10.00	1		1		PTITIVPGPDFNLASHIILDTTPD
l		1				PHDYLSDPPDIHS/TFP/DISFFPV
	1	1				PHPGHTWFNDGSSTRPNRHSPA
		1				KAGHAIVFSTSIIEATALPPSTT
6711	37079	A	6761	189	1201	
6712	37080	Α	6762	1	231	
6713	37081	A	6763	1	834	
6714	37082	Α	6764	470	479	PRNPSSFLQVQVQHRFLQLFVP
1	İ	1				FHFVFFLASLYVMVTLTTWFR*
1			l			DPCVSGMALNCSFLKIASSSGE
6715	37083	A	6765	21	706	YLRPTPSYLNQVVRVTMT
6716	37083	A	6766	1	158	
0710	27004	I'A	0700	1'	1120	L

SEQ ID	Tero In No.	INC.	SEQ ID NO:	Municatida	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		Ļ				
6717	37085	С	6767	78	401	
6718	37086	Α	6768	536	694	
6719	37087	Ċ	6769	1	1410	
6720	37088	В	6770	1	1836	
672I	37089	Α	6771	306	487	VGFLGILF/CFEAIVNVSSLMIW
	i	1			l	LSVCLLSVYKNACDFCTLILYP
6722	37090	A	6772	714	1096	ETLLKLLISSSSLYLW FFLPMSMECSSICLYPL/CISLRS
6/22	37090	A	6/12	/14	1096	GL*FSLKRSFTSLVSWIPRYFILC
		į.				KSQGMRWLGLGSEA*YSCLLIL
					l	IRKITONSVEVLGRRKFLGGGM
						EREWVMFLRAASSGIRGSVGT
l						NFKSESRHOISCASV
6723	37091	c	6773	I	2796	NI KSESKI QISCAS V
6724	37091	A	6774	126	490	FFLPMSMECSSICLYPLLFPGAV
0724	37092	<b> ^</b>	0774	120	490	VCSSP*RGPSHPL*VGFLGILF/C
1		ı				FEAIGNGSSLMIWLSVCLLLVY
1		1				KNACDFCTLILYPETLLKLLISL
i		1			2.	RRFWAETMGFSRYIIMSSANRD
1		1				NLTSSFPN
6725	37093	A	6775	1	550	NETSSI III
6726	37094	A	6776	578	865	MCPRDYGMLCLCSH\CFKEHLY
0720	3,004	l^	0770	570	505	FCLHFVMYPVVIOEQVVOFPCS
	İ	1				*AVLSEFLNPEF*FDCTVV*ETV
ļ		1			!	CYNF*SFTFAEKSFTSNSVVNFG
ŀ		1				IGVVWC
6727	37095	Α	6777	I	2091	
6728	37096	C	6778	I	1458	
6729	37097	В	6779	1	504	
6730	37098	Α	6780	70	511	NHASPGIRNLFLHPRGLRAITIA
		1				VFCKQNTYIRLEPFKINVLEQIT
		1				KHIEKLQCGGVVKQLSRRGNN
1		1				QHISSTYDINRADTQVRRAVNN
İ		1				YDII\A*ATVSMASRSIRCGSVGS
		1				LPSSNLPINSVSIRCRARQEGIM
						SSPGQQVGFIA
6731	37099	A	678 I	3	306	
6732	37100	Α	6782	1	3567	MHIVVETALSASWQNKAKPPA
		1				RVLLQVVPNVWFLVAVVWEL
		1				YPSLDLMDRSIECSSSPATEQS
		1				WTENDYDKLREEGFRRSNYSE
		1				LQEDIQTKGKDVENFEKNLEEC
		1			l	ITRITNTQKCLKELMELKTKAR
		1				ELREECRSLRSRCDQLEERVSV
		1				MEDEMNEMKQEGKFREKRIKR
1						NEQSLQEIWDYVKRPNLRLIGV
						PESDGENGTKLKNTLQDIIQENF
		1				PNLARQAKVQIQEIQRMPQRYS
		<u> </u>				LTRATPRHIIVRFTKVE
6733	37101	Α	6783	386	550	
6734	37102	Α	6784	1	594	

Amino acid sequence (X=Unknown, *-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) MGKKQSRKTGNSKRQSASPPP
MGKKQSRKTGNSKRQSASPPP
KERSSSPAMEQSWMENDFDEL
REEGFRRTNYSELQEGIQTKGK
EVKNFEKNLDECITRITNTEKCI
KELMELKAKARELREECRSLRS
RCDOLEERHHTTPIPKLTTYLE
VKLSPANVKEQVITNCLSDHSA
IKLELRIKKPTQNPSTTWKLNN
LLLNDYWVNKEMKSEIKMFFE
TNENKNTTYONLWDAFKAVCH
GKFIALNAHKGKQERSKIDTLT
SOLRELEKOEOTHSKVSRROEI
TKIRAEPKEIETQKTLQKINESR
SWFFERINKIDRRLARLIKKKRF
KNORDAIKNDEGDITTDPTEIQT
TIREYYKHLYANKLENLKEMD
KFLNTYTLPRLNQEEAESLNRP
AGSEIVAIINSLPTKKSPGPDGFT
AEFYQRYKEKLVFGAGYFGM
WALAALPSNLLKLSQLCQEAA
EVNVLVQFVCIC*SCLNSVRRQ
CD CLONAL NAVIONAL ALL COLUMN
CRCLQMAM*WS*AIALSMKIS MSPRKPEV*IKVLAGLCCL
MSFRRFEV IRVLAGLECEL
KLLODLPFSINSSAVEKISMSTT
GOVIRCKAAILWKPGAPFSIEEV
<b>EVAPPKAKEVRIKVVATGLCGT</b>
EMKVLGSKHLDLLYPTILGHEG
AGIVESIGEGVSTVKPGDKVITL
FLPQCGECTSCLNSEGNFCIQFK
QSKTQLMSDGTSRFTCKGKSIY
HFGNTSTFCEYTVIKEISVAKID
AVAPLEKVCLISCGFSTGFGAAI
NTAKVTPGSTCAVFGLG\GVGL
SVVMGCKAAGAARD/IIGVDVQ
QGRKF*GRAQELGATEC\LNP\Q
ALKKPHFKEVLFDMTDAGIDFC
FEAIGNLDVLAAALASCNESYG
VCVVVGVLPASVQLKISGQLFF
SGRSLKGSVFGGWKSRQHIPKL
VADYMAEKLNLDPLITHTLNL
DKINEAVELMKTGKW
LVYLKVMGRMEPSWKTLCRIL
SRRTSANLSKAGQCSDSGNTEN
TTKILLKKSNSKTHNCOIHOS*N
EGKNVKGSQRERSGYPQRGRPS

SEQ ID	ISEO ID NO.	Mer	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6745	37113	A	6795	3	640	<del></del>
6746	37114	Α	6796	1	996	
6747	37115	Α	6797	I	933	
6748	37116	Α	6798	74	1128	LLLDL*VD*SPSRPLEMRFRV*P
					I	MKRCTILKKNYLSFLVYISRNL
						*NRVKAIM/VGKAEWKTIELPL
						PRKTVNQKQYRIPGGIAEISTTI
		1				KELNNAGMVIPTTSPFNSPIWP
			l		ŀ	VQKIDGSWRMTVDYCKLNQV
		1				VTPIAATVPYVVSSLEQIN/TSPC
					ľ	T/WNRKRFCNRSRLLHKLLCHL
		1				GHMTQQI*CFLRCQWHIGMLF
		l				GPEICGCTSLSGQKL/WKIFVSH
			ĺ		1	AASFEWSPEQEKALQQVQAVV
		l				QAALPLGPYDPADPVLLEMSV
		l				ADRDAVWILWQAPISESQWRPI
		l	ŀ			GFWSKALPSSADNYSPFERQLL
		l			1	ACYWTLVETERLTMGHQVTIP
		1				ELPIMNWVFSDLSSPKMCHPQQ
6749	37117	Α	6799	I	229	
6750	37118	Α	6800	1	1011	MVSTPATLPSLPKPALMASWG
						VPYDQLTKEEKTRVWFTDGSA
		1				RYAGTTQKWTAVALQPLSRTS
						LKDSSEGKSSQWAELQAVYLV
						VHFAWKEKWPDVGLYTDSWA
						VANGLAGWSETWEKQDWKIG
		1				DKEIWGRGMWMDLSEWSKAV
						KIFVSHVSÅHQRVTSAEEEFNN
						QVDRPL/PVFTQWAHEQSGHSG
				l		RDGGYSWAQQT\GLPFTKADL
		l				AMATAECPICQQQRPTLSPLYS
		1			ì	TIPQGDQPATWWQIDYIGPLPS
						WKGQKFVLTVIDTYSRYRFAY
		l				PAHNASAKTTIHGLIECLIHCYG
		1				IPHSIASDQSIHF/TTKEVQ*WAH
						AHGIHWSYHVSHHPEAAGL
6751	37119	Α	6801	2	739	HKMGHAQQHSIIKWK*YICDW
ł		1				ARAGPKGTT\APMASWGVLYD
		l			İ	QLTEEEKTRAWFTDGSARYAG
		l				TTQKWTAAALQPLSRTSLKGS
		l				GEGKSSQWAELQAVHLVVHFS
		l		l		WKDKWPDVRLYIDSWAVANG
1		l	l			LAGWSGTWKKHDWKIGDKEI
1		1	l	l		WGRGMWMDLSEWPKPVKIFG
1		1	l	l		SHVSAHQWVISAEEDFNNQVD
		1	l	l		KMTCSVDITQPLSPATPVITQW
1			l	I		AHKQSGHGGRDGGYTWAQQH
		L	L			GLPLTKTGLAMATAECPI
6752	37120	Α	6802	1	354	
6753	3712I	Α	6803	3	592	

	SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
1	NO:						
EQKKALQ*VQAAVQAALPL YDPADPMVLVVSVAKDVAVQAALPL YDPADPMVLVVSVAKDVADALPL YDPADPMVLVVSVAKDVADALPL YDPADPMVLVVSVAKDVADALPL YDPADPMVLVVSVAKDVADALPL HLSGSDRWRRTYRCL BGFWLSSLDKAMKENDE DSNSQIQKQILSLQSSKIILAL GTVVTQLQNLNSVGIIGSQG GQVAALSLQRQGASFEWSPI EKALQQVQTAVQAALPLCPP PSDPMVFEVSVADGAVWS QAPIGELQWR ILEFWSKALP ADNYSPFGRQLLACYWALV EHLTVDHQVTM*PELPIM    37125				09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
EQKKALQ*VQAAVQAALPL YDPADPMVLVVSVAKDVAVQAALPL YDPADPMVLVVSVAKDVADALPL YDPADPMVLVVSVAKDVADALPL YDPADPMVLVVSVAKDVADALPL YDPADPMVLVVSVAKDVADALPL HLSGSDRWRRTYRCL BGFWLSSLDKAMKENDE DSNSQIQKQILSLQSSKIILAL GTVVTQLQNLNSVGIIGSQG GQVAALSLQRQGASFEWSPI EKALQQVQTAVQAALPLCPP PSDPMVFEVSVADGAVWS QAPIGELQWR ILEFWSKALP ADNYSPFGRQLLACYWALV EHLTVDHQVTM*PELPIM    37125	6754	127122	L_	6804	1126	1365	OLAEDDHWI PD*KGAGEEWGD
YOPADPMYLVSYADKDAY	0754	37122	^	0804	120	303	
FHLSGSDRWRTYRCL			İ				
37123			į .				
EAGWLLLSJDKAMKENDE		07122	١	5005		626	
DSNSQIQKQILSLQSSKIILLN    GTVVTQLQNLNSVGIIGSQG    GQVAALSLQRQGASFEWSP    EKALQQVQTAVQAALPLOP    PSDPMPFESVALQRAVALPLOP    PSDPMPFESVALQRAV TLEFWSKALP    ADNYSPFGRQLLACYWALV     EHLTVDHQVTM*PELPIM     37125	6755	3/123	IA.	6805	Į į	636	
GTVVTQLQNLNSVGIIGSQG   GQVAALSLQRQGASFWSPI   EKALQQVQTAVQAALPLGP    PSDPMVFEVSVADGRAVWS    QAPIGEQWR LLFEWSKALP    ADNYSPFGRQLACYWALV     EHLTVDHQVT7M*PELPIM     37125			1				
GQVAALSLQRQGASFEWSPE			1				
			1				
PSDPMVFEVSVADGANAWS   QAPIGELQWR FLEFWSKALP   ADNYSPFGRQLLACYWALV    ST125			1				
OAPIGELQWR LLEFWSKALP	l		1				
ADNYSPEGROLLACYWALV EHLTVDHQVT/M*PELPIM  37125 A 6806 1 672  37125 A 6807 308 470  37127 A 6809 I 1908  37127 A 6809 I 1218 MGIIGSRGGRQVAALKRQ VTKKAASFEWGPEEKALQ QAAVQALPLGPYDPADPIV VSVADRGAVWSLWQVPIGE QRPLGFWSKALPSSADNDSP RQLLACYCALVETERLDMG VTMRPEVLIINCVLSDPSSH/K WRLCMDSATWTSTYQ/A*PC GHC*VPNLPAAETNTDPSIW SYG*GLASYLOG*LASYLOG*LASYLOG*LASYLOG*LASYLOG*LASYLOG*LASYLOG*LASYLOG*LASYLOG*LASYLOG*LASYLOG*LASYLOG*LASYLOG*LSSSEGCVCSEASNIWYCFSR DSWYQESRGGSGGTHHHE PTSKIFASCELDIMFCW*GC *WRNAATRRINNNFI GPEDLGJEFILSFQDPLL/SHE GEFWLYPSGAA/RASSDAQS VIAVSPLRGLNSWG  37129 B 6811 I 1452  37130 A 6812 122 1838 371310 A 6812 122 1838			1				
		i .	1				
37124			1				
37125							EHLTVDHQVT/M*PELPIM
37126	6756				1		
37127   A   6809   I   1218	6757				308		
VTKKAASFEWGPEEKALO   QAAVQAALPLGPYDPADPIV   VSVADRGAVWSLWQVPIGE   QRPLGFWSKALPSSADNDSP   RQLLACYCAI.VETREILDMG   VTMRPEVLIINCVLSDPSSH/   WRLCMDSATWTSTYQ/A*PC   GHC*VFNLPAAETNTDPSIW    S/VG*LASYLVIG**LHWTSSIN   GAEVCPHWNRHLRI*VCLS   QCFCED/SHPWHIELASYLPSS    ST*HCL*SRHSPVS**RSVAVQ   SWNSLVLPCSPSS**SSWINRN   EWPFEVTITMPTR**QVSAGLA   SSEGCYCSESASNIWYCFSR   DSWYQESRGGGGGTIHHH   PTSKIFASCFLDIMFCW**GG   *WRNAATRRINNNFI    GPEDLGGLFILSFQDPLLISHF   CLEALAPPPSPVVPISSFPPH   GEPWLYPSGAA/RASSDAQS   VIAVSPLRGLNSWG   371129   B 6811   1   1452   1452   1453   1454   1	6758						
QAAVQAALPLGPYDPADPIV	6759	37127	A	6809	11	1218	
VSVADRGAVWSLWQVPIGE   QRPLGFWSKALPSSADNDSP RQLLACYCALVETERLDMG   VTMRPEVLINCVLSDPSSH/WRELACHDSATWTSTYQ/A*PC   GHC*VPNLPAAETNTDPSIW   S/Y/G*LASYLVIG*LHWTSSIN   GAEVCPHWNRHLRI*VCLS   QCFCED/SHPWHIELASYLPSS   ST*HCL*SRHSPYS*FSVAVQ   SWNSLVLPCSPSS*SSWINK   EWPFEVTITMPTR*QVSACLL   SSSEGCVCSESASNIWYCFSR   DSWYQESRGGGGGTHHHH   PTSKIFASCFLDIMFCW*GG   *WRNAATRRINNNFI   GPEDLGGLFISFQDPLL/SHP   GFWLYPSGAA/RASSDAQS   VIAVSPLRGLNSWG   37129   B   6811   1   1452   1			1		1		
ORPLGFWSKALPSSADNDSP							
RQLLACYCALVETRILDMG							
VTMRPEVLIINCVLSDPSSHK   WRLCMDSATWTSTYQA*PC    GHC*VPNLPAAETNTDPSIW    S/YG*LASYLVIG**LHWTSSIN    GAEVCPHWNRHLRI*VCLS    QCFCED/SHPWHIELASYLPSS    ST*HCL*SRHSPYS*RSVAVG    SWNSLVLPCS*RSS*SSWINKN   EWPFEVTITMPTR*QVSAGLA    SSSEGCVCSEASSNIWYCFSR   DSWVQESRGGGGGTIHHH   PTSKIFASCFLDIMFCW*FGC    *WRNAATRRINNNFI    GPEDLQGLFILSFQDPLLISH    CLEALAPPS*PVVPISSFPPH    GEFWLYPSGAA/RASSDAQS    37129   B   6811   1   1452     37130   A   6812   122   1838     371310   A   6812   122   1838     37131   A   6813   101   249   MTHVTALRTSSNLMRN*RK*					1		
WRLCMDSATWTSTYQ(A*PC		l .			1		
GHC*VPNLPAAETNTDPSIW   S7/G*LASYLVIG*LHWTSSIN   GAEVCPHWNRHLRI*VCLS   QCFCED/SHPWHELASYLVES   GAEVCPHWNRHLRI*VCLS   QCFCED/SHPWHELASYLPS   ST*HCL*SRHSPYS*FSVAVQ   SWNSLVLPCSPSS*SSWINK   EWPFEVTITMPTR*QVSAGLL   SSSEGCVGSESASNIWYCFSR   DSW*QESRGGGGGTHHHH   PTSKIFASCFLDIMFCW**GG   *WRNAATRRINNNFI   GPEDLQGLFILSFQDPLL/SHP   CLEALAPPSSPVVPISSFPPH   GEFWLYPSGAA/RASSDAQS   VIAVSPLRGLNSWG   37129   B 6811   1   1452     37130   A 6812   122   1838     371310   A 6811   1249   MTHVTALRTSSNLMRN*RKY							
S//G*LASYLVIG*LHWTSSIN GAEVCPHWNRHLLRI*VCLS   QCFCED/SHPWHIELASYLPSV ST*HCL*SRHSPYS*RSVAVG SWNSLV4PCSPSS*SSWINN EWPEVTITMPTR*QYSAGLI   SSSEGCVCSESASNIWYCFSS DSWVQESRGGSGSGTIHHH PTSKIFASCFLDIMFCWT*GC *WRNAATRRINNNFI GPED/QGLFILSFQDFLUSHF CLEALAPFPSPPVPISSFPPH GEFWLYPSGAA/RASSDAQS VIAVSPLRGLNSWG     37129							
GAEVCPHWNRHLLRI**VCLS   QCFCED/SHPWHE/ASYLPS\							
OCFCED/SHPWIHE/ASYLPS/   ST*HCL*SRHSPYS*RSVAVG   SWNSLVLPCSHSS*SSWINRM					i		
STTHCL*SRHSPYS*RSVAVG   SWNSLVLPCSPSS*SSWINKN   EWPFEVTITMFTR*QYSAGLA   SSSEGCVCSESASNIWYCFSS   DSWVQESRGGSGSGTIHHH   PTSKIFASCFLDIMFCWT*GC   *WRNAATRRINNNFI   OPEDLGGLFILSFOPLL/SHF   CLEALAPFPSPPVVPISSFPPH   GEFWLYPSGAA/RASSDAQS   VIAVSPLRGLNSWG   37129   B 6811   1   1452     37130   A 6812   122   1838     37131   A 6813   101   249   MTHVTALRTSSNLMRN*RKY			ļ.				
SWNSLVLPCSPS\$*SSWINRN							
EWPEVTIMPTR*QYSAGLA   SSSEGCVCSESASNIW;705   D   STILL   SSSEGCVCSESASNIW;705   D   STILL   SSSEGCVCSESASNIW;705   WRNAGTRHINNNFI   D   STILL   STIL			1				
SSSEGCVCSEASNIWYCFS8   DSWVQESRGGGGGTHHHH			1				
DSWYQESRGGGGGTIHHHE   PTSKIFASCFLDIMFCWT*GC	ŀ		1				
PTSKIFASCFLDIMFCWT*GC		i i	1				
\$\frac{\pmu}{\pmu} \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \			1				
37128			1				
CLEALAPEPSPVVPISSPPPH   GEFWLYPSGAA/RASSDAQS   37129			L_				
GEFWLYPSGAA/RASSDAQS   37129   B   6811   I   1452   	6760	37128	Α	6810	901	1142	
VIAVSPLRGLNSWG		i i	1				
37129 B 6811 I 1452 37130 A 6812 122 1838 37131 A 6813 101 249 MTHVTALRTSSNLMRN*RK*	ĺ		ı				GEFWLYPSGAA/RASSDAQSW
2 37130 A 6812 122 1838 37131 A 6813 101 249 MTHVTALRTSSNLMRN*RKV							VIAVSPLRGLNSWG
37131 A 6813 101 249 MTHVTALRTSSNLMRN*RKV	6761		_				
EAKSQQEH*S*QACHLKSRM	6763	37131	A	6813	101	249	MTHVTALRTSSNLMRN*RKVG
	1					1	
SRLWIN							SRLWIN
	6764				·		
	6765	37133	Α	6815	310	397	LTIWQDSNPGSCL*GCSVCAHA
		1				1	CVGGQHMVCF*PSYSLYLKSE/
/CVGGQHMVCF*PSYSLYLK			1			1	PKEGTGRNKDPDLNSQNRKGF
							LEQIHFQ
PKEGTGRNKDPDLNSQNRKO LEQIHFQ	6766	37134	Α	6816	1	583	
SRLWIN   S	6762 6763	37130 37131 37132	A	6812 6813	101	249 1074	EAKSQQEH*S*QACHLI SRLWIN LTIWQDSNPGSCL*GCS
	6766	37134	A	6816	1	583	
PKEGTGRNKDPDLNSQNRKO LEQIHFQ							

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6767	37135	A	6817	h	486	
6768	37136	A	6818	2	1001	
6769	37137	Α	6819	1	2307	
6770	37138	Α	6820	3	393	
6771	37139	Α	6821	I	1776	
6772	37140	Α	6822	1	1140	
6773	37141	Α	6823	1	558	
6774	37142	Α	6824	2	798	PRVRIFFSITWYSLRVLTEISLW
						GGLILVVIITIQYDMTRTRNKYL
						HTNSLVALANMSAQFR\SLHQY
						AA\QRIIRLFSLLSKKHNKVLEQ
						ATOSLRGSLSSNDVPLPDYAOD
						LNVIEEVIRMML\EIINSCL\TNS
						LHHNPNLGITPWLLO\RRSLWN
						NFR\THPSFQGINGKILIWVIF/LS
						/SRLOGLAGKLGAELSVERVLEI
						IKQGVR\SLPKDRLKKFPELKFK
				l		YVEEEOPEEFFIPYVWSLVYNF
						SSRPVLGIPQDIPAVSPWVSD
6775	37143	Α	6825	3	206	PSASRPA WHAPALHPSPVPARG
0775	57143	^	0023	ľ	200	WOPPTGLHPLREORGLGOHM*
						QSSGQQPQGGVGPGSHFPGAL
						WAOL
6776	37144	A	6826	200	601	EMGSCDOWORPCVPWEAVVM
10770	37144	^	0020	200	100,	PRDP/LKMALAVVWPKMKAPR
				ŀ		VTKRTP*LTSTHQLAGLTSSISE
						SLA*MRHSPGKTKMKQAARPP
	ļ					MTEITLPMSGMKS/VQQQGEQE
						PDORLOHSPPPLPPHVLLHWHP
						LVAQPQA
6777	37145	В	6827	25	1407	EVAQIQA
6778	37146	A	6828	1786	1795	HC*LNALPSGETWGOKRGLPG
0,,,0	27110			1,,,,		TQLPLPL/VPLRAPKGRSPKGSK
						GPTHHTWALSSFSLTPSQVTVG
						TEDOATSASGRPWLRIGTGPGG
				1		GRVWAGRDS\RGVPALTVLHV
				i		LSSLGRETP*RPCLRGPTAPAGP
						KRAPGKWLPWSQAPPCGCCPR
						*LSHVL*DRNRCAW*KGGGRG
				-		L/LRAPTPVPELAPHPCGPAPTL
		1	ł			SKPLSSPNMPAOGLTOE*PGSV
		1				ANLPPYGPALLCLGRREWDER
		1	l	1		
		1		1		GQVG*VPTESEME*RRTEPLKT PGDCSAAASKIPSFFSNRTPFPPL
		1				CPHKNKLKGT
(770	27147	ļ	6920		211	CPHKNKLKGI
6779	37147	A	6829 6830	1	311 402	
	37148	Α		1		
6781	37149	A	6831	1	750	
6782	37150	C	6832	130	450	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6783	37151	A	6833	ı	875	MRLLRLKLKVEQHVELYQKYS
		1		1		NNSWRYLSNRLLAPSDSPEWLS
				İ		FDVTGVVRQW/VWSRGGEIEGF
						RLSA\HCSCDSRDNTLOVDINGF
			l	l		TTGRRGDLATIHGMNRPFLLFM
		ļ	i			ATPLERAOHLOSSRHRRALDTK
				l		YCFS\STEKNCCVRQLYIDFRKD
	i		l			LGWK\WIHE\PKGYHANFCLGP
						CPYIWSLDTQYSKVLALYNQH
						NPGASAAPCCVPOALEPLPIVY
						YVGRKPKVEQLSNMIVRSCKC
			ļ			NLGPAPPRPAPAGPAPPRPAPV
						ALPMGAVFKDTRAPSPPGAPLK
	1					MERGKKKKK
6784	37152	В	6834	162	635	
6785	37153	A	6835	2	1846	
6786	37154	Α	6836	322	2104	
6787	37155	Α	6837	1	352	
6788	37156	В	6838	92	1774	
6789	37157	Α	6839	260	1016	
6790	37158	Α	6840	479	1937	DVEHVGKMRRRWRRRVVVAD
1					ł	GNVVKPMSCAGDLQ/PFTRVTV
						HWGKGNDQTFQDLLDTGSELT
				l		LIPGDPKRHCGPPVKIGAYGGQI
				l		INGVLAQVQLTVDAVGPWTHP
			ŀ			VVIFPVPECIIGIDMLSSRQNPHT
						GSLTGRVWTIMVRKAKWKPLE
						LPLPRKIVNQKQYHIPEGIVEIS
						ATIKDLKDAGVVIPTTSPFNSPI
						WPVQKTDGSWRMTVGYCKLN
						QVVTPIAAAVPDVVSLLEQINT
						PPGTWYAAIDLANDF
6791	37159	В	6841	20	26	
6792	37160	В	6842	2	207	
6793	37161	В	6843	187	405	
6794	37162	Α	6844	451	770	LFLFLLSSHPRRSSASWYRHRH
		1				PHHPSAARLPVADSASSSSSPSS
		l			1	SSPSPSSSSSSSSSPPSSSSFVYPHC
1		l				QPPAPHFPH*HSR*QGRLFHFLP
						LPQLPSSPLSPWW
6795	37163	Α	6845	1	417	
6796	37164	Α	6846	191	314	
6797	37165	Α	6847	129	212	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6798	37166	Α	6848	1	192	CALNAGL/IGENEAKKRRSKVT
		ŀ				QEADFPGSMDGASNFVRGDAI
		l				AGILIMVINIVGGLLVGVLQHG
						MSMGHAAESYALLTIGDGLVA
	l	1	l	l		QIPALVISTAAGVIVTRVSTDQD
	l			l		VGEQMVNQLFSNPSVMLLSAA
ŀ				l	ŀ	VLGLLGLVPGMPSLVFLLFTAG
		1				LLGLAWWIRGREQKAPAEPKP
		1		ł		VKMAENNTVVEATWNDVQLE
						DSLGMATGLLT*PIFRAQWTGQ
		l				VTLFAAMPSPGSSSWSLTLSAG
		_				CWSACCNMA
6799	37167	В	6849	65	1129	
6800	37168	В	6850	46	1038	
6801	37169	Α	685I	2	413	PSFQGPVSLPSITVVSIDSQASKP
		l				LKTPQLWCQLRQYSFKHSFLV
		l				VPTCPVPLLG*DTLTKLSASLTI
		l				PGLQPHLIATHLNPQVEDTSIPS
		1				LATYHAPLTISLKPNHPYPSQC
		_				QYPIPQHALKGLKPVITHLLQH
6802	37170	C	6852	35	346	
6803	37171	С	6853	239	484	
6804	37172	A	6854	1	1020	
6805	37173	A	6855	3	131 956	LA CALLED AND DECAME
6806	37174	A	6856	1	956	MAGALPPASLPPCSLISDCCASN
	l .	1		l		ERSSMGIGPSEPCAGYNLLVCR
		1				LTKKKRIRSTNKVWDYVKRPN
		1		ŀ		LRIIGVPEEEENSKSCENILGEIE
		ı				ENFPSLATDLDIQIQEAQRTPQK FITERSLPRYIVIRLSKVKTKERI
		l				LRAVROKHQIFLTORLKTNTAQ
		l				SPOKLPGPSOTLLVTLTREITIVP
		l				GLDFNPASHIIADTTPDPHDCIS
	1	l				LIHLTFIOFPHISFFPVPHPDHTW
l		l			1	FINGSSTRPNRHSPAKAGYAIVS
		l				STSIIEATTLPSSTTSQQAEFIAL
	1	1		ł		TOALILAKGLCINIYADSKY/AF
						HILHHHAVIWAERDTETG
6807	37175	A	6857	1	1269	III EIIIIIA VIWAERDIFIO
6808	37176	A	6858	1	741	
6809	37176	B	6859	411	1257	
0009	12/1//	10	0039	[711	1631	L

SEQ ID	SEQ ID NO:		SEQ ID NO:		Nucleotide location of last	
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6810	37178	A	6860	438	3997	SPLPHSTPISHPAACFKKIKACY
						HLPATAWPFKAYKLSLQFPHFT
						CPKTRQGLQHNSHKNTRALPD
						YRLRLISQTPIPSTKQQLLSFLG
						MVSKVRILTQELGPRPIAFLSKQ
	ŀ					LDLTVLTQPSCLHAAAAAALIL
		ĺ				LKALKITKYAQLTLYSSHNFQN
		l				LFSSSYLMHILSAPWLLQLYSLF
						VESPTITIVPGTDFNPASHIILDT
		1				TPDPHDCISLIHLTFTPFPRISFFP
		1			i .	VPHPNHIWFIDGSSTRPKCHSPA
	1		1		1	KAGY
6811	37179	Α	6861	245	505	
6812	37180	A	6862	346	522	PAPEFWVHG*NVSPLSL*SKEQ
i		ı				EDRGFISQGRSPDLSHGTKFHV
						RPCEETTKQALCEQH
6813	37181	Α	6863	3	879	SGDLPWEINPPSSYTLLCEKDPP
						TTSGPQTNQPKKH\LTNFKSETK
		l				ETRFIRGPTTPAPVTDWEGSLPL
		l				VFNHSRDTSLIIHPGFRGVRPRR
		l				DACLGPSPLAASPTFLGKGPAA
	ł					PRQTELGPNSSSASAPPPYNPFI
1		1				ASPPHTWSGLQFPSMTSPPPPA
		l				OOFTLKKVAGAKGIVKDLINLT
		l				FKVYNNRKKLOFLASTVROTP
						ATSPAHKNFOTPELOOPGVPPE
						PPPRGACYKFQKSGHRAKECLQ
						PRIPPKPHPICVGPHWKSDCPTH
						LAATPRAPGTLAQGSLTPSQIFL
6814	37182	Α	6864	143	331	DTSTPSLVTDHASLTISLKPNHF
						YPD*COYPIPOHALKGLKPVITC
						LLQHGLLKPINSPYPRA
6815	37183	Α	6865	1	783	
6816	37184	A	6866	32	415	WRHALKGLKPVITRLLQHGLL
l		1		1	i	RPINSPYNSPFLLVLEPDKPYRK
		l			1	RK*ISPPNRHILASVEVLKNQVN
		1		1		SHEFERSALIHTLTSGLAPCSLH
		1			1	KMCSKLPRSFLSVGSGTGKEAR
	1	l		1	I	SKILTFRTASRHLVL

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				scquence		
6817	37185	Α	6867	1	1374	MSELPFTIASKRIKYLGIQLTRD
						VKDLFKENYKPLLKEIKEDTNK
		ŀ		İ		WKNIPCSWVGRINIVKMAILPK
						VIYRFNAIPIKLPMTFFTELEKTI
						LKFIWNQKRARIAKSILSQKNK
	1					AGGITLPDFKLYYKPTETKTAW
1						YWYLNRDIDQWNRTEPSEITPH
		1				TYNYLIFDKPEKNKQWGKDSL
	1					FNKWCWENWLAICRKLKLDPF
						FTPYTKINSRWIKDLNVRPETIK
						TLEENLGITIQDIGVGKDFMSKT
		1				PKAMATKDKTGKWDLIKLKSF
1	i	l				CTAKETTIRVNRQRVAALLNSA
	1					VFONAVEVVVWPSSEVHVKFL
	1				!	FCKIISCAGQKQPIKFDGSSSLS
					İ	GVATAMMSATIAHLKRIKACY
						RSPVTAWTFKAYKLSLQFPHFT
						CPKTGQALQ*HT*KGLKPVIAH
						LLQHGLLKPINSPYNSLILPVQK
1						PDKPYRKLESFTSKAIKWHQIPS
						\PGKHLC**GS*RSPVTAWTFKA
						YKLSLQFPHFTCPKTGQALQEA
						GVIHFKGHOMASDPITOGNTYA
				1		NKVAKEAASVLTSVPHGQFFSF
						SSVTPTYFPTEIDFTYMPQVRKL
				1		KHLMV
6818	37186	Α	6868	122	281	
6819	37187	Α	6869	2	2144	
6820	37188	A	6870	224	418	LSQWRHALKGLKSVITRLL*HG
}		1	1			LLKPINSPYNSPIVPVLKPDKTY
L		_				RKVESFTAKTIKRCQIPLL
6821 6822	37189 37190	A A	6871 6872	5	289	
6823	37191	l <del>c</del>	6873	i	2082	
6824	37192	В	6874	i -	1614	
6825	37193	A	6875	i -	2067	
6826	37194	A	6876	i	1152	
6827	37195	A	6877	i	798	
6828	37196	c	6878	488	788	
6829	37197	Ā	6879	90	765	NTVFGLVVLPLELKLRIFRLLD
002)		Ι.	10075	1	1	VRSVLSLSAVCRDLFTASNDPL
		1				LWRFLYLRDFRGDFRNDIYSWT
		1	1			TKDFEYYINLVDKTEARFEKVD
		1			!	SDFESFTVGKMPSNSIACTEKSF
		1				MKGRVSQCDKKPVITRLLQHG
	1	1	1			LLKPINSPYNSPILPVLKPDKPY
1	1	1	1		l	KLVQDLHRINQIVLPIHPCGAQP
						HTLFCPQYLPPQLTIPVPDLKDA
	1	1				FFTIPLQPSSQ\PLFAFT*TDPDT
					L	ITTITEQL 33QUEFAFT TOPDI

SEQ ID	SEQ 1D NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino aeid sequence (X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6830	37198	A	6880	1824	2286	PRVLRPNSPRNISPISNRIFSD*R
						CPIASEASWTITDALG/RLLOWR
						HGLLNPINSPYNSPILPVOKPDK
ŀ						PYRLVOALLSLPOLPLFLAWTSI
l				İ		WPPTLFRITLLNPMTVSL*ST*H
						SLHFPMFPSFLFLTLITLGLLMA
						VPLGLIATHQQRRAML
6831	37199	A	6881	930	1289	LSOWTDGLLKPMNSPYNSPILP
						VLKPDKPYK\*VODLRLINOIVL
		l	l			PIHPVV\PNPYTLLSSIPPSTTHY
		1				SVLDLKLAFFTIPLHPSSOPFFAF
		i				TWTDPDTHQAQQIT*AVLPQSF
		1				SDSPHE
6832	37200	Α	6882	2	196	IHGCKFIQCKRILSNFTEVADHV
1						HDQIRL*TGIRLLTQPQPRLSCR
1						HQVAQHSVCRYLCQLPLL
6833	37201	Α	6883	2	1441	LNQEEGESLNRPITGSEIEAIINS
						LPTKKSPGPDGITAEFYQRYKE
						ELVPFLVKLFQSTEKEGILPNSF
		l				YEASIILIPKPGRDTTKKENFRPI
	l .	l				SLMNIDAKILNKILANRIQQHIK
		1				KLIHNGQHINRTNDKSHIIISIDA
		1	ł			EKTFGKIQQPFMLKTLNKLGID
1		1				GTYLKIIRAIYDKPTANIILTGQ
		1				KLEAFPMKTGTREGCPLSPLLF
ļ.		1				NIVLEVLARAIRQEKEIKGIQLG
						KEEVKLSLFADDMIVYLENPIV
		1				SAQNLLRLISTFSKVSGYKINVQ
	1					KSQAFLYTNNRQTESQILSELPF
						TIASKRIKYLGIQLTRDVKDLFK
						ENYKALLNEIKEDINKWKNIPC
						SWVGRINIVKMAILPKVIYRFN
1						AIPIKLPMTFFTELEKTTLKFIW
1	1					NQKSARIAKSILSQKNKAGGIM
						LPDFKLYYKATVTKTAWYWY
					1	QNRDIDQWNTTEPSEIMLHIYN
	1		1			Y/LIFNKPEKNKKWGKDSLFNK
						WCWENWL

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hed	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6834	37202	A	6884	69	2415	DKTSRGTIRQQRLRFTNIRCSA.
,						TAADIQANRVWRGPPANSNRP
						AA\RVLTVRRKTNKQKGHPHQ
						KPICTSPSSNTKEIQTTIREYYKI
						LYANKLENAEERDKFLNIYTLP
i						RLNQKEVESLNRPITGSEIEAIIK
	1					SLPTKKSPGPDGFTAKFYQRYK
						EELVPFLLKLFQSIEKEGILPNSF
	1					YEASIILIPKPGRDTTKKENFRPI
	1					SLMNIDARILNKILANLIQQHIK
	l					KLIHHDQVGFIPGMQGWFNICK
						SINIIQHMNRTKDKNHMIISIDA
						EKPFDKIQQPFMLKTLNKLDID
						GTYLKIVRAKYDKPTANIILNG
l						QKLEAFPLKTGTRQGCPLSPLL
						FNIVLEVLAREIRQEKEIKGIQL
	ŀ		İ			GKEEVKLSLFVDDMIIYLENPIV
	l					SAQNLLKLISNFSKVSGYKISVQ
	1		!			KSQAFLYTNNRQTESQTMSELP
						FTIASKRIKYLGIQLTRDVKDRF
						KENYKSLLSEIKEDTNKWKNIP
						CSWVGRINIVKMAILPKVIYRF
			l			NAIPIKLPMTFFTELEKTTLKFIR
	1					NQKRARIAKSILSQKNKAGGIT
						LLDFKLYYKATVTKTAWYWY
			1			QNRHVDQWNRTEPSEIMLHIY
						NYLIFEKPDINKQWGKDSLFNK
	1					WCWENWLAICRKLKLDPFLTS
	1		1			YTKINSRWIKDLNVRPKTIKTLE
	1		1		1	ENLGNTIQDIGMGKDFMSKTPK
	1					AMATKAKLDKWDLIKLKSFCT
						AKETTIRVNRQPTGWEKIFATY
6835	37203	Α	6885	1	2358	
6836	37204	В	6886	J	1443	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last endnn for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown. *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6837	37205	A	6887		2913	KMGLAREWILRFLVLILQEIRS MRQKENKDIQOLNSALHQADL IDIYRTLHRKSTEVTFFSAPHCI/ RTYSKIOHTI.GSKALLSKCKITE IITDSQTTVLSELRIKKLTQNRS ATWKLMMILMDYWVHNEMK AEIKMFFETTNENDTTYQNLW DTFKAVCRGKFIALNAHRKY ERSKIDTLMSQLKELEKQEQTH SKVSRRPIPSSEIEAIINSLPTKKS ERSKIDTLMSQLKELEKQEQTH SKVSRRPIPSSEIEAIINSLPTKKS ERSKIDTLMSQLKELEKQEQTH SKVSRRPIPSSEIEAIINSLPTKKS ERSKUSTRNFISSEIEAIINSLPTKKS HOPGOFTAEEDREPISLAMIDA KILNKILANRIQQHIKKLLHHD VGFIPGMGGWFNICKSINVIQHI MRTSDKNHTIISIDAEKAFNKIQ QLFMLKTLNKLGTTNGMYLKIU RAIPGREGOTGLEFVELSA RATYDKPTANILLKGQTKEVKLSL SNFSKVSGYKINLQKSQAFLYR NNRQTESQIMBELPFTTASKRIK YLGIQLTRDVKDLFKENYKPLL NEIKEDTNKWENIPCSWYGRIN IKKMALIPKYTYRFNAIPIKLPM
						TFFTELEKTILKFRWNQKRAHI AKTILSQKNKAGGIRLPDFKLF YKATVTKTARYWYENRDIDQ WNRTEPLEIMPHIYNHLIFDKPD KNKQWGKDSLFNKWCWENWL
6838	37206	A	6888	I	1677	AICRKLKLDPFLTSYTKINSRWI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino neid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6839	37207	A	6889	2	2400	SMRQKENKDIQDLNSALHQAD LIDIYATLHPKSTEYTFFSAPHCI RTYSKIDHTLGSKALLSKCKIT EHTDSQTTVLSELRIKKLTQINK SATWKLNMLLNDYWVHNEM KAEIKMFETNENKDTTYQNL WDTFKAVCRGKFIALNAHRKR QERSKIDTLMSQLKELEKQEQT HSKVSRRPPSSEIEAIINSLPTK KSPGPDGFTAEFYQRYKEELLY ELKLFQSIEKEGILPNSYEASI LIPKPGRDTTEKENFRPISLMNI DAKILNKILANRIQQHIKKLLIII DAKILNKILANRIQQHIKKLLIII ODAKILNKILANRIQQHIKKLLIII CHARLINGENFOKOMENTISLINGENFOKOME
						SRWIEDLNVRPKTIETLEENLG
6840	37208	Α	6890	1	1515	
6841	37209	A	6891	1	1428	

SEO ID	ISEO ID NO:	Met	ISEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide		in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6842	37210	A	6892	150	1920	NYQCREVLKGPDGAENHGTRT
	1					T*RMHK\LSSQFSQLEERVSGM
	1					EDQTNETKDTHRLKIKGWRKIY
						QANGKQKKAEAAILVLDKTDF
						KPTKIKGDKQGHYIMVKGSIQQ
					1	GQLTILNIYAPNTGASRLIKQVL
						RDLQRDLDSHTIIMGDFNTRLS
	1			1		TLDRSTRQRLNKDIQELNSALH
						QVDLIDIYRILHTKSTEYTFFSA
				1	Ì	PHHTYSKIDHTVGSKALLSKGK
						RTEIITNRLSDHSAIKLELRIKEL
				1		TQNRSTTWKLNNLLLNDYWNL
						WDTFKAVCRGKFIALNIQKRK
						QERSKIDTLTSQFKELEKQEQT
						HSKASRRQEITKIRAELKERETQ
						KSLQKISESRSWFFEKINNIDTP
				1		LARLIKKKREKNQIDTIKNDKG
	i i					DITTDPTEIQTTIRQYYKHLYAN
						KQENLEEMNKFLDTYTLPRLN
						WEEAESLNRPITGSEFEAIINSLP
		ı		1		IKKSPGPDGFTAKFYQSYKEEL
						VPFLLKLFQSIEKEGILPNSFYE
						ASIILIPKPGRDTTKKDNFRPISL
				1		MNIDAKILNKILANKIQQHSKK
				1		LIHHNQVGFIPGMQGWFNTCKS
						INIIQHINRTKDKNHMIISIDAEK
				l		AFDKIQQPSC
6843	37211	Α	6893	1	1797	

793

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		<i></i>
6844	37212	Α	6894	2	1880	APNTGAPRFIKQVLSDLQRDLD
		1				SHTIIMGDFNTPLSTLDRSMRO
		1				KVNKDIQELNSALHQADLIDIY
l		l		l		RTLHPKSTEYTFFSATHHTYSKI
		1	l			DHIVGSKALLSKCKRTEIITNCL
l				l		SDHSAIKLELRIKKLTENRSTTW
		1				KLNNLLLNDYWVHNEMKAEIK
		1		ŀ		MVFETNDTLPRLNQEEVESLNR
		1				PKTGSEIEAIINSLPTKKSPGPDG
	1	1				FTAEFYQRYKEELVPFLLKLFQ
	1	1		ŀ	ł	SIEKERILPNSFYEASIILIPKPGR
						DTTKK/EENFRPISLMNIDAKIL
		ļ.				
						NKILANRIQQHIKKLIHHDQLGF
					ł	IPGMQGWFNICKSMNVIQHINS
						PKDKNHMIISVDAEKAFDKIQQ
ļ		ŀ		1	1	PFMLKTLNKLGIDGTYLKIIRAI
l		1				YDKPTASIILNGQKLEAFTLKTG
	1	1				TRQGCPLSPLLFNIVLEVLARAI
1		1				RQEKEIKGIQLGKEEVKLSLFA
			ľ		ł	DDMIVYLENPIISAQNLLKLIGN
ĺ		1				FSKVSGYTINVQKSQAFLYTNN
		1			1	RQTESQIMSELPFTIASKRIKYL
						GIQLTRDVKDFFKENYKPLLNE
1		1				IKEDKNKWKNIPCSWVGRINIV
1		1	ļ.			KMAIPPKVIYRFNAIPIKLPMTF
i		l			i	FGMIFLSQKYGHVTLLFRLLQW
		l				LLNVARNNNKVFYKIYKVGHK
						LSSAYVLCLTCSHFSVSFL
6845	37213	В	6895	13	1506	
6846	37214	Α	6896	1	6635	MTPESRDTTDLSPGGTQEMEGI
		1			1	VIVKVEEEDEEDHFQKERNKVE
	1	ĺ				SSPQVLSRSTTMNERALLSSYL
	1	l				VAYRVAKEKMAHTAAEKIILP
		ı				ACMDMVRTIFDDKSADKLRTIP
		1				LSDNTISRRICTIAKHLEAMLIT
		l				RLOSGIDFAIQLDESTDIASCPTL
		l				LVYVRYIPLKLRLGGLLQPEKPI
			l	l		VLKVESRDGTIQYNSQQHINLS
1		1	1	l	l	AAWLKTAVOGREAPGKOPSKO
		i i		1	1	QHSAKRKTHRTQLKKESGDGP
		l		1		HPKFGGGNLASP
6847	37215	В	6897	1	3045	
004/	121213	ь	0077	11	2042	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6848	37216	A	6898	1	2764	MARELHDKCTSFSSRFDOLEES
0848	3/210	l^-	0898	1'	2704	
		1	ļ		l	LSAMEDQMNEMMREEKFREK
ļ.	1					RRKRNEQSLQEIWDYVKRPNL
ļ						HLIGVPESDRENGPKLENTLQDI
l						IQENFPNLARQGNIQIQEIQRMP
					l	QRYSSRRATPRHIIVRFTKVEM
						KEKMLRAAREKEIQTTIREYYK
1						HFYANELENLEEMDKFFETYTL
	i i	1				PRLNQEEVESLNRPITGSAIEAII
	i .			1	I	NSLPTKKSPGPDGFTAEFYQRY
	l .					KEELVPFLLKLFQSIEKEGILPNS
						FHEASIILIP
6849	37217	В	6899	1	3549	
6850	37218	Α	6900	387	541	
6851	37219	A	1090	1	545	
6852	37220	A	6902	71	370	RRCKVRPSARGVLRYAVCVCV
1	1					CVCVYPCVHVCTCVRMCLCVC
1	1					VCVCE/CSVEIHCGGQGCARCIC
l				t .		LQPQEGGCTEQAVALHCAAQL
						WRNRLKLMKQPVARV
6853	37221	Α	6904	1	738	
6854	37222	Α	6905	1	567	
6855	37223	Α	6906	1	1416	
6856	37224	Α	6907	3	1267	
6857	37225	Α	6908	1	552	NALPGRKSRVFSGCVSADTWK
1					i	PPSSAKVTETKGASPAFLRAGQ
						PRLVPGETLEKSLGPGKDPQVE
	1				I	PQHPVHLPGISSEGFPWDGFNE
					l	QTPKD\LPNRDGGAWVLGYRA
					i	GPACPFLLHEEREKSNRSELYL
					ŀ	DLHPDHSLTEQDDRTPGRLQA
		1			ŀ	VWPPPKTKDTEEKVGLKYTEA
		1			ŀ	EYQAAILHLKRE
6858	37226	Α	6909	1	561	
6859	37227	Α	6910	219	1343	RRLCHTQPTLGMRERSELVNV
		1				CVHSVFSLPSVQAMQEKDEAK
						AETIQALYHQTLEALQTLLKAL
1				1		FIEDPTPAGLKSILEALGPWMNS
						GKAHERARAVNTNVSVLNHM
ł						LLTLPFFMPLGFPALGLLLGRLI
	1	1				LHIGDPDEEIGCEALDGIIILYTI
						LELOKRARDKEETNKKELYES
i	1					NKHFLGPYNPVSPCONILRVIEE
1	1					FGDFLGPQQIKDLLLAALEGLK
						GSSEAPGKDSREMMQLASEVM
	1					LSSVLEWYRHRALEVIPEIMQGI
	1	1			1	YMOLSHIQEPRARQVALLPVSL
ŀ	1		1			LASSFMTEVVVALLMCPLPLNR
			1		1	QPAACASSCPSTAAWAV*GAST
1	1		1			LSCSWPCSFRSITTSASTCLAAW
	1	1	1			
L	1			l		LLPRTPRRVHSPLPSYLCAGW

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first coden for peptide	eodon for last amino acid of peptide sequence	*=Stop endnn, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or permue sequence	deteron, (-possible interestide insertion)
				·		
6860	37228	Α	6911	3	730	
6861	37229	A	6912	2	1218	ERKCMQGKYAGAMESEPCVCT
				•	[	EADFDCDYGYERHSNGQCLPA
1	1				İ	FWFNPSSLSKDCSLGQSYLNST
						GYRKVVSNNCTDGVREQYTAK
1						PQKCPGKAPRGLR\VVTADGKL
						TA\EQGHNVTLMVQLEEGDVQ
1						RTLIQVDFGDGIAVSYVNLSSM
						EDGIKHVYQNVGIFRVTVQALV
						RLPPHISQCDEVFRFFEARPEDV
l		1				NPPKDQALLLGELGPAVELCLK
1						EERFADAIILAQAGGTDLLKQT
l		ŀ				QERYLAKKKTKISSLLACVVQK
	į.					NWKDVVCTCSLKNWREALAL
		1			Ì	LLTYSGTEKFPELCDMLGTRME
		1				QEGSRALTSEARLCYVCSGSVE
		1				RLVECWAKCHQALSPMALQD
						MHVISTDENQVFAAVQEWNQN
l		1				DTYNLYISDTRGVYFTLALENV
		_				QSSRGPEGNIMIDLYEVTI
6862	37230	Α	6913	1	1659	V-0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.
6863	37231	Α	6914	540	824	KPRLENYVKNAEASGADAINW
l		1				KKGY/LVMEDEMNEMKREGKF
		1				REKRIKRNEQSLQEIWDYVKDQ
				į		IYVRLVYLKVTGRMEPSWKTL
6864	37232	١.	6915	1	939	CRILSRRTSPI
6865	37232	A	6916	285	458	OVFSOLEGRIALGKFORPSSLPT
0803	3/233	^	0910	203	430	GKWTQRCWWGAQWE*D*LFG
		1				LHGWWVRPVIAGFP
6866	37234	A	6917	32	171	CHG W W VRT VIAGIT
6867	37235	A	6918	294	461	
6868	37236	A	6919	2	255	LIPCPATVNNVSDIMGMYMKE
				F		CSASLITREMOIRTTIMRHHLTS
		1				IGTEMIRK/SKNNECWSGRECO
						TVGAGQCVRAPCASRSRARH
6869	37237	Α	6920	2	393	
6870	37238	В	6921	87	633	
6871	37239	A	6922	78	260	TQYLRWKCRNHRLLRRSCWEL
1						*TRAVPIRPSWLQNRYQGTSRF
		1				CVCFEESSGTPSTQLEI
6872	37240	Α	6923	1	369	FVLHEKCLGPFIWTGNTNVEM
		1				VKKICAPT*TKHVVW*LES*M
						WEEPRWPN\GKAPVYSSQREQR
						RRRVISAFPSEGVLPSTFKNKKF
l						TVKQPQVGRSVGIPEEGIVIIGD
						GQLQGCLLPLKTF
6873	37241	Α	6924	3	201	LKEMQINTTMRYHS\TPSRTS*\I
l		1				KKTDNNKFWMRMTEKLETSY
						CWWECETMQPRWKVSLQYLL
						PLI
					<u> </u>	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
6874	37242	Α	6925	1	2064	
6875	37243	Α	6926	95	752	
6876	37244	Α	6927	2237	5072	RAKSPANIIMTGSNSHITILTLN
		1			1	VNGLNSPIKRHRLASWIKSQDP
		i				SVCCIQETHLMCRDTHRLKIKG
		1				WRKIYQANGKQKKAGVAILVS
	1				1	DKTDFKPTKIKRDKEGHYMMV
						KGSIQQEELTILNMYAPNTGAP
ļ	1					RFIKQVLSDLQRDLDSHTLIMG
		l				DFNTPLSTLDRSTRQKVNKDTQ
	i .					ELNSALHQADLIDIYRTLHPKST
ŀ		1			1	EYTFFSAPHHSYSKIDHILGSEA
ĺ		1				LLSKCKRTEIITNYLSDHSAIKL
		1				ELRIKNLTQSR
6877	37245	A	6928	3	331	
6878	37246	Α	6929	364	853	
6879	37247	A	6930	2	531	RPRVRELVGGSAIQALKEWNTT
		1				GKLRINH*KRCGSTQHHGSKYA
		1				TDKEERPD\ACPLQPQPPQIQNG
		1				PMNGCEKDSSSTDSANEKPALI
		1				PREKKISILEEPSKALRGVTGPNI
		1				EKSAKDLQRCTVSLTRYRVMIK
						EEVDSSVKKITAAFAELHNCIID
						KEASLMAEMGTVNEQAMRC
6880	37248	Α	6931	1	456	ISILEEPSKALRG\VTEGNRLLQ
		1				QKLSLDGNPKPIHGTTERSDGL
		1				QWSAEQPCNPSKPKAKTSPVKS
		Į.				NTPAAHLEIKPDELAKKRGPNI
						EKSVKDLQRCTVSLTRYRVMIK
						GEVDSSVKNIKAACAEFPICIID
		l				KEVSLMAEM\DKVKGRKPW
6881	37249	Α	6932	333	964	
6882	37250	Α	6933	240	691	
6883	37251	Α	6934	1	2076	
6884	37252	Α	6935	14	485	RRSLESVLSRKLNPF*KATGTSR
		1			1	SESAVWAIIDAVSSPQKRLLDSE
					į.	FIDPLMNKKARISHLTNRVPPTL
		ı			į.	NGHLNPTSEKSAAGLPLPPAAA
		1				AIPTPPPLPSTYLPISHPPQIADS
		ı				HSPAAPVQGIQPFLTADQYWLE
		ــــــــــــــــــــــــــــــــــــــ				NRYPSQHLSRVTASRARHQT
6885	37253	A	6936	1	643	
6886	37254	В	6937	1	408	
6887	37255	A	6938	2	197	or wit Former conservation
6888	37256	A	6939	103	298	CLWLFQEEEEEEEEEED*EEE
						EEE/EEEEEEEEEEEEE
1			l			EEEEEEEEEEEEEEEE
1000	0.000.0	ļ	6040	1117	200	FLGHRVGI
6889	37257	Α	6940	117	257	L

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
6890	37258	Α	6941	46	219	LKECNCIVCNSKNKCLKG*KKK
		1		i	}	EEEEEEEEEEEEEEEE
		1				EEEEEEEEEGRRGRGRGRRR
				l		RRRRRKKK
6891	37259	Α	6942	1	1314	MVSRIWSWISEAQCPLCRPSGT
						YGPGEAALLLWLCIEAAAAAA
						AARSTTTPIITNHQSNTIAEQNP
		l				PRHENGDPKTYIIHVLAEOVLE
						RLPHGVALRHDPLAPVVSRAG
		1		l		GVGHORCAADDALOPLLOGRP
		1		l		EPGLAERHGVODNLILKVSHTH
		1				TOKSAEKRAVSDPSSTVHRPOP
ļ		1		l		LPPSTVHQSTIPSNPDSSSAYCL
						PSTRHGFSSYTDSFVPPSGPSNP
						MNPTIGNGLSPORVHYOHLPTH
1		1				AGGKRNAALEYGVPRKYYHM
1		1				LKITASDYEKTKPFOVGDKVM
						GSGWRKVGMQT*FL*LKKEEE
						EEREEEE\EEEEEEEEEEE
				l		ECECECECECECECECEC
						EEEEENSLSLTE
6892	37260	Α	6943	1	160	
6893	37261	Α	6944	1	306	
6894	37262	Α	6945	1	933	MWLARELEESLAVSLQGEPGL
		l		l		LAGAGRLQGSPFSHPMEPGRQS
						ETLSQKKKKKEEEEEEEEEE
		l				EEEEEEEEEEEEE
						EEEEEEEEEEEEEEE
		ı		l		DQLDTM\FGTHQQTSPTQRSAR
						RRPCSVQGPRS*SPFSHPMEPGR
		1				QSETLSQKKKKKEEEEEEEEE
		1				EEEEEEEEEEEEEE
						EEEEEEEEEEEEEE
						EEDQLDTMLWDSSTNLTNTAL
		1				SKEKTMFSSRAKIVKPNGEKPD
						EFESGISQALLELEMNLDLKAQ
		1				LWELNITAAKEIEVGGGRKAIII
		1				FVPVPQLKSFQKTQVQLRRILP
		1				KPTQKSCTNNKQKLPRSCTLTA
		1		l =		VHDAILEDLVFPSEIVGKRIHVK
		l	1			LDGSHLIKIHLDEAQQNNVEHK
						VEPFSGVYKKLMGKDVNFEFP
6895	37263	Α	6946	1	1365	
6896	37264	Α	6947.	416	610	EFKKPVLEGGA*RGEGGSPCV
						WSFFDPVHFNYQAGLFRVALP
		_				GEQCRTGRLVARVYTGISGASF
6897	37265	A	6948	1	846	

	SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
5090   37268   B   6951   446   625	6898	37266	A	6949	3	620	WFIVPISCVICNDIMAYMFGFFF GRTPLIKLSPKKTWEGFIGGFFA TVGFGLLLSYVMSGYRCFVCP VEYNNDTNSFTVDCEPSDLFRL QEYNIFGVIQSAUGWKTVRMY PFQHSIALSTFASLIGPFGGFF ASGFKRAFKIKDFANTIPGHGGI MDRFDCQYLMATFVNVYIACV
	6899	37267	Α	6950	50	554	
	6900	37268	В	6951	446	625	
5903   37271	6901	37269	Α	6952	1	2149	
6904 37272 A 6955 I 1305 MYKGSIPGELTILNIYALNTGA PRFIKQVLRDLQRDLDSHTIIMG DFNTPLSTSDRSTRQKVNKDIQ ELNSALHQADIIDIYRTLHFKST EYTFFSAPHHTYSKIDHIVOSKA LLSKCQRIEHTNCLSDYSAIKLE LRIQKLTQNCSTHWKLNNLLIN DYWYHKEMKAEKMFFETNEN KDTTYHHLWDTFKAVCRGKFI ALNAHKRKQERFEMPTLTSQL KELKKQEQTHSKASRRQEITKI RAERKEIETQKTLQKINESGSW FVEKINKIDRPLARLIKKKREKN QIDAIKNDKGVITTDFTEIQTTIR EYYKHLYANKLIKKREKN QIDAIKNDKGVITTDFTEIQTTIR SEEAIINSLPTKKSPQNOGFIA KFVGELTILNIYALNGAPRT KQVLRDLQRDLDSHTIIMGDFN TPLSTSDRSTRQKVNKDIQELN SALHQADIIDIYRTLHFKSTEYT FFSAPHHTYSKIDHIVGSKALLS KQQREITINCLSDYSAIKLERI QKLTQNCSTIWKLNILLINDY WYHKEMKAEIKMFFETNEND TTYHHLWDTFKAVCRGKFIAL NAHRKQGRFEMDTLTSQLKE LKXQGQFISHKARRQERFEMDTLTSQLKE LKXQGQTISKASRQEITKIRA ERKEIETOKTLQKINESGSWFV EKINKIDRPLARLIKKKREKNQI DAJKNOKQVITTPOFTEQTTIRE	6902	37270	Α		I		
PRFIKOVLRDLORDLOSHTIMO DFNTPLSTSDRSTROKVNKDIQ ELNSALHQADIDIYRTLHPKST EYTFFSAPHHTYSKIDHIVOSKA LLSKCQREIITINCLSDYSAIKLE LRIQKLTONCSTIWKLNNLLLN DYWYHKEMKAEIKMFFETNEN KDTTYHHLWDTFKAVCRGKFII ALNAHKRKQERFEMDTLTSQL KELKKQEQTHISKASRRQEITKII RAERKEIETQKTLQKINESGSW FYEKINKIDRPLARLIKKKREKN QIDAIKNDKGVITTDPTEIQTTIR EYYKHLYANKLENLEEMDKFL DTYYHLRLNQGVESLSNRFITG SEEAINSLPTKKSPOPNGFTA KFF*QEELTILIIYALNTGAPRFI KQVLRDLQRDLDSHTIMGDFN TPLSTSDRSTRQKVNKDIQELN SALHQADIDIYTLHPKSTEYT FFSAPHIHTYSKIDHIVOSKALLS KCQREIITINCLSDYSAIKLELRI QKLTQNCSTIWKLNNLLLNDY WYHKEMKAEIKMFFETNEND TTYHHLWDTFKAVCRGKFIAL NAHRKRQERFEMDTLTSQLKE LKKQGTHSKARRQETKIRA ERKEIETQKTLQKINESGSWFV EKINKIDRPLARLIKKKREKNQI DAIKNOKGVITTOPTEQLTTRE			A		1		
	6904	37272	A	6955		1305	PREIKQVLRDLOSHTIMO DENTPLSTSDRSTRQKVNKDIQ ELNSALHQADIIDIYRTLHPKST EVTFFSAPHHITYSKIDHIVOSKA LISKCQRIEITINCLSDYSAIKLE LRIQKLTQNCSTIWKLNKLLLN DYWVHKEMKAEIKMFFETNEN KOTTYHHLWDTFKAVCRGKFI ALNAHKRKQERFEMDTLTSQL KELKKQCQTIPIKSASRRQEITKI RAERKEIETOKTLQKINESGSW PVEKINKIDFDLARLIKKRENQ QIDAIKNDKGVITTDPTEIQTTIR EYYKHLYANKLENLEEMDKFL DYTVNLRRLNQGEVESLNRPITG SEIFAIINSLPTKKSFONGFTA KF-QEELTLINYALNTGAPREI KQVLRDLQRDLDSHTIIMGDFN TPLSTSDRSTRQKVNKDIQELN TPLSTSDRSTRQKVNKDIQELN KCQRIEITINCLSDYSAIKLELRI QKLTQNCSTIWKLNNLLLNDY WVHKEMKAEIKMFTETNENKD TYHHLWDTFKAVCRGKFIAL NAHKRQERFEMDTLTSQLKE EKKQCTISTIKKASRRQEITKIRA ERKEIETOKTLQKINESGSWFV EKINKIDRIVALNTGSGSWFV EKINKIDRIVALNTGSGSWFV EKINKIDRIVALNTGSGSWFV EKINKIDRIVALNTGSGSWFV EKINKIDRIVALNTGSGSWFV EKINKIDRIVALNTGSTRIKER

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		Sequence		
6906	37274	Α	6957	2	1025	WRRIYQANGK*KNK/QKKAGV
		1				VILVSDKTDFKPTKIKRDKEGH
		ŀ	l	1	l	YIMVKGSIQQEELTVLNIYAPN
		1		1		TGAPRFMKQVLRDLQRDLDPH
		ŀ			l .	TTIMGDFNTPLSTLDRSARQKV
	1	ļ.				NKDIQELNSALHQADLINIYRIL
		1				HPKSTEYTFISAPHRTYSKIDHI
	l					VGRKALLRKYKRTEIITDCLSD
				1		HSAIKLELRIKKLTQNSSTTWK
		1		l		LNNLLLNDYWIHNKTKAEIKM
	1	ŀ				CFETSENKDTTYQNLWDTCKA
	1					VCREKFIALNAHKRKQERSKID
		ŀ				TLTSQLKE/LEKQEQTHSKASRF
						NLEEMDKYLDTYTLPRLNQEE
l	1	1	ľ			FESLNRPITGSEIEAIINSLPTKKS
ŀ		1		ŀ		SGPDGFTAKFYQ
6907	37275	Α	6958	1	1661	
6908	37276	Α	6959	2	1632	WRKIYQANGK/HKKAGVAIRV
		l				SDKTDFKPTKIKRDKEGHYLM
l		l			1	VKGSIQQEELTILNIYATNTGAP
				l		GFIKQVLSDLQRDLDSHTIIMED
		l		l	1	FNTPLSTLDISMRQKVNKDTQE
		1				LNSALHQEDLIDIYRTLHPKSTE
		l		i		YTFFSAPHHTYSKIDHILGSKAL
		l		ł		LSKCKRTEIITNYLSDHSAIKLE
						LRIKNLTQSRSTTWKLNNLLLN
ŀ		1		İ		DYWVHKEMKADIKMFFETNES
	1		ŀ	ŀ		KDTTYQNLWDAFKAEELESLN
		1				RPITASEIVAIINSLPSKKSPGPD
		ŀ				GFTAKFYQRYKEELVPFLLKLF
		į į				QSIEKEGILPNSFDEASIILIPKLG
		1				RDTTKKENFRPISLMNIDAKILN
		ı				KILANQIQQHIKKLIHHDQVGFI
		1				PGMQGWFNIHKSINVIQHINRT
	l	l				KDKNHMIISIDAEKAFDKIQQSF
	1	i				MLKTRNKLGIDGTYLKIIRAIYD
						KPTANIILNGQKLEAFPLKTGTR
	1	1		l		QGCPLSPLLFNIVLEVLARAIRQ
		l		l		EKEIKGIQLGKEDVKLSLFADD
			l	1		MIVYLENPIVSAPNPLKLISNFS
		L_				KVSGYKINVQKSQAFLYTNNR
6909	37277	Α	6960	1	2169	

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540.217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		097,540,217	sequence	or permit sequence	detection, * possible indeceding insertion)
6910	37278	A	6961	2	1255	EGKFRENRIKRNEOSLOEIWDY
						VKRTNLRLIGVPESDWENGTKI
						ENTLODIIQENFPNLAR*AKIOR
						RSQDPSTHLTSRDTHRLKIKGW
		l				RKIYQANGKQKKAAVTILVSD
					'	KTNFKPTKIKRDNEGHYIMVKO
					1	SNQQEELTILNIYAPNTGAPRFI
i	l					KOVLRDLQRDLDSHTIITGDINI
	ı					PLSTLDRSTKOKVNKDTOELNS
	ŀ			i .		ALHQVDLIDIYRTLHPKSIEYTF
	1					FSAPHHTYSKVDHILGSKALLS
						KCERIEIITNCLSDHSAIKLELRI
						KNLTONHSITWKLNNLFLNDY
	1	1		l		WVHNEMKAEIKMFFETSENKD
		1				TTYONLWDAFKAVCRGKFIAL
		ı				NAHKRKOERSKIYTLTSOLKEL
	1	l				EKQEQTHSKASRRQEIIKÎRAEL
		ŀ				KEIETOKTLOKLNESISHQLEW
		1				QSLKSQKTTGAGEDVEK
6911	37279	Α	6962	1	1122	
6912	37280	Α	6963	551	1536	EILSPPGLPYKSS*KKH*TWKGT
		ŀ				TGTSCC/INHAKIVTHRLKIKGW
		ŀ				RKIYQANGKQKKAGVANLVSD
		ŀ				KTDFKPTKIKRDKEGHYIMVKG
						SIQQEELTTLNIYAPNTGAPRFI
		ŀ				KQVLSDLQRDLDSHTLIMGDFN
						TPLLTLDRSTRQKVNKDTQELN
		l		i		SALHQADLIDIYRTLHPKSTEYT
						FFSAPHHIYSKTDHILGSKALLS
		1				KCKRTEIITNYLSDHSAIKLELRI
		į.	ļ		1	KNLTKNRSTTWKLNNLLLNDY
						WVHNEMKAEMKMFFETNENK
						DTTYQNLWDTFKAMCRGKFIA
		1			1	VNAHKRKQERSKIDTLTSQLKE
	1	1				
		_				LEKQEQTHSKASRRQEITKI
6913	37281	В	6964	28	1209	LEKQEQTHSKASRRQEITKI
6914	37282	Α	6965	ī	1284	LEKQEQTHSKASRRQEITKI
6914 6915	37282 37283	A B	6965 6966	1	1284 1056	LEKQEQTHSKASRRQEITKI
6914 6915 6916	37282 37283 37284	A B B	6965 6966 6967	1 1 124	1284 1056 963	LEKQEQTHSKASRRQEITKI
6914 6915 6916 6917	37282 37283 37284 37285	A B B	6965 6966 6967 6968	1 1 124 3	1284 1056 963 1162	LEKQEQTHSKASRRQEITKI
6914 6915 6916 6917 6918	37282 37283 37284 37285 37286	A B B A	6965 6966 6967 6968 6969	1 1 124 3	1284 1056 963 1162 1364	LEKQEQTHSKASRRQEITKI
6914 6915 6916 6917	37282 37283 37284 37285	A B B	6965 6966 6967 6968	1 1 124 3	1284 1056 963 1162	LEKQEQTHSKASRRQEITKI

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	detetion, (=possible nucleotide insertion)
				sequence		
6921	37289	Α	6972	1	1917	MVKGSIQQEELTILNTYAAHTG
		ĺ				APRLIKQVLSDLQRDLDSHTIIM
						GDFNTPLSTLDRSTRQKVNKDT
l						QELKSALHQADLTDIYRTLHHK
						STEYTFFSAPHHIYSKIDHILGSK
						ALLSKCKRTEIITNYLSDHSAIK
		1				LELWIKNLTQNHSTTWELNNLL
			]			LNDYWVHNEMKAEIKMFFETN
						ENKDTTYHNLWDTFKAVCRGK
		1				FIPLNAHKRKQERSKIDTLTSQL
		Ì				KELEKQEQTHSKASRRQEITKIR
		ł		i		AELKEIETQKTLQKINESRSWFF
						ERINKIDRLLARLIKKKREKNQI
İ		1				DAIKNDKGDITTDPTEIQTTIRE
	1	ŀ				YCKHLYANKLENLEEMDKFLD
		1				TYTLPRLNQEEVESLNRPITGAE
ĺ		1				IVAIINSLPTKKSPGPDGFTAKF
				ĺ		YQRYKEELVPFLLKLFQSIEKE
		ł			ļ	GILPNSFYEASHLIPKPGRDTTK
		l				KENFRPISLMNIDAKILNKKLA
						KRIQQHIKKLIHHDQVGFIPGM
						QGWFNIRKSINVIQHINRAKDK
					i	NHMIISIDAEKAFDKIQQPFMLK
						TLNKL\GIKYLGIHLTRDVKDLF
						KENYKPLLKEIKEDTNKWKNIP
						CSWVGRINIVKMAILPKMCL*R
		1		1		RWTPLCLLTAAASLNRE*ERLV
		1		1		QPLLWRQMYCGPRHCRQVPQH
						RRLNWSPSLRLS
6922	37290	Α	6973	1	2673	-

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6923	37291		6974	261	2667	TWCSGRYMVGCR/DWHLLLV/ KGLRKLTIVAEGEGGAGMSLG ESGNKIKRDKEGHYIMVNGSIQ QEELTILNIYAPNTGAPRFIKQV LENDLGREIDDSHTIIMRDFNTPLS ALERSTREKVNKDIQELMSALI- ALERSTREKVNKDIQELMSALI- KRTEIITKCLSDHSTIKLELRIKK KRTEIITKCLSDHSTIKLELRIKK LTQNRSTTWKLNSLLLNDYWV HNEMKAEIKMFFETIENKDITTY QNLWDTFKAECRGKFIALNAH KRKQERSKIDTLTSQLKEI-EKQ EQTHSKASRGETIKIRAELKET ETQKTLQKINESRSWFFERINKI DRPLARLIKKKREKNLIDAIKN DRPLARLIKKKREKNLIDAIKN DRPLARLIKKKREKNLIDAIKN SLPTKLSPGPGSKINFTIGSEIVSTYLP RLNGEEVESINRPITGSEIVSTYLP RLNGEEVESINRPITGSEIVSTYLP RLNGEEVESINRPITGSEIVSTYLP VSILISYCQGGSLMSQVYWNQG EXPPSSNAPPOLSVNKAQHRH VCCRGEMLKRVQVHYVRAGES DASSHCVAGOPBAFGKPLILS KENHLLTVTAIAKLNHKLCEIK SMOVPINTEHLTSTIMSKAVIPML SLPTOSKQIPSTQFLISTSTAGRESKVIPML SLPTOSKQIPSTGAGRESKULLS KENHLLTVTAIAKLNHKLCEIK SMOVPINTEHLTSTIMSKAKIPML SLTPGSSQIVESSLAPSPAGKFQG
						HLGGLPGGSQERPSRQYLYESA RTTVLLGLGCPLKQIQLRSQHS SPLEYLESLPKKDRKKREKIOIN

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Uaknowa.
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
NO:	sequence	nou	09/540,217	codon for peptide	of peptide sequence	deletion. \=possible nucleotide insertion)
	sequence	1	03/10/40/41	sequence		
6924	37292	Α	6975	1	1687	MLKGSIQQEELTVLNIYAPNTG
					\	APRCIKQVLSDVQRDLDSNTLI
		l				MGDFNTPLSTLDRSTRQKVNK
	1	1				DTQELNSALHQADLIDIYRTLH
						PKSTEYTFFSAPHHTYSKIDHIL
		l				GSKALLSKCKRTEIITNSLSDHS
ŀ		l				AIKLELRIKNLTQNRSTTWKLN
						NLLLNDYWVHNEMKAEIKMFF
l	1					ETKENKDTTYQNLWDAFKAVC
		1				RGKFIALNAYKRKQERSKIDTL
1	ì	ŀ				TSQLKELEKQEQTHSKEIQTTIR
ŀ		İ	ŀ			EYYKHLYTNKLENLEEMDKFL
İ						DTYTLPRLNQEEVESLNRPITGS
ŀ	l	l				EIVAIINSLPTKKSPGPDGFTAEF
	Ì	1				YQRYKEEMHINRAKDKNHMIIS
1		1				IDAEKAFDKIQQPFMLKTLNKL
		l				GIDGTYFKIIRAIYDKPTVNIILN
						GQKLEAFPLKTGTRQGCPLSPL
						LFNIVLEVLARAIRQEKEIKGIQ
		1				LGKEEVKLS\LFADDMIVYVEN
	l	1				PLPSQPQNLL*GWLSNFSK/MSS
						GYKINVQKSQAFLYTNNRQTES
		1	1			QIMSELPFTIASKRIKYLGIQFTR
		1				DVKDLFKENYKPLLNEIKEDTN
						KWKNIPCSWVGRINIVK\MAILP
6925	37293	В	6976	1	2431	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	or peptiac sequence	deletion, \=possible nucleotide insertion)
				s.cque.ee		
6926	37294	Α	6977	1	1921	MGESVQSLLTLAQKRSMMIQV
	l				1	AVAPRTPTLLLKLYKEKASKTQ
	1					LKKVNLVVQDGQSLESIEVHD
		1				HEPADTYKLLSLVKEPAEEIPR
						VIQNVFGHRSKKENLKDSYGLF
						QSSTMVATTWNNVSLMQHHSL
		l				RRPNRHLTASYPHFHFQEIPVNF
		ı				FHSGRDSESFGWNQHIKKDKE
	1					GHHIMVKGSIQQEELTMLNIYA
						PNTGAPRFINQVLSDIERDLDSH
		i				KIIMGDFNTPLSTLDRSTRQKV
	H					NKDTQELNSALHQADLTDIYRT
						LHPKSTEYTLFSAPHHTYSKIDH
	I					IVGSKALLSKWKRTEIITNCLSD
	l.					PRAIKLELRIKKLTQNRSSIWKL
						NNVLLNDYWVHNEMKAEIKIF
	l .					FETNENKDTSCQNLWDTFKAV
						CRGKFIALNAHRRKQERSKIDT
						LTSQLKELEKQERTHSKASRRQ
					0	EITKIRAEMKEIETQK\TLQKINE
						SRSWFFEKINKIDRPLARLIKKK
	l .					REKNQIDAIKNNKGDITTDPTEI
	į.					ETTIREYYKHLYTNKLENLEEM
	ı					DKFLDTYTLPRLNQEEVESLNR
					:	PITGSEVVAIINSLPTKKSPGPDG
						FTAEFHQRYKEKLISELLPMPN
						HTALKKQTQDLSDCKAMFLYY
						QSVSVQTAIINYHRLRGLNNRN
	1					LFLTVLEYSSLRSGCEHSRVL

SEQ ID				Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first codon for peptide	of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	scauence	or peptide sequence	deletion, (-possible nucleotide insertion)
				,		
6927	37295	Α	6978	I	1848	MSLTKMLICAALLGLFCMLLGI
1						RWQVAELIGMTLALSSTAIAM
						QAMNERNLMVTQMGRSAFAV
						LLFQDIAAIPLVAMIPLLATSSA
					į.	STTMGAFALSALKVAGALVLV
						VLLGRYVTRPALRFVARSGLRE
		1				VFSAVALFLVFGFGLLLEEVGL
						SMAMGAFLAGVLLASSEYRHA
						LESDIEPFKGLLLGAVFTPRVVV
		l			İ	NIYSSELRTAKNYQANGKQKK
l		1				PGVAILVSDKTAF/KPTEIKRDK
		1				EGHY\IMVKGSIQQEELTILNIY
		1			ł	APNTGAPRFIKQVLSDLQRDLD
					ł	SHTLMMGDFNTPLSTLD\RSTR
		l				QKVNKDTQELNSALHQADLIDI
		l				YRILHPKSTEYTFFSAPHHTYSK
		1			ľ	IDHIVGSKALLSKCKRTEIITNY
	r	l			İ	LSDHSAIKLELRIKNLTQSRSTT
		1			ĺ	WKLNNLLLNDYWVHNEMKAE
		1			İ	IKMFFETNENKDMTYQNLWDT
					1	FKAVCRGKFIALNAHKRKQERS
					İ	KIDTLTSQLKELEKQEQTHSKA
l						SRRQEITKIRAELKEIETQKAIQ
		1			l	KINESRSWGPPGNCQQNYRNSE
				1		SGEKSAPEGQAQHAGPTEGKV
		1			l	PTFLYVGKEKFPPSYLLTRKSSH
					l	LPTCGDPICGEKCWRVPTTSGQ
						GNKADQWGGVGIGDTDHDSA
6928	37296	Α	6979	1	2235	
6929	37297	Α	6980	1	2955	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide focation of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6930	37298	A	6981	3	2156	KSLKOLMELKIMAGELCDEWT SLSSRCNQLEERVSVMEDEMN EMKDKHRPKIKEWRKIVQANG QQKKTRVANLVSDKTEFKPTKI KRDKEGHYIMVKGSIQQEELTI VNIVAPNTGAPRFIKKVLSDLQ RALDSHTIMGDFNTPLSTLDRS TROKVNKDIGELNSALHQADLI DIYRTLHPKSTEVTFFSAPHYTY PKIDHIVGSKALLSKCKRTEIIT NCLSOHSAIKLELKIKKLTQNL STTWKLNNLLKDVWYHKEM KAEIKMFFETINKNKDTTYQNF WDTFKAVCRGKFIALNAHKRK QEGFKIDTLTLQLKELEKQEQT HSKASRRINKIDRPLARLIKKRK QEGFKIDTLTLQLKELEKQEQT HSKASRRINKIDRPLARLIKKRK PKENQIDTIKNDKGDITTOPTEIQ TTIREYYKHLYANKLENLEEM DKFLDTYLLPRLNQEEVESLNR PTGAEIVAIINSLFTKKSPGPDG FTAKFYQRYKEELVPFLKLEP GMGGWFNIHKSINNIDAELINKI LASQMQQHIKKLIYHNQVGFIH GMGGWFNIHKSINNIOHINTIK DKNHTIISLDAEKAFDKIQOFF MLKLKTLNKLGIGDMYLKIIRA VJKRFTANIILHWQKLEAFPLXT GTRQGCPLSPLLENIVLEVLA AVRKEKEIKRTQIGREEIKLSLF ADDMIVYLENIVSKQNLLKILS ADDMIVYLENIVSKQNLLKLI
6931	37299	A	6982	3721	8717	MLPIKRHELANWIKISQDPSVC CIEETHLT CEDAHRHKIKGWR KIYQANGKQNKTKQQKKQGLQ LUVSDKRDFKPTKIKRDKEGHYI MVKGPIQQUELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLD MGOIPTPILSTLDRSMRQKVNK DTQELNSALHQADLIDIYRTLH KSTEYTEFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDH SAUKLKLRIKNLTQNHSTT\WK LNNL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleolide insertion)
6932	37300	IA	6983	599	1074	NPRAWEKQQPPTSPQEFCLVCF
						VVHLQKSTREALNNKNIKPLLS
		1			i	TFSQVPG/SINHSSCENVLAHSL
	ŀ	1				AIGGVTEGICTASTPFVLLGDVL
		1				DCLPLDQCDTIFTFVEKNVATW
		1				KSGTASLPAAFMAGVEHLWLF
		ŀ				QVNGANCQWIYPSGVWRTVAL
		1				FSQLH
6933	37301	Α	6984	1	312	
6934	37302	Α	6985	2	484	QSRALLWPMLVDVIQPKPWKA
		1		1		PGSLGLPSCISAITVQSSPGLRLC
		1				SCGQGPRVNTPGTKLPQPNRPV
		ŀ				SLSFSQMKLLTSSHWKSFHCPA
		1				*INPAQSSPGPWP*PQLSGCPAF
		1				QFLSFG*KSLLSSGNTASSSPLW
		1				FLCWCFLNLVLQAKLPDGFRPA
	1	1				HRV
6935	37303	Α	6986	234	405	ELKICSCOPITVRYNADDSTVSL
						SFSQMKLLTSSHWKSFHCPA*I
		1				NPAQSSPGPWP
6936	37304	Α	6987	1	2021	PTRPAAAQWRARAAEKMSPTP
		1				PLFSLPEARTRFTKSTREALNNK
		ŀ				NIKPLLSTFSQVPGSENEKKCTL
		1				DQAFRGILEEEIINHSSCENVLAI
		1				VISLAMGEVTEGICTASTHFVLL
	i	1				GDVLDCLPLDQCDTIFTFVEKN
		1				VATWKSNTFYSAGKNYLLRMC
		1				NDLLRRLSKSQNTVFCGRIQLF
		ł			i	LARLFPLSEKSGLNLQSQFNLE
		ĺ				NVTVFNTNEQESTLGQKHTED
1		I				REEGMDVEEGEMGDEEAPTTC
	l	1				SIPIDYNLYRKFWSLQDYFRNP
						VQCYEKISWKTFLKYSEEVLAV
						FKSYKLDDTQASRKKMEELKT
						GGEHVYFAKFLTSEKLMDLQL
						SDSNFRRHILLQYLILFQYLKGQ
						VKFKSSNYVLTDEQSLWIEDTT
						KSVYQLLSENPPDGERFSKMVE
						HILNTEENWNSWKNEGCPSFV
						KERTSDTKPTRIIRKRTAPEDFL
	-	İ				GKGPTKKILTGNEELTRLWNLC
		1				PDNMEACKSETREHMPTLEEFF
			l			EEAIEQADPENMAENEYKAMN
l		1	l	1		NSNYGWRALKLLARRSPHFFQP
1		1	1	I		TNQQFKSLQEYLENMVIKLAKE
			1	I		LPPPSEEIKTGEDEDEEDNDALL
1		1	1	I		KENESPDVRRDKPVTGEQIEVF
		1	1	I		ANKLGEQWKILAPYLEMKDSEI
						RQIECDSEDMKMRAKQLLVAW
		1		I		QDQEGVHATPENLINALNKSGL
L	L			L		SDLAESLTNDNETNS

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
	ļ	<u> </u>				
6937	37305	Α	6988	155	811	EFYRTGKVHRAPGVQEVTEDP
	1			i		RDPLAQLATRDRKERRGSLDH
1						LALRVREAQLDQLVPPESVAA
		1				KDLKAPRAPKAPVVPLGSPALR
l	1	1				APVGTQAPRAHQAKRDSPALR
						ALLASRDFRAPLGSLGCLDLGD
		1				CQACLGYQACQAPRAPPALLA
		1				HQERWCPWPCRMSQPQHRRT
						MAARLTGRTSQTNATIFQLRKK
1	1		1			FLRMQSFSVKTSLHILFS*TLER
						NSNG
6938	37306	A	6989	91	918	
6939	37307	A	6990	199	380	CSTSSRTY*IPSRCFSKG*HWRH
1	l .					TVNSNFGPMGNPSHPTTSSAHH
	i .					TVPLIESQPSSTSKK
6940	37308	A	6991	1	483	
6941	37309	A	6992	178	298	
6942	37310	Α	6993	864	1298	RLQNRTILASDLSGSDRWRRTY
		1				RCL*RHGPRFSSCRLSCRRPFDK
ļ	1	1		1		TCRLMCHQRLSGFPQEQTQRDS
1	1					RCIQLLFRORFAAASCPTHOVH
l	ŀ					VHRWRKPMVFLILESDLKYTV
	ŀ					LSLPEECHTGAHEQSSHCLLLSL
ŀ		1				ASVDVHCSQRP
6943	37311	A	6995	2	348	KKKRKKKIEEEEEEEEEEE!
		1				REEEGDEEOEEEEE\EEEEEEE
		1				EEEEEEEEDDDDDNGLLOTL
	1					PGLHEMRVNLTRSDGIISVWHF
	1					PFWHFSFLMPYEEGALLRLHLP
6944	37312	A	6996	1	192	
6945	37313	Α	6997	1	507	MEKNEKEQEEEEKKEKNSKKK
ŀ	1	1				EEEEEEGGGEEEEEGEGGEE
1		i				EEEEEEEEEEEEEEEEE
	1	1			1	EEE/DKEEEEEEEEEEEEE
		1				EEEEEEEEEEEEE\EEEEKVVE
1		1				EEDEFIWFLGNSLYFPSFSHFA
		1				WSOIPSREDEGERRLRVNSMIM
		1				DFTSNTNHVQLIVAR
6946	37314	A	6998	1	257	MGPIHKISHYVYANISKSEKVL
10,70	15,5.4	Ι.,	0,,,0	I.	[	KSEHFRSQAFQPGQQSETVSEK/
		1				EEEDEEEEEEEEEEEEEE
1	1	1		1	1	EEEEEEEEEEEEEEEEEE
		1				EEEEEEEEEEEEE
6947	37315	A	6999	1	156	CECECECECECE
6948	37316	В	7000	1	757	
6949	37317	A	7001	1	279	
0949	D/31/	I'A	7001	II	1417	L

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6950	37318	A	7002		1226	MPSSKGVHVHSPPRYLAAKDF KMINKELTAATFMEVIAEDNRF IYDGIDSNFEPELVFLEFFEALLS FAFICVTDQMTKSYTNVPADD VSGNKHEITVILNODOA,MSS SAVMSHESDAAHSDSARSSSK LELSPDVNKIRKSEAMVKEKKK SAVMSHESDAAHSDSARSSSK LELSPDVNKIRKSEAMVKEKKK KQDKGKARSPSSLSDNLDFS KQDGMTTRGEMSPAGVPLLGM QLNEVKPKKDRQNVQQNE/GC QLNEVKPKKDRQNVQQNE/GC VPFENLQGGEGBILCEECPDEP RRVHVAGRSMYEGEVVNGMR NGFGMFKCSTQPVSYIGHWCN GRKHGKVGEVATWRAEKKK EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
6951	37319	Α	7003	3	123	
6952	37320	Α	7004	2	458	
6953	37321	Α	7005	239	432	CLWLFQEEEEEEEEEEED*EEE EEE/EEEEEEEEEEEEEEE EEEEEEEEKIFLGHRVGI
6954	37322	С	7006	7	162	
6955	37323	Α	7007	39	2154	
6956	37324	Α	7008	1	639	
6957	37325	Α	7009	I	651	
6958	37326	В	7010	ı	684	
6959	37327	A	7011	3	428	TRPGGVYLPLLWEQSF/CWKSP/ ALGYTRGHFSALVAMENDGYG NRGAGANLNTDDDVTITFLPLV DSERKLLHVHFLSAQELGNEEQ QEKLLREWLDCCVTEGGVLVA MQKSSRRNHPLVTQMVEKW LDRYROIRPCTSLF
6960	37328	A	7012	2	800	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon,/-possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	1			sequence		
		L.,				
6961	37329	Α	7013	1	930	DHNSSPAMEQNWMENAFDELT
						EVGFRRWVITNFSKLKEHVLTQ
1						CKEAKKLEKRLEELLTRITSLEK
1						NINDLMELKNTSQELREAYTTE
1						ERISEIEDQLNEIKHEDRIREK/R/
		1			1	VKRNEQSLQEIWDY VKRPNLH
1						LT/GVPESDGENGTKLENTLQDI
1		1				IOENFPNLARQANIQIQEIORTP
1		1				ORYSSRRATPRHIJIRFTKVEMK
		1				EKMLRAAREKGQVTHKGKPIR
l		1				LTADPLAETLOARREWGPIFNIL
						KEKNFOHRMSYPAKLSFISVGE
						IKYFTDKOMLRDFVTTRPALOE
1	1					LLKDALNMERNNONQSLQKHA
1		1				KL
6962	37330	A	7014	1	870	
6963	37331	A	7015	i	585	
6964	37332	A	7016	1	1032 .	
6965	37333	Α	7017	2	770	
6966	37334	A	7018	I	2910	
6967	37335	В	7019	239	462	
6968	37336	Ā	7020	3	694	
6969	37337	Α	7021	1	1212	
6970	37338	Α	7022	1	1140	
6971	37339	Α	7023	1	570	
6972	37340	Α	7024	1	486	
6973	37341	Α	7025	1	1476	MEVNREKQLNELEVIGSEEQNL
						EEEGLMIGGVAVRLVPDDIVIP
				į .		GGVNATNGTEARDALRVKVA
1						MSVTLLSGIIQYLLSALGWSYY
	1					TVDGVSQKNPRALGVTADQLH
1						AIFTTMSDEQASFRFGFVAIYLT
l l						EPLVRGFTTAAAVHVFTSMLK
						YLFGVKTKRYSGIFSVVYSTVA
				1		VLQNVKNLNVCSLGVGLMVFG
1	1	1		İ		LLLGGKEFNERFKEKLPAPIPLE
				1	i .	FFADHNSSPAREOK WMENEFD
1						EWTEVSFRRWVITNSSELKEHI
		1			1	LTOCKEAKNLEKRLEELLTRITS
	1				1	LEKNINDLMELKNTAGEFHEA
1	1	1			I	YTSINS/RNQTEERVSEIEDQLN
		1			I	EI*CKDKIR\EKKRMKRNEQSLQ
1		1				EIWDCVKRPNLRLTGVPESDGE
	1	1	1			NGTKLENTLODIIQENFHNLAR
		1				QANSQIQEIQRTPQRYSSRRATP
	1	1				RHIJIRFTKVEMKEKMLRAARE
1		1				KGRVTHKGNPIRLIADLSADTL
		1		I		QARRQWEPIFNILKENFQTRISH
6974	37342	A	7026	1	1080	Quanta and a superior of the superior
07/4	157542	<u>'^</u>	1.020	<u>ı.                                    </u>	11000	

SEQ ID	SEQ ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	:	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
6975	37343	A	7027	T .	3501	MIVYLENPIVSAONLLKLISNFS
0,715	3,3,3	ľ.		ľ		KVSGYKIYKIDVQKSQAFLYTN
						NRQTESQIMSELPFTIASKRIKY
		i				PGIOLTRNVKDLFKENYKPLLN
	ŀ	ŀ				EIKEDTNKWKNIPCSWIGRINIV
	l					KMAILPKVIYRFNAIPIKLPMTS
	i					FTELEKTTLKFIWNQKGARIAK
		-				TILSKKNKVGGITLPDFKLYYK
ŀ	1					ATVTKTAWYWYQNRDIDQWN
						RTEASEITPPIYNHLIFDKPDKN
l						KKWGKDSLFNKWCWENWLAI
						CRKLKLDPFLTS
6976	37344	A	7028	164	714	IGVNRHLIQESPSWNLAGAPLE
				l		QIFQRKEQAAIFAILQPLLVISRQ
		1				TGSGVDPQQTPADLQK/SGSDS
						REQNKTENEFDELTEIGCRRWV
		1				ITNSSELKEHVVTQCKEAKNLE
				ŀ		KMLQELLTRITSLEKNINDLME
		1				LKNTAQELREAYTIINSQTDQA
						EERISEIEDQLNEIKGEDNIREKT
						VKRNE
6977	37345	В	7029	1	579	
6978	37346	A	7030	1	927 1362	MAAGRIN BUGARBUN IGEGEG
6979	37347	Α	7031	1	1362	MAAGRHLPVGADRHLIQESTG WHLAGAPLGWSFORKEOTAIF
						AVLQPLLVIPROTGYGVDLQO
		1				MPADLQQRFLTVRRKTNKQKG
						IVSTSTKRTSSEGHQHQRRKVD
	i	1				KFTEMGRNOHKKAENSKNON
						ASSP\PKDHNSLPAREONWTEN
						EFDELTEIDFRRWVITNSSQTKG
						SMF*P*CKEAKNLEKRLDELLT
						RITSLEKNINDPMELKNTAREL
				l		REANKSINS*IDOGRKERV\SEIE
						DOLNEIKREDKIREKRMORNK
						OTLOEIWDYVKRPNLHLIGVPE
						SDRENGTKLENTLQDII\QENFP
						NLARQANIQIOEIORTPORYSSR
		1		1		RATPRHIIVRFTKVEMKEKMLR
		1				AARKKGQVTHKGKSIRLSADFS
		1				AETLOARREWGPIFNILKEKNF
	1	1		1		QPKISYPAKLSFISEEEITSFTDK
l		1		1	1	OTLRDFVTTRPALQELLKEAVN
						MERKNQYQPLQKHTKM
6980	37348	Α	7032	1	598	
6981	37349	Α	7033	3	787	
6982	37350	Α	7034	61	284	RLLEPQGPLRAGSSPAGK/IGGT
		1				LERRGMPWPGP/HSEGGLSPLL
	1					LGASLA A A PHGEMPS VR VHP V
						RPSSRDCSSRV
6983	37351	В	7035	743	1683	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6984	37352	Α	7036	1	1137	
6985	37353	Α	7037	-1	663	
6986	37354	Α	7038	1	197	
6987	37355	Α	7039	1	291	
6988	37356	A	7040	3	342	
6989	37357	Α	7041	1	439	
6990	37358	Α	7042	3	253	
6991	37359	С	7043	1	210	
6992	37360	A	7044	I	165	
6993	37361	Α	7045	I	346	
6994	37362	Α	7046	1	389	
6995	37363	С	7047	1	464	
6996	37364	Α	7048	1	1806	
6997	37365	A	7049	491	1640	
6998	37366	Α	705 I	188	383	
6999	37367	A	7052	I	759	
7000	37368	Α	7053	I	1683	
7001	37369	Α	7054	I	972	
7002	37370	Α	7055	1	429	
7003	37371	Α	7056	3	753	DOTTWGLLETG/S/ELMLIPGOP KCHICOPPVKOA YGGGEIKGV LAQVQITVGPVGTRTHPVVISP VPECHIGIDILSSWOPPHTGSLTG KRVYIMVEKAKWKPLELPLPR KIVNGKQYCIPGGIAEISATIKD LKDTGYMIPTSPRSPIWQK KTDGSWRITVDYQVYTPIAAA VPDVVSLLEQINTSPGTWQHIT HLDVLLWRIYQVTQKAASFEW GPEQEKALQQVQAAVQA\LCH LGHMTOQIOWCL
7004	37372	Α	7057	2	430	
7005	37373	Α	7058	1	1515	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hođ	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
7006	37374	A	7059	h	1523	MGEERRWRPSSNGKHGAFAEL
7000	3/3/4	<u> </u> ^	1039	ľ	1323	DKGWLVWLEGKGVIGARRSW
						RAHSALIKICVQQIKDSLPGKM
		1				SKGLLQQQQKPKHLLHDLYKA
						MSTRWGVQKARLNCTALPPTG
		1				CVTLDPSFLTEPOFPROLSEDLL
						LTREALEKEVQLRRQLQQEKEE
	ŀ	1				LLYRVLGANASPAFPLAPVTPT
	ŀ					EVEKERELELRDRLDEOORVLE
						GKNEEALQDPRLVDPLTSCTVH
						FEKPOMLNARLWKHAGREAV
						ACKVRGSELPKTMGTYPLHOH
		1				DLDVRHGVKGDHFGALRFDCP
		1				AGFWTCMGPLAPSFWPISPIWN
		1				GPPLDISGYPATSTQKSTMCLRI
						IDTRLHPESRLKQQSNFALNAR
						EKALQQVQAAVQAALPLGPYD
	1					PADPMVLEVSLADRDAVWSL
	1	l				WQAPIGESQQRPLGFWGKALPS
						SADNNSPLERQLLARYWALVE
						TEYLTMGHQVTM*P/ELPIMNW
		1		1		VLSDPSSHKVVYAWQHSIKW
						K\DRA*AGLAGTSKLHEEVAQ
		L				MPIVSTPATLPSCRIL
7007	37375	Α	7060	1	2190	
7008	37376	Α	7061	286	430	
7009	37377	A	7062	205	514	LWSLCAPVLQVPCLRAAFPVFT
	1	1				RRHAPSAGRGFTRSYVSAGSW
		1		1		TETQQGLWGSLTKLGADGLLL
		1				GISKHLVEFLQIFQISGCWGHYC
		1			1	YLQILFFALNSISPSYHVLLFNV OFGFIFNFMVLCVP*AGTHIAPC
						KSSSRTRGMSSCENWKGCSKA
		1				RHLQYWSTKTPQSLSFFCCGIH
		1				FVTAVCOP
7010	37378	A	7063	1	487	. Thirteg.
7011	37379	A	7064	1	1212	
7012	37380	Α	7066	140	453	
7013	37381	Α	7067	1	3341	MGKKQNRKTGNSKNQSASPPP
	1	ı	i			KERSSSPATEQSWMENDFDELR
		1				EEGFRLSNYSELPEDIQTKGKE
						VENFEKNLEECITRITNKRNFKP
1	1	1	1	1		TKIKRDKEGHYIMVKGSIQQEE
	1	1	l	1		LTILNIYAPTGAPRFIKQVLSDR
l	1	1	l	1		QRDLDFHTLIMGDFNTPLSTLD
l	I		1	I		RSTRQKVNKDTQELNSALHQA
l	1	1	l	I		DLIDIYRTLHSKSTEYRFFSAPH
l	1	1	l	I		HTYSKIDHLLGSKAFLSKCKRT
1		1	l	l		EHTNYLSDHSAIKLELRIKNLTQ
	0.000	L_	70.00	ļ.———	1705	NRSTTWKLNN
7014	37382	В	7068	11	1785	L

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				ocquence		
7015	37383	A	7069	Ţī	1141	MVTWNFIQERNGSGMDQCDD
		1				GGGKILDPVYILTVELTGFAKG
		1				WKMFSVKDQSVNVLGFAGYPI
		1				ITQTARKGAGKIPTWASLRQYQ
		1				KGLGSKYQLRRALRPDCALGN
						GQGVRYCNSLDEEEKRELKLFS
		1		l		SQRKRENLGRGNVRPFPVTMT
		l				GAICEQCGGQINGGDIAVFASR
		1				AGHGVCWHPPCFVCTVCNELL
İ						VDLIYFYQDGKIYCGRHHAECL
		1				KPRCAACDEIIFADECTEAEGR
						HWHMKHFCCFECETVLGGQRY
						IMKEGRPYCCHCFESLYAEYCD
						TCAQHIGHAGSFIKEC/SRRLLP
		1		l		GEAEI/SRRATVICLVRVSVRPE
		1				AASKSPNMRRKRKRKGACPLS
						SVGPVIPSVP*NTQRT*RPQSRP
						LGAPWNPWPCLMQ
7016	37384	Α	7070	1	2388	VHQYYSCLPEEKVPYVNSPGEK
						LRIKQLLHQLPPHDNEVRYCNS
						LDEEEKRELKLFSSQRKRENLG
		İ				RGNVRPFPVTMTGAICEQCGG
						QINGGDIAVFASRAGHGVCWH
		1				PPCFVCTVCNELLVDLIYFYQD
		1				GKIYCGRHHAECLKPRCAACD
						EIIFADECTEAEGRHWHMKHFC
1						CFECETVLGGQRYIMKEGRPYC
		1				CHCFESLYAEYCDTCAQHIGID
		1				QGQMTYDGQHWHATETCFCC
						AHCKKSLLGRPFLPKQGQIFCS
1						RACSAGEDPNGSDSSDSAFQNA
						\GPRSPGAVPKLARTRARR\GAH
		l				AEPAQPAASEF*PAVSRRRPPVT
ļ.		1				ADGHAQPVQPDTQPQPGPHLE
		1				EPGRALPLWEQDGAEPDPEPSA
						AP\RQCNIRTSYSPGGQGAGAQ
						PEMWGKHFSNPKRSSSLAMTG
		l				HAGSFIKECREDYYPGRLRSQE
		1		l	i	SYSDMSSQSFSETRGSIQVPKYE
1				l	1	EEEEEEGGLSTQQCRTRHPISSL
1				1		KYTEDMTPTEQTPRGSMESLAL
		1				SNATGLSADGGAKRQEHLSRFS
l					1	MPDLSKDSGMNVSEKLSNMGT
					I .	LNSSMQFRSAESVRSLLSAQQY
1						QEMEGNLHQLSNPIGYRDLQSH
				1		GRMHQSFDFDGGMAGSKLPGQ
		1				EGVRIQPMSERTRRRATSRDDN
		1		l		RRFRPHRSRRSRRSRSDNALHL
				1		ASEREAISRLKDRPPLRAREDY
				l		DQFMRQRSFQESMGHGSRRDL
7017	37385	Λ	7071	1	807	

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hed	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /-possible nucleotide detetion, \=possible nucleotide insertion)
7018	37386	Α	7072	500	2666	YCLRLAQVGIFPAPSRAWPVDL
		1				DPESRLCCFPSLGSLANPTAVG
						LEEDREQDVGTSSRGGAWDTRI
		1				KRELEKMSEKCGGQINGGDIAV
						FASRAGHGVCWHPPCFVCTVC
						NELLVDLIYFYQDGKIYCGRHH
}		l		1		AECLKPRCAACDEIIFADECTEA
Ì	1	1		}		EGRHWHMKHFCCFECETVLGG
l		1	ŀ			QRYIMKEGRPYCCHCFESLYAE
		ı				YCDTCAQHIGEAIFGSQLGPSV
1		l				MRSPLFWGVGIAAAALDAVLIR
						AHQRTQGCHHELSALLAFEKG
ļ.						SEKKEEEEGGQVSRSSSLKVQA
						QELSATEDKGHISPFFWEAVYH
	İ					YASGECRGPGPPYSHSLRLYSQ
		l				QALPTGRGPSSSQFPFCQFYCC
		ł				YKKSLLCDCLSKSPALEKAMR
		l				GIDQGQMTYDGQHWHATETCF
	ļ					CCAHCKKSLLGRPFLPKQGQIF
		ı	1	l .		CSRACSAGEDPNGSDSSDSAFQ
	1	l	ļ			NA\GPRSPGAVPKLARTRARR\G
			į			AHAEPAQPAASEF*PAVSRRRP
						PVTADGHAQPVQPDTQPQPGP
		ı				HLEEPGRALPLWEQDGAEPDPE
		ı		i		PSAAP\RQCNIRTSYSPGGQGAG
1		1	1	l		AQPEMWGKHFSNPKRSSSLAM
İ		1		1		TGHAGSFIKECREDYYPGRLRS
		l				QESYSDMSSQSFSETRGSIQVPK
1		l		!		YEEEEEEGGLSTQQCRTRHPIS
		l		l		SLKYTEDMTPTEQTPRGSMESL
		l		l		ALSNATGTKTCSVTFQAKETCR
		1				YQDAQFGKVKARVKERQSLWS
7019	37387	Α	7073	1	2239	
7020	37388	Α	7074	I	282	
7021	37389	A	7075	2	430	GFGAQDPKSLALRTHCQTSGW/
		l		l		SLTEQDPYNNVIRTTIEALAATL
		ı		l		GGTQSLHTNVFDEALGLPTDFS
		ı		i		ARIARNTQIIIQEESELCRTVDPL
		ı				AGSYGGAIIQQIDVAGGLAKRI
		I		I		EAGLSKRMIEEASAREQALIDQ
1		1		l		GKRVIVGVT

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide Incation of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7022	37390	A	7076		1561	MVTLILYFRFYRLNGDTLRRIQI HLLDKYRKVPPEVHADIPYGA KRFSRPCSWFLRITKRGYRRTV HAMAGQKEKILLGAGMSDYLA KPIEERELINILLRYKPGSGISS RVVTPEYNEIVVNPNATLDWQ LALRQAAGKTDLARDMLQML LDFLEPVRNKVEGOLJGENPEG LVDLIHKLHGSCGYSGVPRMK NLCQLIEQQLRSGTKEEDLEPEL LELLDEMDNVAREASKILGPDK THILRIRRDVLATDPPANDRR KACLHACVLTPPLGAARAIIQ QIDEAGGMAKAIEAGLPKRMIE EASAREQSLIDQGKRVIYGVNK YKLDHEDETDVLEIDNWWRN EQIASLERIRATRDDAAVTAAL NALTHAAQHINENLLAAAVNA ARWRATLGEISDALEVAFDRYL VPSQCVTGVIAQSYHOSEKSAS EFDAIVAQTEGFLADNGRPPR LIAKMGQDGHDRGRPRI LIAKMGQDGHDRGRVIASAY SDLGFDVILSPEEIARLA SUNDHYVGANSSLAAGRSR
7023	37391	Α	7077	1	354	
7024	37392	Λ	7078	1	1116	
7025	37393	Α	7079	1	450	
7026	37394	Α	7080	1	252	
7027	37395	Α	7081	1	242	
7028	37396	Α	7082	1	242	
7029	37397	A	7083	1	9228	
7030	37398	A	7084	3	664	
7031	37399	A	7085	3	718	
7032	37400	A	7086	380	1038	WTRWRASAADNLAHGRWGEG KLVYTTGASGAPDRQAARCAA SAKISWYRŚKGSKIPLTPKEVE KTGWGLKIPG/MGQQQLPERV KEAARILEL GOLLKRRPPELS GQRQRVAMARAIVRDPAVFLF DEPLSNLDAKLRVQMKLELQQ LHRRDQVEAMTLAGRWMMN GGVAEQIGTPVEVDGDDTLEIL GADNLAHDAGRAEAGGDWRI RSARRSSTGA

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		_				
7033	37401	Α	7087	380	920	WTRWRASAADNLAHGRWGEQ
						KLVVTTGASGAPDRQAARCGC
İ		1				IWRKISWYRSKGSKHPLTPKEV
1		1				EKTGWGLKIPG/MGQQQLPERV
		1				KEAARILELDGLLKRRPRELSG
		1				GQRQRVAMARAIVRDPAVFLF
		1				DEPLSNLDAKLRVQMRLELQQ
		1				LHRRDQVEAMTLAQRVMVMN
						GGVAEQIGTPVE
7034	37402	Α	7088	1	258	
7035	37403	Α	7089	3	208	
7036	37404	Α	7090	34	125	
7037	37405	Α	7091	1	393	
7038	37406	Α	7092	1	690	MVAPVYIRDQYSALITNIGKGD
		1				HTTFVKPNIPATGEFKGVGFLE
		ļ				APRGMLSHWMVIKDGIISNYQ
		1				AVVPSTWNSGPRNFNDDVGPY
		1				EQSLVGTPVADPNKPLEVVRTI
						HSFDPCMAWVGNILLTDEAIGV
	1	1				RIVEALEQRYILPDYVEILDGGT
	ł	1				AGMELLGDMANRDHLIIADAIV
		1				SKKNAPGTMMILRDEEVPALFT
		1				NKISPHQLGLADVLSDLRFT\GE
		1				FPKKLPWVQA
7039	37407	A	7093	82	224	
7040	37408	Α	7094	1	239	
7041	37409	Α	7095	1	1062	
7042	37410	Α	7096	1	221	
7043	37411	A	7097	1	1067	
7044	37412	Α	7098	1	1545	
7045	37413	Α	7099	1	2820	
7046	37414	Α	7100	1	1223	
7047	37415	A	7101	1	3087	
7048	37416	A	7102	1	1182	MDKFLDTYTLPRLNQEEVESLN
		1				RPITGSEIVAIINSLPTKKSPGPD
		1				GFTAEFYQRYKEELVPFLLKLF
ŀ						QSIEKEGILPNSFYEASIILIPKPG
						RDTTKKENFRPISLMNIDAKILY
		1				KILAKRIQQHIKKLIHHDQVGFI
	į.					PGMQGWFNIRKSINVIQHINRA
	i	1				KDKNHMIISIDAEKAFDKIQQPF
	ŀ		1			MLKTLNKLAQNLLKLISNFNKV
	1	1				SGYKINVOKSOAFLYTSNROTE
1	1	1				SOIMSELPFTIASKRIKYLGIOLT
ĺ	ŀ	1				RDVKDLFKENYKPLLKEIKEDT
1	1	1	1			NKWKNIPCSWVGRINIVKMAIL
l	1	1				PKVIYRFNAIPIKLPMTFFTELE
l	1		ŀ			KTTLKFIWNQKRAHIAKSILSQ
			1			KNKAGGITLPDFKLYYKATVT
1	1	1	1	1		KTAWYCYQNRHIDQWNR\PSEI
l				1		TPHIYNYLIF
	L	<u>L.</u>		L		TEULINICIE

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
7049	37417	IB	7103	1	1722	
7050	37418	A	7104	i -	3513	
7051	37419	A	7105	i	2546	MSELPFTIATKRIKYLGIOLKSD
/031	37419	l^	/103	l'	2540	VKDLFKENYKPLLNEIREDTYK
1		l	İ			WKNTPCSWIGRINIMNMAILPK
						VIYGFNAILIKLPLTFFTELEKTT
1						LKFTQSLKRAHIAKTILSKKNK
1						AGGIMLPDFKLYYKATVTKTA
ļ	[					CTIHNSKDLEPTEMPSNDTLDK
						ENVAYIHHGILCSHSKGRVHIL
	ł	1			]	CRDMDEAGNHHSRQTNTGTEN
	1	1			İ	QTLHVLTHKWELNDENTWTO
					1	GGEHHISGPVRTNNKNHMIISIG
		l				AEKAFDKIQQPFMLKTLNQLGI
1		l		1		DGTYLKIIRDIFDRPIANILLNGO
	1					KREASPLKTGTRQGCPLPPLLF
		1			1	NIVLEILARAIRQEKEIKGIQLG
		1				KEEVKLSLFADDMIIYLENPIVS
						AQNLLKLISNFSKVSGYKINVQ
		1				KSQAFLYTNNRQTESQILSELPF TIASKRIKYLGIOLTRDVKDLFK
						ENYKPLLNEIKEDTNKWKNIPC
	İ			1		
1		1		1		LSIGKINIMKMAILPKVIYRFNA
		1			i	PIKLPMTFFTELEKTTLKFIWNQ KRARIAKTILSQKNKDGGITLPD
	l	1				FKLYYKATVTKTAWYQYQNR
		l				
1		1			1	DIDQWNRTEPSEIIPHVYNHLIF
						DKPDKNKKWGKDSLFNKWCW ENWLAICGKLKLDPFLTPYTKI
l		1			l	
1	1	l				NSRWIKDLNVRPKTIKTLEENL
						GNTIQDIGMGKDFMSKIPKAM
				l		ATKAKIDKWNLIELKSFCTAKE
1					İ	TTISVNRQPTEWEKIFAICLSDK GLISRIYKELKQRHKKKTNNPIK
7052	37420	A	7106	1	2575	OLISKI I KELKOKHKKK I NINFIK
7053	37421	A	7107	li -	875	
7054	37422	В	7108	1	3421	
7055	37423	Α	7109	1	3790	MELKTKARELREECRSLRSRRN
		1				OLEERVSAMEDEMNEMKREG
		1				KFREKRIKRNEQSLQEIWDYVK
		1			l	RPNLRLIGVPESDAENGTKLEN
		1		l		TLQDIIQEDFPNLARQANVQIQE
	1	l	l	I		IQRTPQRYSSRRATPRHIIVRFT
		1	l	I		KVEMKOKMLRAAREKDFKPT
	1	1		l		KIKRDKEGHYIMVKGSIQQEEL
		1	l	I		TILNIYAPNTGAPRFIKQVLSDL
	1	1		1		QRDLDSHTLIMGDFNTPLSTLD
		1	1	1		RSTROKVNKDTOELNSALHQA
		1	1			DLIDIYRTLHPKSTE
7056	37424	Α	7110	134	307	DEDITION NOTE
7050	127424	١^.	17.110	1154	507	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7057	37425	Ā	7111	2	173	RPPRSEVPGPLSPGRPPAAGLRG
		l				R*PAGVRGLREPRAFSGVRVER
		1				RSLFIGKDMFDS
7058	37426	Α	7112	888	1016	VPGEIHALHSADRQHENA*NAR
		1				TRWQHAQSGRSPLFLALSRE
7059	37427	A	7113	573	872	SPSLLPDPDAHVGC*SRSRKRPD
						RIRRFDSR*NGLFYCRKTS*PFH
	i	1				*G*MCQ*YQTDPRSNAQCHPVL
						LRLWWPGDEYDFLCRSGSVGS
						VRQSGRASGL
7060	37428	A	7114	I	654	
7061	37429	Α	7115	71	2776	
7062	37430	Α	7116	31	1016	TVLPERPYNRKSSRRNRCGNGP
						PARSFCPSSGRSRRRSSSPATGP/
						HTAIASALPRIAFGKISDSSTQH
						TGPQDMAKAAT*NSLRGSMRY
		l			1	SFKPMVGRWIKSCLRPVWC
7063	37431	Α	7117	279	1243	SVLLMCAADYLPRPPDVQTCN
			l		i	AVRVWLRYHRSNHGTPPDFSP
	1					GPVSAWYYAH/QPKIPIWSQ/QR
	l .					GFTD/R*TRHKCPQRFAVPDK*I
	1		1			SSPD*AMNYYRKIHRPAPRHTA
	į.		l			PTQKARLMADKSSLRHRHNSA
		ĺ				NKRRSASPLSSAGYP/GKRIRAQ
	1					NLIPASTTNGQLRIRQRRISQAR
						**TKRMARKGSISPISAVSNSLN
						SS*ASIIVSSCIRCSALSPLSNIHK
	i .				!	S*TAGPWGASSRKTNIGLSRQRI
	1				1	FPA WOSPCSRRTVKSSROCAVT
						AAISSSVAFRNAAFNPEGISVAS
	1					SNSLRGSMRYSFKPMVGRWIKS
			ŀ			CLRPVWCIRPK
7064	37432	В	7118	1	726	
7065	37433	A	7119	1	138	
7066	37434	Α	7120	56	133	
7067	37435	В	7121	1	1524	
7068	37436	В	7122	1	1521	
7069	37437	Α	7123	1	1494	
7070	37438	В	7124	4	1698	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide			location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
7071	37439	A	7125	I	1725	MELKTKARELREECRSLRSRCD
						QLEERPNLRLIGVPESDGENGT
						KLENTLQDIIQENFPNLAKQVN
						VQIQEIQRTPQRYSLRRATPRHII
						VRFTKVEMKEKMLRAAREKGR
						VTLKGKPIRLTADLSAETLQAR
						REWGPIFNILKEKNFQPRISYPA
						KLSFISEGEIKSFTDKQMLRDFV
						TTRPALQELLKEALNMERNNRS
						WFFEKINKIDRPLARVIKKKRE
						KNQIDAIKNDKEDITTNPTEIQTI
						IREYYKHLYPNKLENLEEMDTF
						LDTYTFPRLNQEEVESLNTSITG
						SEIVAIISIAYQPKKVQDQMDPQ
						PNSTRVLEVLARAIRQEKEIKGI
		1				QLGKEEVKLSLFADDMIVYLEN
						PIVSAQNLLKLISNFSKVSGYKI
		l				NVQKSQAFLYTNNRQTESQIMS
	ĺ					ELPFTIASKRIKCLGIQLTRDVK
	ľ					DLFKENYKPLLKEIKEDTNKW
						KNIPCSWVGRINIVKMAILPKVI
			ŀ			YRFNAIPIKLPMTFFTDLEKTTL
			ŀ			NFIWNQKRARITKSILSQKNKA
		1				GGITLPDFKLYYTATVTKTAW
		l				YWYQN/RWYWYQNRDIDQWN
		l				RTEPSEITPHVYNYLIF
7072	37440	Α	7126	I	2478	

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SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
						L.,
7073	37441	Α	7127	1	1746	METQKTLQKINESRSWFFEKIN
		1				KIDRPLARLIKKKREKNQIDTIK
						NDKGDITTDPTEIQTTIREYYKH
						LYANKLENLEEMDKFLDTYTL
						PRLNQEEAESLNKPITGPEIEAII
						NSLPTKKIPGPDGFTAEFYQRY
					1	KEELQHIKKLIHHDQVGFIPGM
		l			1	QGWFNIHKLINVIQYINRTKDK
						NHMIISIDAEKASDKIQQPFMLK
						TLNKLGIDGTYLKIIRAIYDKPT
						ANIILNGQKLEAFPLKTGTRQG
						CLLSPLLFNIVLEVLARAIRQEK
i						EKKCIRLGKEEVKLSLFADDMI
						VYLENPIVSAQNLLKLISNFSKV
				ĺ		SGYKINVQKSQAFLYTNNRQIE
				1		SQIMSELPFTIASKRIQYLGIQLT
						RDVKDLFKENYKPLLNEIKEDT
						NKWKNIPCSWIGRINIMKMAM
1						LPKVIYRFDAIPIKLPMTFFTELE
						KTTLKFIWNQKRARIAKSILSQ
				l		KNKAGGITLPDFKLYYKAIVTK
1				i		TAWYWYOKRDVDOWNRIEPS
ŀ		1				ETIPHICNHLIFDKPDKNKQWG
						KDSLFNKWCWEIWLAIGRKRK
						LDPFLTPYTKINSRWIKDFNIRP
						KTIKTLEESLG\IQDISMGKKFTS
7074	37442	Α	7128	1	1908	
7075	37443	Α	7129	I	1494	
7076	37444	Α	7130	2	1562	
7077	37445	В	7131	1	1569	
7078	37446	Α	7132	1	1593	
7079	37447	Α	7133	1	1520	
7080	37448	В	7134	I	2796	

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7081	37449	A	7135	101	1686	SIAYQPKRVQDQMDSQPNSTR
		1				ANIILNGQKLEAFPLK\TGTRQF
1		į .				SKENFE\PLSPLLFNIVLEVLARA
		1				IROEKEIKGIOLGKEEIKLSLFA
		1				DDMIVYLENPIVSAQNLLKLISM
						FSKVSGYKINVQKSQAFLYTNN
						ROTESOIMSELPFTIASKRIKYL
	1					GIOLTROVKOLFKONYKPRLKI
						IKEDTNK WKNIPCSWVERIYIV
						KMAILPKVIYRFSAIPIKLPMTFI
						TELEKTTLKFIWNQKRARIAKS
		1				LSQKNKAGGITLPDFKLYYKDT
						VTKTAWYWYQNRDIDQWNRT
						EPSEIMPHIYNYLIFDKPEKNKQ
						WGKDSLFNKWCWENWLALCR
	l .					KLKLNPFLTPYTKINSRWIKDL
						NVRPQTIKTLEENLGITIQDIGM
		1				GKDFRSKTPKAMATKAKSDK
						WDLIKLKSFCTAKETTIRMNRQ
						PTKWEKIFATYSSDKGLISRIYN
						ELKQIYKKKTNNPIKKWAKDIN
				1		RHFSKEDIYAAKRIIMKKCSSSL
		1				AIRQMQIKTTMRYHLTPVRMAI
						IKKSGNNRDMDEIGNHPSQ
7082	37450	Α	7136	1364	3024	TEPKTKTT*LSQ*MQKRPLTKF
					1	NNASC*KLSIN/IVLEVLARAIRQ
						EKEIKGVQLGKEEVKLSLFADD
		1				MIVYLENPIVSAQNLLNLISNFS
						KVSGYKINVQKSQAFLYTNNR
		1				QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNER
						KEDTNKWKNIPCSWVERINIVK
						MAILPKVIYRFNAIPIKLPMTFF
						TELEKTTLKFIWNOKRARIAKSI
	1					LSOKNKAGGITLPDFKLYYKAT
	1	1				VTKTAWYSYQNRDIDQWNRTE
						PSEILPRIYNYLIFDKPEKNKQW
						GKDSLFNKWCWENWLAICRKL
						KLDPFLKPYTKIKSGWIKDLNV
						RPKTIKTLEENLGITIQDIGMGK
						DFMSKTPKAMATKAKIDKWDL
	ļ					IKLKSFCTAKETTIRVNROPTER
						EKIFATYSSDKGLISRIYKELKO
				1		YKKRTNNLIKKWYKDMNRHFS
	1	1	1	1		KEDVYAAKKHMKKCSSSLAIR
						EMOIKTTMRYHLTPVRMAIIKK
						SGNNRITIVLLPGSLIVRSFHVTL
						NAILLHPGLTLFSPSAGRRDIPR
				0.0		VAFSYLAFSAQPSHNTPVN
7083	37451	Α	7137	1	2274	
7084	37452	Α	7138	2	2348	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
7085	37453	Α	7139	1	2202	
7086	37454	Α	7140	1	2823	
7087	37455	A	7141	1052	3831	EHKKPFKKSMNPGAGFFERINK IDRPLARLTKRKREKNQIHAIK NDKGDITTDPTEIQTTIREYYKH LYANKLENLEEMDKFLDTYTL PRLNGEEIBSLNRPITGAEIVAII NSLITKKSPGPDGFTAEFYQRY KEELPFLLKLPGSIEKEGILPNS FYEASINLIPKGRDTTKENFR PISLMNIDAKILSKILANRIQQHI KKLIHDQVGFIPGMQGWFNIC KSINVIQHINRTKOKNHMIISID
7088	37456	Α	7142	1	327	
7089	37457	A	7143	1	446	
7090	37458	Α	7144	382	1485	
7091	37459	A	7145	1	378	
7092	37460	Α	7146	2	217	
7093	37461	Α	7147	1	483	
7094	37462	Α	7148	1	1260	
7095	37463	Α	7149	1	891	
7096	37464	Α	7150	5	182	RQGLLVSPRLVQKGEIRTPGLK RSSRLDLQKC*DYRHEPSSLAS EAPSVWVLLPPWRQS
7097	37465	A	7151	1	1914	

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SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7098	37466	IA	7152	1	2200	MKLTTHRENMALTNGFCHHIA
1000	37,100			l'	2200	AQQNLYTNTLLAARIKQRLTEQ
						FELMLRQAQIDFAGKAHSLTEA
	1	l				QANTTQVSAERDRLFKNYORY
	į.	1				LKGSQAAVNPFSERDIDDARON
					1	FLAQDALAQIQSQLDSLVNGEO
	1					SQIVSLKAQLAEAKYNLEQTIV
						RAPSNGYVTQVLIRPGTYAASL
		1				PLRPVMVFIPDQKRQIVAQFRQ
						NSLLRLAPGDDAEVVFNALPG
		1				KVFSGKLAAISPAVPGGAYOST
1						GTLQTLNTAPGSDGVIATIELDE
						HTDLSALPDGIYAQNPKNLKIV
		1				ELKAPQLPRSLDDAQIALAVIN
		l				TTYASQIGLTPAKDGIFVEDKES
						PYVNLIVTREDNKDAENVKKF
	İ	ŀ				
	l	ļ.				VQAYQSDEIPCRTRSKHCTPAE
		į.				SGACKTESAARHAGPNLYQCR RIRSANRSAISVKGWRTPCIPDS
		ŀ			1	LPAVEWLTYGSGYLAGMKLGD
		1			l .	TPLVEYTRDRLHRETLRSFGRY
	1					ELTTAYTPAGQLQSQHLNSLLS
						DRDYTWNDNGELIRISSPROTR
		ı				SYSYSTTGRLTGVHTTAANLDI
1						RIPYATDPAGNRLPDPELHPDST
		1				
						LSMWPDNRIARDDNYLYRYDR HGRLTEKTDLIPEGVIRTDDERT
ł						HRYHYDSQHRLVHYTRTQYEE
		1				PLVESRYLYDPLG\RRVAKRVW
		1		1		RRERDLTGWMSLSRKPQVTWY
		1				GWDGDRLTTIQNDRTRIQTIYQ
7000	07167	<del>  -</del>	7152	710	1404	PGSFTPLIRVETATGELAKTQRR
7099	37467 37468	A	7153 7154	719	1575 239	
7101	37469	A	7155	i -	735	FNDDSPEARKITRRWRIGEAAD
////	37409	l^	1,133	l*	/33	LVGVSSQAIRDAEKAGR\LP\HP
1	l					D\MEIRGRVEQRVGYTIEQINH
	1	1				MRDVFGTRLRRAEDVFPPVIGV
	1	l		l		AAHKELNNDYTSKKVMKPLIT
		l				SNTVTDEIERANVLKMNGKWY
	1					LFTDSRGSKMTIDGINSNDIYM
	l					LGYVSNSLTGPYKPLNKTGLVL
		l				QMALDPNDVTFTYSHFAVPQT
ŀ	1					KGNNVVITSYMTNRGFFEDKK
1		1		l		
						ATFAPSFLMNIKGNKTSVVKNS ILEQGQLT
7102	37470	A	7156	1	4368	
7103	37471	Α	7157	1	1452	
7104	37472	Α	7158	1	516	
7105	37473	Α	7159	1	743	
		_				

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7106	37474	A	7160	13	1743	DSPE\ARKITRRWRIGEA ADI.V
						GVSSQAIRDAEKAGRLPHPDME
1						IRGRVEQRVGYTIEQINHMRDV
	1					FGTRLRRAEDVFPPVIGVAAHK
1				l		GNDPQGTASMYHGWVPDLHIH
						AEDTLLPFYLGEKDDVTYAIKP
						TCWPGLDIIPSCLALHRIETELM
	1					GKFDEAOPNLGIGTINVVCAAD
	1				ł	VLIVPTPAELFDYTSALQFFDM
	l					LRDLLKNVDLKGFEPDVRILLT
						KYSNSNGSQSPWMEEQIRDAW
				ŀ		GSMVLKNVVRETDEVGKGOIR
	1					MRTVFEQAIDQRSSTDTSLSTP
İ	1					AAPMVDSLIARVGVMARGNAI
	1					TLPVCGRDVKFTLEVLRGDSVE
						KTSRVWSGNERDQELLTEDAL
	1			İ		DDLIPSFLLTGQQTPAFGRRVSG
ļ	1					VIEIADGSRRRKAAALTESDYR
	1			l		VLVGELDDEQMAALSRLGNDY
			]	l		RPTSAYERGQRYASRLQNEFAG
						KYFLRWLMRKIFHIITRCINTAK
	i		ĺ	l .		LPKSVVALFSHPGELSARSGDA
			ľ			LQKAFTDKEELLKQQASNLHE
			ŀ	l		OKKAGVIFEAEEVITLLTSVLKT
İ	İ	1				SSASRTSLSSRHOFAPGATVLY
	l	l		l		KGDKMVLNLDRSRVPTECIEKI
				l		EAILKELEKPAP
7107	37475	A	7161	I	438	
7108	37476	Α	7162	I	3216	MKLMETLNQCINAGHEMTKAI
						AIAQFNDDSPEARKITRRWRIG
		1		l		EAADLVGVSSQAIRDAEKAGR
l						LPHPDMEIRGRVEQRVGYTIEQI
ļ				l		NHMRDVFGTRLRRAEDVFPPG
1						FGDFADFGTTIKQDFRLLGQTS
l	i					VDRLLQLSQGQAVKGNQLLPV
1	ļ			ł		SLVKRKTTLAPNTQTASPRALA
	İ					DSLMQLARQVSRL/VKRAPTC
1	1	1	1	I		WPGLDIIPSC\LALPRIETELMGK
						FDEGKLPTDPHLMLRLAIETVA
		1				HDYDVIVIDSAPNLG
7109	37477	A	7163	I	513	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	١.			sequence		,
7110	37478	Α	7164	1	2027	MRGHREKAAACKPRTRASEGT
						TPASTFILDFQPPNCNYTSGDNH
İ	l					TLRDPHYVEDKGHKYLVFEAN
	l					TGTENGYQGEESLFNKAYYGG
1						GTNFFRKESQKLQQSAKKRDA
		ŀ				ELANGALGHELNNDYTLKKVM
		1	l			KPLITSNTVTDEIERANVFKMN
						GKWYLFTDSRGSKMTIDGINSN
		l				DIYMLGYVSNSLTGPYKPLNKT
		1	l.			GLVLQMGLDPNDVTFTYSHFA
		l	ŀ			VPQAKGILCEEDNYTAGDNHM
		1				MRAPHCEEDRAHKFVVFDANA
		l				GTESGHQGESSLFNRACGGGGT
1	1					
						FFFSKESQKLQQSAKKRDCINA
		1	l			GHEMTKAIAIAQFNDDSPEARK
1		1				ITRRWRIGEAADLVGVSSQAIR
		1				DAEKAGRLPHPDMEIRGRVEQ
		1				RVGYTIEQINHMRDVFGTRLKR
		1				AEDVFPPVIGVAAHKGGVYKT
		ŀ				SVSVHLAQDLALKGSLLLPKND
		ļ				FLFKLGLEGHLPLGKIHSPPTGA
		l				DVARGSSGLPKSELFLPERNTQ
		ŀ				ELQQDSEEGPLALQVLQSNLM
						DFADFGTTIKQDFRLLGQTSVD
1		l				RLLQLSQGQAVKGNQLLPVSL
	1					VKRKTTLAPNTQTASPRALADS
			l			LMQLARQVSRLESGONNDGIC
		l				EIHVAKYVEIFGLTSAEASKDIR
		l	İ	l		OALKSFAGKLVVFYRPE/VGCR
		l	İ			R*KRL*IFSLVYOTCAOSIORAL
		1	l			OCTYOPISHSLLYRVTEPVYAV
7111	37479	<del>ا</del> ـ	7165	1	750	QCTTQFISHSLLTKVTEFVTAV
7112	37480	A A	7166	1	723	
7112	37480	В	7167	1	1156	
7114	37481	A	7168	1	999	
		A		1	529	MICL METE NOCINIA CHENTRAL
7115	37483	l <sup>A</sup>	7169	l'	329	MKLMETLNQCINAGHEMTKAI
1		l	l	1	l	AIAQFNDDSPEARKITRRWRIG
1	1	1		1		EAADLVGVSSQAIRDAEKAGR
1	1	ı		1		LPHPDMEIRGRVEQRVGYTIEQI
1	}	ı		1		NHMRDVFVAGDEKGYESFPWF
1		l		1		IKTCA\HPSRGLYSVHINPYLIPS
1		1	l	1		LSGYRTGLRSFGLVKQKKSPIR
		1	l .	1		MPCVYTNPCVSIVSRMAQASSL
7116	37484	Α	7170	1	1038	
7117	37485	A	7171	1	1098	· · · · · · · · · · · · · · · · · · ·
		r-	L	ı:		

SEO ID	ISEO ID NO:	Tates	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
7118	37486	A	7172	1	838	MKLMETLNQCINAGHEMTKAI
		ı		ļ		AIAQFNDDSPEARKITRRWRIG
l						EAADLVGVSSQAIRDAEKAGR
1						LPHPDMEIRGRVEQRVGYTIEQ
1		1				NHMRDVFGTRLRRAEDVFPPVI
		l				GVAAHKGGVYKTSVSVHLAQ
1		ı				DLALKGLRVLLVEGNDPQGTE
						TMYHGWVPDLHIHAEDTLLPF
						YLGEKDDVTYAIKPTCWPGLDI
						IPSCLALHRIETELMGKFDEGSL
						PTDPHLMYYYQAPCMKSNNAL
1						IVILGTVTLDAVGIGLVMPV\CR
						ASCGISSIPTASPVTMACC
7119	37487	В	7173	1	1212	
7120	37488	Α	7174	1	738	
7121	37489	A	7175	1	654	
7122	37490	Α	7176	1	448	MKLMETLNQCINAGHEMTKAI
		1				AIAQFNDDSPEARKITRRWRIG
1		ŀ				EAADLVGVSSQAIRDAEKAGR
1		1				LPHPDMEIRGRVEQRVGYTIEQ
i		t			į.	NHMRDVFGTRLRRAEDVFPPVI
1						GVAAHK\AGNLSCOLH**IGOR
						AGRGGLRIGRQGGFSFHQ
7123	37491	В	7177	1	753	-
7124	37492	Α	7178	1	345	
7125	37493	Α	7179	1	516	
7126	37494	Α	7180	1	1989	
7127	37495	В	7181	1	1191	
7128	37496	Α	7182	1	669	
7129	37497	Α	7183	1	574	
7130	37498	Α	7184	1	934	
7131	37499	A	7185	1	1281	
7132	37500	Α	7186	1	324	
7133	37501	Α	7187	3	817	
7134	37502	Α	7188	1	587	
7135	37503	В	7189	1	610	
7136	37504	A	7190	1	882	
7137	37505	Α	7191	1	1077	
7138	37506	Α	7192	1	418	
7139	37507	Α	7193	1	840	
7140	37508	A	7194	1	337	MKLMETLNQCINAGHEMTKAI
1		i				AIAQFNDDSPEARKITRRWRIG
		ŀ				EAADLVGVSSQAIRDAEKAGR
		1				LPHPDMEIRGRVEQRVGYTIEQI
		ł	l			NHMRN\VFGSGLRRPTAELKCA
1		l		l		SQT
7141	37509	Α	7195	1	1142	
7142	37510	A	7196	1	1080	
7143	37511	Α	7197	1	1170	
7144	37512	В	7198	1	1296	
7145	37513	A	7199	1	1179	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop eodon, /=passible nucleotide
l	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7146	37514	Α	7200	ı	507	
7147	37515	Α	7201	1	411	
7148	37516	Α	7202	1	793	
7149	37517	В	7203	366	1502	
7150	37518	Α	7204	1	1107	
7151	37519	Α	7205	Ï	2388	
7152	37520	В	7206	1	2260	
7153	37521	Α	7207	1	1067	
7154	37522	В	7208	563	1467	
7155	37523	В	7209	1	1272	
7156	37524	Α	7210	1	1722	
7157	37525	В	7211	I	1917	
7158	37526	Α	7212	1	2679	
7159	37527	Α	7213	1	1207	MKLMETLNQCINAGHEMTKAI
	l	l			1	AIAQFNDDSPEARKITRRWRIG
		ı				EAADLVGVSSQAIRDAEKAGR
	1	1	ŀ			LPHPDMEIRGRVEQRVGYTIEQI
	l .	l				NHMRDVFGTRLRRAEDVFPPG
		1	ŀ			FGDFA\HFGNHHQNRIFALLGQ
		1				TSVDRLLQLSQGQAVKGNQLL
	1					PVSLVKRKTTLAPNTQTASPRA
		l				LADSLMQLARQVSRLESGQAIR
1		l				DAEKAGRLPHPDMEIRGRVEQ
				i		RVGYTIEQINHMRDVFGTRLRR
						AEDVFPPVIGVAAHKGGVYKT
		l				SVSVHLAQDLALKGLRVLLVE
1	1	1	l			AARGLKKRGLAGTAQGPGEPG
		1		1		EAPKGKKGKTEPGHERKGNWT
				1		GKGPQIREGTSPNPPREHGGEC
!		1			1	APPPPSAKRKQPKAQKRKANSN
		1				AHPRQPKPKKKRPKRQTNSRTN
l	l					TRSGKRQNKQPEEPK
7160	37528	Α	7214	1	2757	
7161	37529	Α	7215	1	2984	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7162	37530	A	7216	I I	2387	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI MANDEYGTRLRRAEDVFGYTIEQI MANDEYGTRLRRAEDVFGYDWYA KRNSSKPLAGVQEEDSAWHPE CLQKTRQAWCDNLKTCHTSHG SYMAETAVINHKRKNSPRIVQ SYNDLTEAAYSLSDQKRMLYL FVDQIRKSDGTLQEHDGICEIHW KYAEJFGLTSAEASSURGQAL KSFAGKEVVFYRPEEDAGDEK GYESPFWFIKRAHSPSRGLYSV HINPYLIPFFIGLQWPLTQFRLSE TKEITNPYAMRLVESLCOYRKP HINPYLIPFIGLQWPLTQFRLSE TKEITNPYAMRLVESLCOYRKP MIGEAADLVGVSSQAIRDAEKA GRLPHPDMEIRGRVEGRAFRITRRW RIGEAADLVGVSSQAIRDAEKA GRLPHPDMEIRGRVEGRVGVT PVIGVAAHKGGVYKTLISVHL AQDLALKGLPGLREGNDPGG TTSMYHGWYDLHIHAEDTIL PFYLGEKDDVPYAIKFTCWAG DEGKLPTDPHLMLRLAIETVAH
						DYDVIVIDSAPNLGIGTINVVCA ADVLIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFEPDVFIRD
7163	37531	A	7217	1	917	KLMERRNRRTGRTEKARIWEV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleutide insertion)
7164	37532	A	7218	1	1862	MKLMETLNHCINAGHEMTKA
						AIAOFNDDSPEARKITRRWRIG
						EAADLVGVSSQAIRDAEKAGR
	1			1		LPHPDMEIRGRVEORVGYTIEG
				l		NHMRDVFGTRLRRAEDVFPPV
				1		GVAAHKGGVYKTSVSVHLAY
						DLALKGLRVLLVEGNDPOGTA
				l	l .	SMYHGWVPDLHIHAEDTLLPF
						YLGEKDDVTYAIKPTCWPGLD
			ļ			IPSCLALHRIETELWGK/FDEGR
		l			İ	SFMPGPP/HHHPLGRSSQ*QVS
						SLDRAAKGN*KPLCHCPCSGT
					1	HATLRLIKEORPYVPYAHLOO
						VVDPRRGGHMVLI/NVVRVTG
		1				DVGKGOIRMRTVVEOAIDORS
		l				TGAWRNALSIWEPVCNEIFYRI
		l				IKPRWEIRWGKRAPVIPKHTLN
		l				TQPVEDTSLSTPAAPMVDSLIA
		l				RVGVMARGNAITLPVCGRDV
	į	1			i	FTLEVLRGDSVEKTSRVWSGN
		l		1		RDQELLTEDALDDLIPSFLLTG
				1		QTPAFGRRVSGVIEIADGSRRR
				1		KAAALTESDYRVLVGELDDEC
						MAALSRLGNDYRPTSAYERGO
		i		l		RYASRLQNEFAGNISALADAEN
				l		ISRKIITRCINTAKL PKSVVALES
				l		HPGEAICPVRMFRMKLMETLN
		ļ.				OCINAGHEMTKAIAIAOFNDDS
						PGSEENNPALENR
7165	37533	Α	7219	1	2724	
7166	37534	Α	7220	ı	3252	FNDDSPEARKITRRWRIGEAAD
						LVGVSSQAIRDAEKAGRLPHPE
						MEIRGRVEORVGYTIEOINHME
						DVFGTRLRRAEDVFPPFNDDSF
						EARKITRRWRIGEAADLVGVSS
					ŀ	QAIRDAEKAGRSTATRILEIRGI
						VEQRVGYTIEQINHMRDVFGTI
						LRRAEDVFPPVIGVAAHKGGV
						YKTSVSVHLAQDLALKGLRVL
				į.		LVEGRSFPOTEACLLOYSSWDV
						SSEKPAALNKNKSEMRGDFAD
						FGTTIKQDFRLLGQT
7167	37535	Α	7221	1	465	.,,-
7168	37536	Α	7222	I	291	

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \= possible nucleotide insertion)
7169	37537	Α	7223	1	1710	MLCTKWDKLGLEKNAGKNKN
		1		1		AYKWYGWPANAPDEPHIEQLV
l		l	l			GECRVMRQLKRLISRIAPSPSSV
		1				MVVGESGTAIPVVSHAEFKGGF
		1				ADIGVHYLDWTSRTTEKSSTKS
l						HKDDFGYLEFEGGANFSWGEM
		1		l		YGFFDWENFYNGRHNKPGSEQ
		1				RYTFKNTNRIYLGDTGFNLYLH
		ı			İ	AYGTYGSANRVNFHDDM\FLA
l		l				GFGFQF*PAGGW/WGSNPFFAK
						RYTRSKPYYT\GDNGYV\AGWV
		l				AGYNFMLGSEKFTLTNWNEYE
		l				FDRDATYAADFLPLYDVDCQD
		l				NGNLEYDTYSQPEWKHNLFDH
					1	YLAVLYRFKDESGKEQFSGAV
		1				VKTREATPGKEIEAITRRMLDFS
1		1		l		PRLKKLADCPSPRPVFEALCICS
		1				MLDALLLLCPLDYHASCDNYS
						YALLDPQGFPLPHRRLWGPYID
		1				VDVPMLHLIQHAWAQDALLSC
1	Ì	ŀ		İ		LYSDLLYMSSFPYPAGTLTRLM
	1					GVTSYNHKNTLLTYCITLMSTI
1						RFAYDGDEEIAMKYTDFLKGE
						LSMNIRPLHDRVIVKRKEVETK
1	-					SAGGIVLTGSASAKSTRGEVLA
						VGNGRILENGEVKPLDVKIGDI
						VFFNDGYRGEI
7170	37538	A	7224	678	1588	RTQHKASLHGRASAFCPPRLFA
		l				PQAPRLFDHRGFLTFASANFAA
		1				VAFCPPRLFPPTGAAAVCPLPLF
1						APRRFLPPPPPRLFRCHGFFPPC
						LGFLTSAAFFLPPPRLFALRRRG
		1				FLPFAAAAAFFPTRLFAPPPTQL
		1				FAPSPPWLFAAAAFCPPWLSAP
		1				TPPRLFVPAAAAFCCRDFLPPSP
		1				PLFRHRDFLPPPPRIFVPAAAAL
						RAGAADSAAGSTGVLGQDLWS
ŀ		1	[			RCVVGTGMEAPGSRGGGGGLR
		l				EDIPLPPEFPSGPALSSCR*GNRR
		l				PEGEMTCQEPLLS/CSWIP*VKE
I		I	l			FETNPDNIVRPH

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
7171	37539	IA	7225	1	1627	MTKQLELPQSPGEVPGSDYPLL
/1/1	31339	l^	1223	ľ	1027	IACAYIGELTWGGGFSGSMPLL
	ĺ	1		l	1	AATPGNPVEHIAGLIPVGDTLFS
		1		l		GFNIFITVALIVVMPFITRMMMF
		1				KPSDVVSIDPKLLMEEADFQKQ
					1	LPKDAPPSERLEESRILTLIIGAL
		1				GIAYLAMYFSEHGFNITINTVNL
		1				MFMIAGLLLHKTPMAYMRAIS
		l			l	
		l				AAARSTAGILVQFPFYAGIQLM MEHSVTGIEAAMLDLLGQHLG
		1		l		
1	ŀ	1				VNVASLLGDGQQRSEVEMLGY
		l			İ	LFFVGNRKATPLPYQSQPDDSC
	ł	1				DWYRLRHEEAMTPDAVVRLAE
		l				AAYEKYGFNDFKLKGGVLAGE
	İ	1		l		EEAESIVALAQRFPQARITLDPN
		l				GA\WSLNEAIKIGKYLKGSLAY
						AEDPCGAEQGFSGREVMAEFR
		1				RATGLPTATNMIATNWREMGH
1		1				AVIAQ\SVDIPLADPHFWTMQG
1		1		l		SVRVAQMCHEFGLTWGSHSNN
1		1				HFDISLAMFTHVGAAAPGNPTA
1						IDTHWIWQEGDCRLTQNPLEIK
		1		l		KGKIAVPDAPGLGVELDWEQV
		1				QKAHEAYKRLPGGARNDAGP
7172	37540	ļ.	7226	3	655	MQYLIPGWTFDRKRPVFGRH
7172	37541	A	7227	1	633	
7174	37542	A	7228	1	630	
7175	37543	A	7229	362	1491	PTLSVIHESMRFFIRHOPENLTL
1,,,,		ļ.,				VVLSRNLPQLALPICVFVINCW
l				l		KLAVSNWHLPISTGCAVTKDG
i		1				RWSPEFTITGQA/WDLPVVGYR
		1		i	Ì	NGVAOPLRLWOATHAHPFDLT
		1		l		KFNDGDFLRAEQQGINAEKLTK
		1				VLYPNDNHTAGKKLRLMQQYF
i		1				QCACSVADILRRHHLAGRKLH
i		1				ELADYEVIQUENDTHPTIAIPELL
		1				RVLIDEHOMSWDDAWAITSKT
		1		ł		FAYTNHTLMPEALERWDVKLV
I		1				KGPLPRHMQIINEINTRFKTLDL
1	l	1				QDAEHRPLKMRGCLLCQCHTL
1	l	l	l			FOGKHRFFTGAGGNRONNVIE
1	1		l			
	İ					HLVAASRYRFTTASRRPLFTAG
1	l	1	l	I		FTLLTAFLFHSNFAEGVNSLMF
						MKNLTISGGFLLLAITGPGAYSI
1000	22544	ļ.	7220		660	DRLLNKKW
7176	37544	Α	7230	1	000	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7177	37545	A	7231	545	1322	KHAEHLGQATHAHPFILTKFNP GYFLIRRQTTRGINAEKLAKIFF PYKANHFAGKKLRLMQQYFQC ACSVADILRRHHLAGKKLHEL ADVEVIQLNDTHFITAIPELLTA LIDEHQMSWDDAWATISKTAT YTNIHTLMPEALERWDVKLVKG LLPRHMQIINEINTRFKTLVEKT WPGDEEV WAKLAVVHBQVM MANLCVVGGFAVNGV AALHS DLVVKDLFPEYHQLWPNKFHN VTNGITPRRWIKQCNPALAALL
7178	37546	A	7232	641	874	KYPTPGRDLRMFITGLSERL*EI TSLLKRSITGDKYSLRPLTANSV TSVTHFSFGRVALKSLSSVRAV SLDLNRCFK
7179	37547	A	7233	1	693	
7180	37548	A	7234	980	1305	TWLRICSIRHSKSLILTSI/HVLH SDQGWQYRMRRYQNILKEHGI KQSMSRKGNCLDNAVVECFFG TLKSECFYLDEFSNISELKDAVT EYIEYYNSRRISLKLKGSDSN
7181	37549	Α	7235	1	3219	
7182	37550	С	7236	1	7521	
7183	37551	A	7237	1351	2117	CDRILCSACCAEPQPVSHLHRL RRSFSERQPDGNGSQNPASRDR DVVDVTV1AWIEHRGGHEAPS GPGEDGMDAPAIAAGTFSPREA STLPVQVS*VCRLNCCSRDVPK ATRVPLJEKLAGPLRHPLFMLF QTCLHLSLFTHHFADDSRRLQIF SVGFVAGLKQQYRRDLLQGDV NPRMATAVGNDQVWFQSGNG FQARLRARSDGLPRFQVRTHFG QDAFCIVIVGNTDRDDVHGGQ RIGEREFQHINDLWRFFEC
7184	37552	A	7238	690	868	

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7185	37553	A	7239	2607	3692	TWLRICSIRHSKSLILTSI/HVLH
/185	3/553	A	1239	2607	3092	SDQGWQYRMRRYQNILKEHGI
1					l	KOSMSRKGNCLDNAVVECFFG
1			i		1	
1					1	TLKSECFYLDEFSNISELKDAV1 EYIEYYNSRRISLKLKGLTPIEY
1						RNQTYMPRVNCPLFDTLRIPDI GGVVRARAIAKLLNDTDMAIID
		1				KRRPRANVSOVMHIIGDVAGR
1	i	ŀ				DCVLVDDMIDTGGTLCKAAEA
1						LKERGAKRVFAYATHPIFSGNA
1		ŀ		1		ANNLRNSVIDEVVVCDTIPLSD
	l	1				EIKSLPNVRTLTLSEKYTAARFT
1		1				RDLIAGITYGIIAIPLAMALAIGS
	ł	1				GVAPQYGLYTAAVAGIVIALTG
		1		i		GSRFSVSGPTAAFVVILYPVSO
						OFGLAGLLVATLLLGDLFDSDG
7186	37554	A	7240	1326	3930	NVLRGISAAFFVG*AKAPRNGT
		1				lo
7187	37555	A	7241	3	195	RVDDFVGGAGAPASPGL*OCG
		1				QLQKLIGISIGSLRGLGTKCAVS
		1				NDLTEQEIRTLEHCPNSFF
7188	37556	В	7242	75	402	
7189	37557	Α	7243	1	309	
7190	37558	Α	7244	3	187	
7191	37559	Α	7245	383	1778	
7192	37560	Α	7246	2	447	IREKLIRLQHENKMLKLNQEGS
		1				DNEKIALLQSLLDDANLRKNEL
		1				ETE/Q*VLVPINFPLTTAFAVSH
		1				RFRLVNQRLLEVQSQVEELQKS LODOGSKAEDSVLLKKKLEEH
		1				LEKLHEANNELOKKRAIIEDLE
		1				PRFNNSSLKIEELOEALR
7193	37561	В	7247	80	1042	PRINNSSERIEEEQEAER
7194	37562	A	7248	1	192	
7195	37563	A	7249	3	62	
7196	37564	В	7250	219	230	
7197	37565	Ā	7251	246	594	
7198	37566	Α	7252	I	316	
7199	37567	Α	7253	1	1059	
7200	37568	Α	7254	1	516	EDALEQEKKELQIQVEHYEFQT
		1				RQLELKAKNYADQISRLEERES
1	İ	ļ.				EMKKEYNALHQRHTEMIQTYV
		1				EHIERSKMQQVGGNSQTESSLP
						GRSRKERPTSLNVFPLADGT/CT
		1				CTDRGQARACGGPLAPE*PRPA
		1				AVQLQLPGFVAVPWSERLLPV
						AGVPRSLGREPRLQAALHGS
7201	37569	Α	7255	1	1176	
7202	37570	Α	7256	1	749	
7203	37571	A	7257	]1	691	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequence	Nucleotide location of last codon for last amino aeid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7204	37572	A	7258	2	810	VMMTGYNNGRCPRNSLYSDCII EKETVYLQKKDNEGGGFVLRG AKADTPIEEFTPIPAFPALQYL ESVDEGGVAWQAGLRTGDFL EVNNENVVKGHRQVVNMIR QGGNHLFLKVVTVTINLDPDD TARKKAPPPPKRAPTTALTLRS KSMTSELEELVDKASVRKKKD KPEEIPVASKYBRA-BRMAVEP RVATIKQRPSSCEPAGSDMNS VYERQGIA VMTPTVPGSPKAPF LGIPRGTMRRQKSIGKKCGTPP QKLPLEFGFGT
7205	37573	Α	7259	1	1416	
7206	37574	A	7260	2	1142	
7207	37575	Α	7261	1	576	
7208	37576	Α	7262	21	289	
7209	37577	A	7263	2	372	
7210	37578	A	7264	170	655	VRRRILGALETWICSVTRESTSK PLSSALLSAKLLHRARSRTGLS GRPPKTISQDLOFAAIGSPLTES LNLHSRQALRDCCWTHTIPPPW PICTHARRWRDCCWTHTIPPPW DTVWRFPLSSPVSAAPKQERAS SEPCSWSHWCRCSLSWLSSIPTE GCTPVCSSICLLMATFPMFSLIK IVR
7211	37579	Α	7265	]]	1725	
7212	37580	Α	7266	307	686	PRRTPMKSCKIKEVPIFVFPLRT TRENCLRPIKGYAIYEKAPRSIL KDVHLTRNQCVPIPDRYKWWS WQVCRRPKQWGWTQGPVAPK RSAEFFAAHA*KRRVMLNLR GLDVDSLVIEHIQVNKAP
7213	37581	Α	7267	1	276	
7214	37582	A	7268	1	726	
7215	37583	A	7269	3	231	
7216	37584 37585	A A	7270 7271	3	217	KRKTEGDAKGDKAKVKDESQR
						KKK LEGDAKGDKAKVKDESQK RSARLSAKPAPPKPEPKPKKAP AKKGEKVPKGKKRKADAGKE REGYWRSQVKCIHFL*LYFW*L YSLKYYFI
7218	37586	A	7272	1	1188	
7219	37587	A	7273	5	365	
7220	37588	A	7274	1	453	

SEQ ID	ISEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide Incation of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \spossible nucleotide insertion)
				sequence		
7221	37589	ĪΑ	7275	1	441	RQPAHPGTSSAAAAPRKRSAAA
						HAGVAVAASARLPPCAGCGLR
						AAPPLLASSARLRALRRP\GGL
		l				WAAGCAPAAGQLCTAAGSAAF
						GALQRCGGRHGITRPWCAEIAS
		1				AG*GSGGSRWGCWPCPCLLRT
						CTSHPLSSPLPFTHGSLQASFSL
					1	TRDCVSSTKTLWVWLEVQR
7222	37590	Α	7276	2	1957	
7223	37591	Α	7277	1	678	
7224	37592	Α	7278	1	720	
7225	37593	A	7279	190	2947	QALQRGLLSR/DRAPCSSKLSW
						RS/SPRRRAGTGPVQEEVALKP
						VLLRHPVQPVIRVKLPRICLLEE
1	İ	1				AGQLRGVHRLESVEEYYEADG
1						AEWGPPDTAMLESLPEMAGKH
						SLPQLLDSSSASQPGAIQIIYS\IL
						YQIHYLKHLLSSYWGASQWKH
1						TRHTHYFESLW*EHLPS*KYQK
	į.					REKWADLTRSLENP\GQQPRDS
1	1					WEPSGFWALPQAGDSCQTSQSF
1						RKPTGPPKPSPPPEEGRLLR/CPT
1						MPVMRKSLTE
7226	37594	A	7280	3	439	
7227	37595	Α	7281	1	273	
7228	37596	A	7282	2	1664	
7229	37597	A	7283	1	7511	
7230	37598	A	7284	1	5046	
7231	37599	A	7285	42	8716	
7232	37600	A	7286	2	201	COLORDO COMO DILLI
7233	37601	A	7287	2	797	CS/GSPPTCRQAQTSLEVALYM
						FLQNPDTEAVLVAMSCFCHLCE
						EADTQCGVDEVSVHNLLPNSN
1						TFMEFACQQCDVNSPPVGPVSE
						HKGSMISVMSSEGNADTPVSK
l	1				1	YMDQLLSLMVCNLEKVGLQIP
1					1	TNDKDLVLLTDTNTQFVEQTL
1	1				1	DIMKNLLDNHTEGSPEHLEQAS
1						IETMMLNLVRNKMVEYLTDW
			1			VMGTSNQAADDDVKCLTSRI/D
1						HPGGTLL*GQPRPELPAGLPRQ
						PASPGPRHPGASCGWPRAPPDS
7224	27602	_	7288	56	9660	APGGPGRER
7234	37602 37603	A B	7289	278	8669 2333	
7236	37603	A	7290	1	423	
1230	3/604	I <sup>A</sup>	1290	1	1443	L

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	tocation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
		<u>_</u>				
7237	37605	A	7291	2	1688	PLYFHSPPAWLCSPSPPSARLYL
		l				ELRKLPATLPWSSVTDTGSYSA
1					ŀ	GRRERGGEGEGRGRRVRVADH
						RSALPRTGPQGSEEELANMQGL
						\VERLERAVSRLESL\SAESHRPP
						GN\CGEVNGVIA\GVAPSRGKPL
						HKLMDSMVAEF\LKNSRILSGD
						VETLAEIVHSAFQAQRAFLLMA
						SQYQQPHENDVAALLKPISEKI\
l		l				KEIQTFQRE/RTRGSNMFNHLSA
1	l				ŀ	VSESIPALGW\IAVSPKPGPYVK
						EMNDAATFYTNRVLKDYKHSD
					Î	LRHVDWVKSYLNIWSELQAYI
		l				KEHHTTGLTWSKTGPVASTVS
						AFSVLSSGPGLPPPPPPLPPPGPP
						PLFENEGKKEESSPSRSALFAQL
		1			1	NOGEAITKGLRHVTDDOKTYK
						NPSLRAQGGQTQSPTKSHTPSP
		l		l		TSPKSYPSQKHAPVLELEGKKW
1		1				RVEYQEDRNDLVISETELKQVA
						YIFKCEKSTIOIKGKVNSIIIDNC
		1				KKLGLVFDNVVGIVEVINSQDI
İ						OIOVMGRVPTISINKTEGCHIYL
l				l		SEDALDCEIVSAKSSEMNILIPQ
						DGDYREFPIPEOFKTAWDGSKL
7238	37606	В	7292	44	355	DOD TREET IN EQUALITY IN DOCKE
7239	37607	Ā	7293	1	3623	SEKEKEELERLQKEEEERKKRL
1.20		Γ.		ľ		OLYVFVMRCIAYPFNAKOPTD
1						MARRQQKISKQQLQTVKDRFQ
		l				AFLNGETQIMADEAFMNAVOS
						YYEVFLKSDRVARMVQSGGCS
		l				ANDSREVFKKHIEKRVRSLPEID
				ł		GLSKETVLSSWMAKFDAIYRG
				ì		EEDPRKQQARMTASAASELILS
1		1				KEOLYEMFONILGIKKFEHOLL
						YNACQLDNPDEQAAQIRRELD
		1				GRLOMADOIARERKFPKFVSKE
			1			MENMYIEELKSSVNLLMA
7240	37608	В	7294	1	1555	MENNTTEELKSSVILLIMA
7241	37609	A	7294	1	1056	
7242	37610	В	7296	54	2173	
7242	37611	A	7297	1	984	
7243	37612	В	7298	95	1350	
7244	37012	ь	1270	73	1330	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	Incation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7245	37613	Α	7299	1	2569	MDGAKAFFSAVAAGFVHLTCQ
						LQWQWQHGGVHAHQLWQLA
	l					SGYRDACFCVSTYSSGPSEFPGF
ł						TLGTLNELAIDLEERKHRRKAK
	İ					VWKGEGGGLRSPRQSLLAFRA
						VLASRGTRSCHVSPYLGVSGAL
1						SSPNPHPSTTGAGPIPPVQRWGL
						PQINQKNREIAIPLTLGMSTHLR
				ŀ		RGCKNMSRFSPSLHCCTTPISTN
	l					FTDPGSHCKGAHGDICLLIQNL
	1					KGALPMSINRSYFNAHPLLQISE
						AVTFKDVAVVFTEEELGLLDPA
						QRKLYRDVMLENFRNLLSVGN
		ŀ			1	QPFHQDTFHFLGKEKFWKMKT
		1			1	TSQREGNSGGKIQIEMETVPEA
1	1	l				GPHEEWSCQQIWEQIASDLTRS
	1			1		QNSIRNSSQFFKEGDVPCQIEAR
		ŀ		1		LSISHVQQKPYRCNECKQSFSD
				1		VSVFDLHQQSHSGEKSHTCGEC
						GKSFCYSPALHIHQRVHMGEK
		ŀ				CYKCDVCGKEFNQSSHLQTHQ
			İ			RVHTGEKPFKCGQCGKGFHSRS
					1	ALNVHCKLHTGEKPYNCEECG
						KAFIHDSQLQEHQRIHTGEKPF
						KCDICGKSFRVRSRLNRHSMVH
		l				TGEKAFRCDTCGKNFRQRSAL
1				1		NSHSMVHIEEKPYKCEQCGKGF
1						ICRRDFCKHQMVHTGEKPYNC
		1				KECGKTFRWSSCLLNHQQVHS
1		1	1		1	GQKSFKCEECGKGFYTNSRRSS
1		1		1		HQRSHNGEKPYNCEECGKDYK
		1				RRLDLEFHQRVHTGERPYNCK
7246	37614	Α	7300	2	326	
7247	37615	Α	7301	166	443	

sequence   09/540,217   codum for peptide   sequence   detetion,   possible nucleotide insertion)   sequence     detetion,   possible nucleotide insertion)   sequence     detetion,   possible nucleotide insertion)	SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
1   2692	NO:		hod				
LKRRNIOTSWORLTPIIKWHYV LMIGPGEKEAGRNLGIFGKWT FPKIPAKRLRESNCPVDAQEIW LPQAFREYLGRRONFGFGRT FEWEYSICSVESWEL WLRQA DSGDSGKCSPDACGIIDTSGLR ACHCVLTRLWHVSGRIPPSFKI HHPGVCKFPKVSGKMTTFKE, VTFKDVAVVFTEELGLLDPA RKLYDWMLENFRNLLSVGH FPHQDTCHFLRE\EKFWMGT ATQREGNSGKQHTEMETVPE AGTTHEETSCRQWEQIASDLT SQDTTISNSQLFEQDDNSQIK, RLSIHWXTETSEGRTCKKSFSI VSVLDHQULQSREKSHTCDE GKSFCYSSALRIHQRVHMGEK YNCDVCGKEFNGSHQQHLOR HTGEKPFKCEQCGKGFSRSGI YVHRKLHTGVKPHICEKGGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANLNRISMYHM REKPFRCDTCGKSFGLKSALN HRWHTGEKRYKCEEGGKFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHVRVISG ETTFKCEEGGKFTYNSQRYSI QRAHSGEKPYTCEECGKGFF RLDLDFHQRVHRGEK CKSFGWSSALLHORHINGE FFKCECGKFTYNSQRYSI QRAHSGERPYTCEECGKGFF RLDLDFHQRVHRGEKPYNCKE CKSFGWASGLLNHQRIHSGE PFKCEECGKFTONSQLYTHRI TANDAT TO THE TOTAL		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
LMIGGEREAGRNLGIFGKWT FPKIPAKRLRESNCPVDAQEIW LPQAFREYLGRGNTGFGRTT EFWEVESICSVESWELWLRQA DSGOSGKCSPAGCIIDTSGIR AGHCYLTRLWHVSGRIPPSFKI HHPGVCKFPKVGGKMTTFKE/ VTFKDVAVVFTEELGLLDPA RKLYRDWMLENFRNLLSVGH PPHQDTCHFLREKFWMMGT ATQREGNSGKIQTEMETTVPE AGTHEEFSCKQIWEQIASDLTR SQDTTISNSQLFEQDDNPSQIK, RLSIHWKTETSEGRTCKKSFSE VSVLDLHQQLGSRESHTCDE GKSPCYSSALRIHGRVHMGEK YNCDVGKEFNSGSHQQHROG HTGEKPFKCEQCGKGFSRRSGI YVHRKLHTGVKPHICEKCGKA FIHDSQLGEHGRHTGEKPFKC DICCKSFRSRANLNRHSWHM REKPFRCDTCGKSFGLKSALN HRMVHTGEKRYKCEECGKFFI YKQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHIVRVIBG ETTFKCEECGKCFYTNSQRYSI QRAHSGERPYRCEECGKOFK RLDLDFPHQRVHRGEK PYNCKE CGKSFGWASGLLNHQRIHSGE PFKCEECGKFTQNSQLYTHRI  7249 37617 A 7303 I 585 KRTAISPROAFCTRODLNEEEA AQVMGVKDPAPASTGSVLAD TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGRGRI MKTVTQGSQC/SLADPASHLE VCDHLTYSNETEPVRALLPDEI KEVKPALSMSNLHEATMPVL LDHLRETRADKKRLRKALRFE EQFFKQTGRSPQKEDRIPMADE	7248	37616	A	7302	1	2692	MDPGTLQSASQGPTAINPCDYV
PFKIPAKRURESNCPVDAQEIW LPQAFREYLGRGNTGPGRRT EFWEVESICSVESWELWLRQA DSGDSGKCSPDACGIIDTSGLR AGHCVLTRL WHYSGRIPPSKI HHPGVCKFPKVGGKMTTFKE/ VTFKDVA VVFTEELGLILDPA RRL VRDVMLENFRNLLSVGH PFHQDTCHFLREEKFWMMGT ATQREGNSGGKIQTEMETVPE AGTHEEFSCKQIWEQIASDLTR SQDTTISNSQLFEQDDNIPSQIK. RLSIHWXTETSEGRTCKKSFSE VSVLDLHQQLQSREKSHTCDE GKSFCYSSALRIHQRVHMGEK YNCDVCGKEFNQSSHQQHHQR HTGEKPFKCEQCGKGFSRRSGI YVHRKLHTGVKHIECKSGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANLNRHSMVHM REKPFRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEEGGKFF YRQDLYKHQIDHTGEKPYNCK EGGKSFRWASGLSRIKVNHSG ETTFKCEECGKGFYTNSQRYSI QRAHSGEKPYRCEECGKGYF RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLSRIKVNHSG ETTFKCEECGKGFTYNSCRYSI QRAHSGEKPYRCEECGKGYF RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLSHIKVNHSG ETTFKCEECGKGFTNSQRYSI QRAHSGEKPYRCEECGKGYF RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLSHIKVNHSG ETTFKCEECGKGFTNSQRYSI QRAHSGEKPYRCEECGKGYF RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLSHIKVNHSG ETTFKCEECGKGFTNSQRYSI QRAHSGERPYRCEECGKGYF RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLSHIKVNHSG ETTFKCEECGKGFTNSQRYSI QRAHSGERPYRCEECGKGYF RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLSHIKVNHSG ETTFKCEECGKGFTNSQRYSI QRAHSGERPYRCEECGKGYF RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLSHIKPNHSQL ETTFKCEECGKGTTNSQLYTHRI VGDMLTVSNSTEPVRALLPDEI KEVFRPALSMSNLHGATMPVU LDHLETRADKKRLRKALRFE EQFFKKTGRSPQKEDRIPMADE YY			1			1	LKRRNIQTSWQRLTPIIKWHVY
LPQAFREYLGRRGNFGPGRTT EFWEVESICSVESWELWLRQA DSGDSGKCSPDACGIIDTSGLR AGHCYLTRLWHVSGRIPPSEKI HHPGVCKFPKYGGKMTTFEKE, VTFKDVAVVFTEELGLLDPA RKLYRDVMLENFRNLLSVGHC PFHQDTCHFLREEKFWMMGT ATQREGNSGCKQTEMETVPE AGTHEEFSCKQUFGOJASDLTR SQDTTISNSQLFEQDDNSQLK. RLSIHVKTETSEGRTCKKSFSL VSVLDLHQQLGSREKSHTCDE GKSFCYSSALRIHGRVHMGEK YNCDVGGKEFNGSSHQCHGM HTGEKPFKCEQGGKGFSRSGI YVHRKLHTGVKPHICEKCGKA FIHDSQLQEHGRIHTGEKPFKC DICCKSFRSRANLNRISMVHM REKPFRCDTCGKSFGLKSALN HRWVHTGEKRYKCEEGGKFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRIHVRVHSG ETTFKCEEGGKCFYTNSQRYSI QRAHSGEKPYRCEEGGKGFK RLDLDFHQRVHRGEK CGKSFGWASCLLNHQRIHSGEI PFKCEECGKFTQNSQLYTHRI  7249 37617 A 7303 I 585 KRTAISPROAFETRQDLNEEEA AQVHGVKDPAPASTGSVLAD TDSAGN*ARGEPHKAAL*PIQN YQANLVNTFPYSNNSGRGRRI MKTVTQGSQQPSLADPASHLE VCDHLITYSNETEPVRALLPDEI KEVKPALSMSNLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE			l				LMIGPGEKEAGRNLGIFGKWTP
EFWEVESICSVESWEL WLRQA DGGDSGKCSPDACGIIDTSGLR AGHCVLTRLWHVSGRIPPSTSKI HHPGVCKFFKVGGKMTTFKE VTFRDVAVVTFEEELGLLDPA RKLYRDVMLENFRNLLSVGH PPHQDTCHELREERFWMMGT ATQREGNSGGKIQTEMET.VPE AGTHEFSCKQIWEQIASDLTR SQDTTISNSQLFEQDDNS9QIK, RLSIIHVKTETSEGRTCKKSFSE VSVLDLHQQLQSRESKHTCDE GKSFCYSSALRIHORVHMGEK YNCDVCGKEFNQSSHQHOR HTGEVFKCEQGGKGFRSRSGI YYHRKLHTGVKPHICEKGGKA FIHDSQLGEHGRHTGEFFFKC DICCKSFRSRANLNRIHSWHM REKPFRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEEGGKFT YRQDLYKHQIDHTGEKPYNCK EGGSFRWASGLSRIHVRIVES ETTFKCEEGGKGFYTNSQRYSI QRAHSGERPYRCEEGGKGYK RLDLDFHQRVHRGEKPYNCK CGKSFGWASCLLNHQRIHSGEI PFKCEECGKFTPRONQLYTHRI  7249 37617 A 7303 I 585 KRTAISPROAFSTRODLNEEA AQVHGVKDPAPASTGSVLAD TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGGGRI MKTVTQGSQQPSLADPASHLE VGDHLTYSNETEPVRALLPDEI KEVKPALISMSLIEATMPUL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			1				FPKIPAKRLRESNCPVDAQEIW
DSGDSGKCSPDACGIIDTSGIR AGHCYLTRLWHVSGRIPPSFKI HHPGVCKPFKVGGKMTTFKE, VTFKDVAVVFTEELGLLDPA RKLVRDVMLENFRNLLSVGH PHOPOTCHFLREEKFWMMGT ATQREGNSGGKIQTEMETVPE AGTHEEFSCKQIWEQIASDLTR SQDTTISNSQLFEQDDNPSQIK. RLSIHWXTETSEGRTCKKSPSI VSVLDLHQLQSREKSHTCDE GKSFCYSSALRIHQRVHMGEK YNCDVCGKETNQSHQQHOR HTGEKPFKCEQCGKGFSRSGI VYHRKLHTGVKPHICEKGGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANINRISMVHM REKPFRCDTCGSFGLKSALN HRMVHTGEKRYKCEECGKFF YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHVRVISG ETTFKCELEGGKGFYTNSQRYSI QRAHSGEKPYRCEECGKGFF RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLLMHQRIHSGE PFKCECGKFTRONSQLYTHRI TATAL TATA						į .	LPQAFREYLGRRGNFGPGRRTC
AGHCYLTRL WHVSGRIPPSEKI HHPROVCKPPKVGGKMTTFKE VTFKDVAVVFTEELEGLLDPA RKLYRDWALENFRNLLSVGH PPHQDTCHELREEKFWMMGT ATQREGNSGGKIQTEMETTVE AGTHEEFSCKQIWEQIAS DLTR SQDTTISNSQLFEQDDNPSQIK. RLSIHWKTETSEGRTCKKSFSL VSVLDLHQQLQSRESHTCDE GKSPCYSSALRIHORVHMGEK YNCDVCGKEFNQSSHQQIHQR HITGEKPFKCEQCGKGFSRASGI YYHRLHTGVKPHICEKGGKA FIHDSQLQEHQRHITGEKPFKC DICCKSFRSRANLNRHSWHM REKPFRCDTCGKSFGLKSALN HRMVHTGEKRYKCEECGKRFI YRQDLYKHQIDHTGEKPYNCK EGGSFRWASGLSSRINKVHSG ETTFKCEECGKGFTNSQRYSI QRAHSGEKPYRCEECGKGFF RLDLDFPHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRIHSGE PFKCEECGKFTTNSQRYSI QRAHSGEKPYRCEECGKGFT KRUDLFFROMOLYTHENGE FFKCEECGKFTTNSQRYSI QRAHSGEKPYRCEECGKGFT RLDLDFPHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRIHSGE PFKCEECGKFTTNSQRYSI QRAHSGERPTRANSOLYTHEL VQDHLTYSNETEPVRALLPDEI KEVKPPALSMSNLIEATMPVU LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY						ŀ	EFWEVESICSVESWELWLRQA
HHPGVCKFPKVGGKMTTFKE/ VTFKDVAVVFTEELGILDPA RRLYRDVMLENFRNLLSVGH PPHODTCHFLREEKFWMMGT ATQRGNSGGKJGTMETVYP AGTHEFSCKQIWEQIASDLTR SQDTTINNSQLFEQDDNPSQIK. RLSIHVXTETSEGRTCKKSFSI VSVLDLHQQLQSREKSHTCDE GKSPCYSSALRIHORVHMGEK YNCDVCGKEFNQSSHQQIHQR HTGEKPFKCEQCGKGFSRSGI YVHRKLHTGVKHJECKGKGK FIHDSQLQEHQRIHTGEKPFKC DICKSFRSRANLNRISMVHM REKPFRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEECGKEF YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRIHVNHSG ETTFKCEECGKGFYTNSQRYSI QRAHSGEKPYRCEECGKGYFR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLLSHANDRIHSGE PFKCECGKGFTQNSQLYTHRI CGKSFGWASGLLSHANDRIHSGE PFKCECCGKFTQNSQLYTHRI TOSAGN*ARGEPHKAAL*PIQN YQANLVNTFPYSNNSGGRGRI MKTVTQGSQQPSLADPASHLE VGDHLTYSNETEPVRALLPDEI KEVKPALSMSNLIEATMPVU LDHLRETRADKKRLRKALRFE EQFFKKTGRSPQKEDRIPMADE YY			1				DSGDSGKCSPDACGIIDTSGLR
VTFKDVAVVFTEELGLLDPA RKLYRDVMLENFRNLLSVGHE PFHQDTCHFLREEKFWMMCT ATQREGNSGCKIQTEMETVPE AGTHEEFSCKJWEGOLSDLTR SQDTTISNSQLFEQDDNPSQIK. RLSIHVKTETSEGRTCKKSFSL VSVJ.DLHQQLQSREKSHTCDE GKSPCYSSALRIHQRVHMGEK YNCDVCGKEFNQSSHQQHING HTGEKPFKCEQGGKGFSRSG YVHRKLHTGVKPHICEKCGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANLNRISMVHM REKPFRCDTCGSFGLKSALN HRMVHTGEKRYKCEEGGKFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRIHVRVHSG ETTFKCEEGGKFFYNNSQRYSI QRAHSGEKPYRCEEGGKFFK RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRIHSGE PFKCEECGKFTQNSQLYTHRI 7249 37617 A 7303 1 585 KRTAISPRDAFETRQDLNEEEA AQVHGVKDPAPASTQSVLAD TDSAGN*ARGEPHKAAL*PIQN YQANLVNTFPYSNNSGRGRIR MKTVTQGSQQPSLADPASHLE VCDHLTYSNETEPVRALLPDEI KEVKPALSMSNLIEATMPVL LDHLRETRADKKRLRKALRFE EQFFKQTGRSPQKEDRIPMADE YY			1				AGHCYLTRLWHVSGRIPPSFKL
RELYRDWILENFRNLLSVGHK PFHQDTCHFEREIKFWMMGT ATQREGNSGKIQTEMETVPP AGTHEEFSCKQIWEQIASDLTR SQDTTISNSQLFEQDONPSQLK. RLSIIHVKTETSEGRTCKKSFSE VSVLDHQQLQSREKSHTOE GKSFCYSSALRIHQRVHMGEK YYCDVCGKEFNQSSHQQHQK HTGEKPFKCEQCGKGFSRRSG YYHRKLHTGVKPHICEKGKA FIHDSQLGEHQRHTGEKPFKC DICCKSFRSRANLNRHSWYHM REKPFRCDTCGKSFGLKSALNS HKMVHTGEKRYKCEECGKEFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHIVRYHSC ETTFKCEECGKCFYTNSQRYSI QRAHSGEKPYRCEECGKGFYRNSQRYSI QRAHSGEKPYRCEECGKGFYRNSQRYSI QRAHSGEKPYRCEECGKGFYRNSQRYSI QRAHSGEKPYRCEECGKGFYNCE CGKSFGWASCLLNHQRHINGGE PFKCEECGKFFTQNSQLYTHRI  7249 37617 A 7303 I 585 KRTAISPROAFETRQDLDEEEA AQVMGVKDPAPASTGSVLAD TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGGGRI MKTVTQGSQCGSLADPASHLE VGDHLTYSNETEPVRALLPDEI KEVKPALISMSLHEATMPUL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY						ŀ	HHPGVCKFPKVGGKMTTFKEA
PPHQDTCHFLREEKFWMMGT ATQREGNSGGKIQTEMETVPE AGTHEEFSCKQIWEQIASDLTR SQDTTISNSQLFEQDDNPSQIK. RLSIIHVXTETSEGRTCKKSFSI VSVLDLHQQLQREKSHTCDE GKSFCYSSALRIHQRVHMGEK YYNCDVCGKEFNQSSHQQHHQR HTGEKPFKCEQGKGFSRRSGI YVHRKLHTGVKPHICEKGGKA FIHDSQLQEHQRIHTGEKPFKC DICKSFRSRANIN,RISHMYHM REKFPRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEEGGKFI YRQDLYKHQIDHTGEKPYNCK ECGKSFR WASGLSRHVRVISG ETTFKCELEGGKGFYTNSQRYSI QRAHSGEKPYRCEEGGKGYFR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLKLMQRHINGE FFKCEEGGKGFTYNSQRYSI QRAHSGEKPYRCEEGGKGYFR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLKHQRHINGE FFKCEEGGKFTNSQLYTHRI TZ249 37617 A 7303 1 585 KRTAISPKDAFETRQDLNEEEA AQVHGVKDPAPASTGSVLAD TDSAGN*ARGEPHKAAL*PIQN YQANLVNTFPYSNNSGGRGRI MKTVTQGSQQPSLADPASHLE VCDHLTYSNETEPVRALLPDEI KEVKPALSMSNLHEATMPVU LDHLRETRADKKRLRKALRFE EQFFKKTGRSPQKEDRIPMADE YY	1						VTFKDVAVVFTEEELGLLDPAQ
ATQREGNSGCKIQTEMETTVPE AGTHEEFSCKQIWEQIASDLTR SQDTTISNSQLFEQDDNPSQIK. RLSIHWKTETSEGRTCKKSFSE VSVLDLHQQLQSRESHTCDE GKSFCYSSALRIHORVHMGEK YNCDVCGKEFNOSSHQQHING HTGEKPFKCEQCGKGFSRRSGI YYHRKLHTGVKPHICEKCGKA FIHDSQLQEHQRHITGEKPFKC DICCKSFRSRANLNRHSWYHM REKPFRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEECGKRFI YKQDLYKHQIDHTGEKPYNCK EGGSFRWASGLSRHIVRVIBG ETTFKCEECGKGFYTNSQRYSI QRAHSGEKPYRCEECGKGFK RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRIHSGE PFKCEECGKFTQNSQLYTHRI 7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLDEEEA AQVHGVKDPAPASTQSVLAD TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGGGRI MKTVTQGSQQPSLADPASHLE VCDHLTYSNETEPVRALLPDEI KEVKPALSMSNLIEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			l				RKLYRDVMLENFRNLLSVGHQ
AGTHEEFSCKQIWEQIASDLTR SQDTTISNSQLFEQDDNPSQIK. RLSIHVKTETSEGRTCKKSPSIK VSVLDLHQQLQREKSHTCDE GKSFCYSSALRIHORVHMGEK YNCDVCGKEFNQSSHQQIHQR HTGEKPFKCEQCGKGFSRSGI YVHRKLHTGVKPHIGEKCGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANI,NRIHMVHM REKPFRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEECGKEF YNQDLYKHQIDHTGEKPYNC ECGKSFRWASGLSRIHVRHSG ETTFKCEECGKGFYTNSQRYSI QRAHSGEKPYRCEECGKGYFR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLIKHNQRIHSGE PFKCEECGKGFTQNSQLYTHRI CGKSFGWASGLIKHQRIHSGE PFKCEECGKFTQNSQLYTHRI TZ249 37617 A 7303 I 585 KRTAISPKDAFETRQDLEEEA AQVHGVKDPAPASTGSVLAD TDSAGN*ARGEPHKAAL*PIQN YQANLVNTFPYSNNSGGRGRI MKTV/TQGSQQPSLADPASHLE VCDHLT/NSNETEPVRALLPDEI KEVKPALSMSNLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKKTGRSPQKEDRIPMADE YY			l				PFHQDTCHFLRE\EKFWMMGT
SODTTISNSQLFEQDDNPSQIK. RLSIHVKTETSEGRTCKKFSEL VSVLDLHQQLQSREKSHTCDE GKSPCYSSALRIHQRVHMGEK YNCDVCGKETNQSSHQQHING HTGEKPFKCEQGGKGFSRSGI YVHRKLHTGVKPHICEKCGKA FIHDSQLQEHQRIHTGEKPFKCE DICCKSFRSRANLNRISMVHM REKPFRCDTCGSFGGLKSALN HRWHTGEKRYKCEEGGKFI YRQDLYKHQIDHTGEKPPNCK ECGKSFRWASGLSRIHVRVHSG ETTFKCEEGGKFTYNSQRYSI QRAHSGEKPYRCEEGGKGYFR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRIHSGEI PFKCEECGRFTQNSQLYTHRI 7249 37617 A 7303 I 585 KRTAISPRDAFETRQDLNEEEA AQVHGVKDPAPASTQSVLAD TDSAGN*ARGEPHKAAL*PIQN YQANLVNTFPYSNNSGRGRRI MKTVTQGSQQPSLADPASHLE VCDHLTYSNETEPVRALLPDEI KEVKPALSMSLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY					l		ATQREGNSGGKIQTEMET\VPE
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VSV.DLHOQLOREKSHTCDE GKSFCYSSALRIHQRVHMGEK YYNCDVCGKEFNQSSHQQHIPG HTGEKPFKCEQGKGFSRRSGI YVHRKLHTGVKPHICEKGGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANLNRISMYHM REKPFRCDTCGSFGLKSALN HRMVHTGEKRYKCEECGKFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHVRVISG ETTFKCEECGKGFYTNSQRYSI QRAHSGEKPYRCEECGKGYFR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLLSHANDRIHSGE PFKCEECGKFTRONSQLYTHRI GRAHSGEKPYRCHECTOR TÖDAGN*ARGEPHKAAL*PIQN YQANLVNTFPYSNNSGGRGRI MKTVTQGSQQPSLADPASHLE VCDHLTYSNETEPVRALLPDEI KEVKPPALSMSNLIEATMPVU LDHLRETRADKKRLRKALRFE EQFFRKTGRSPQKEDRIPMADE YY			1	i		i	SQDTTISNSQLFEQDDNPSQIKA
GKSFCYSSÄLRIHORVHMGEK YNCDVCKEFNQSSHQQIHOR HTGEKPFKCEQGGKGFSRASGI YYHRKLHTGVKPHICEKGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANLNRIHSMYHM REKPFRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEECGKRFI YRQDLYKHQIDHTGEKPYNCK EGGSFRWASGLSRIHVRYHSG ETTFKCEECGKGFTNSQRYSI QRAHSGEKPYRCEECGKGFY RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRIHSGE PFKCEECGKFTGNSQLYTHRI 7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLDEEA AQVHGVKDPAPASTGSVLAD TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGGRI MKTVTQGSQQPSLADPASHLE VGDHLTYSNETEPVRALLPDEI KEVKPPALSMSLIEATMYUL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			ŀ		l		RLSIIHVKTETSEGRTCKKSFSD
YNCDVCGKEFNQSSHQQIHOR HTGEKPFKCEQCGKGFSRRSGI YYHRKLHTGVKPHICEKCGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANI,RNISMVHM REKPFRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEECGKEFI YRQDLYKHQIDHTGEKPYNC ECGKSFRWASGLSRIHYNISG ETTFKCEECGKGFYTNSQRYSI QRAHSGEKPYRCEECGKGYKR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLISHIVNISG ETFKCEECGKGFYNSQRYSI QRAHSGEKPYRCEECGKGYKR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASGLINHQRIHSGE PFKCEECGKFTQNSQLYTHRI AQVHGVKDPAPIASTGSVLAD TDSAGN*ARGEPHKAAL*PIQN YQANLVNTFPSYSNSGGRGRI MKTV/TQGSQQPSLADPASHLE VGDHLTYSNETEPVRALLPDEI KEVKPPALSMSNLIEATMPVU LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY		ľ					VSVLDLHQQLQSREKSHTCDEC
T7249 37617 A 7303 I 585 KRTAISPROAFSTQOLSEFA AQVHGVKDPHKGEKGKA PIHOSQLOEHGRUHTGEKPFKC DICCKSFRANLNRISMVHM REKPFACHTGKSFGLKSALN. HRMVHTGEKRYKGEEGGKFI YRQDLYKHQIDHTGEKPYNCK EEGKSFRWASGLSRIVRVHSGE ETTFKCEEGGKFFYTNSQRYSI QRAHSGEKPYRCEEGGKFF RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRIHSGE PFKCEEGGKFTQNSQLYTHRF RLDLDFHQRVHRGEKPYNCKE AQVHGVKDPAPASTQSVLAD TDSAGN*ARGEPHKAAL*PIQN YQANLVNTFPYSNNSGRGRI MKTVTQGSQQPSLADPASHLEVGDHLTYSNETEPVRALLPDEF KEVKPALSMSNLIFATMPVL LDHLRETRADKKRLRKALRFE EQFFKQTGRSPQKEDRIPMADE YY			l		ł		GKSFCYSSALRIHQRVHMGEKL
YVHRKL HTGVKPHICEKCGKA FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANLNRISMVHM REKPFRCDTCGSSFGLKSALN HRMVHTGEKRYKCEEGKRFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRIHVRVIBG ETTFKCEEGKGFFYTNSQRYSI QRAHSGEKPYRCEEGKGYK RLDLDFHQRVHRGEKPYNCKE CCKSFGWASCLLNHQRIHSGEI PFKCEEGKRFTQNSQLYTHRI 7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLNEEEA AQVHGVKDPAP/ASTQSVLAD TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPSYNSGGGRGI MKTV/TQGSQQPSLADPASHLF VGDHLTVSNETEPVRALLPDEI KEVKPPALSMSLHEATMPUL LDHLRETRADKKRLRKALREF EQFFRKQTGRSPQKEDRIPMADE YY			1			1	YNCDVCGKEFNQSSHQQIHQRI
FIHDSQLQEHQRIHTGEKPFKC DICCKSFRSRANLNRHSMVHM REKPFRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEECGKEFI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHVRVISG ETTTKCEECGKGFYTNSQRYSI QRAHSGEKPYRCEECGKGFYR RLDLDFHQRYHRGEKPYNCKE CGKSFGWASGLNHQRHISGE PFKCEECGKGFTYNSQLYTHRI 7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLNEEEA AQVHGWKDPAPASTGSVLADH TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGRGRI MKTVTQGSQQPSLADPASHLE VCDHLTYSNETEPVRALLPDEI KEVKPPALSMSNLIEATMPVU LDHLRETRADKKRLRKALREF EQFFRKTGRSPQKEDRIPMADE YY	i						HTGEKPFKCEQCGKGFSRRSGL
DICCKSFRSRANLRRIHMVHM REKPRCDTCGKSFGLKSALNS HRMVHTGEKRYKCEEGKKFI YRQDLYKHQIDHTGEKPYNCK EGGSFRWASGLSSRHIVRVISG ETTFKCEEGGKCFTYNSQRYSI QRAHSGEKPYRCEEGGKCYKFI RLDLDFHQRVHRGEKPYNCKE GCKSFGWASCLLNHQRIHSGE PFKCEEGKBTFQNSQLYTHET 7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLNEEA AQVHGVKDPAPASTQSVLAD TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGGRI MKTVTQGSQCPSLADPASHLE VGDHLTYSNETEPVRALLPDEI KEVKPPALSMSALIEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY		ŀ					YVHRKLHTGVKPHICEKCGKA
REKPRCDTCGKSFGLKSALNS HRMVHTGEKPYKCECGKFI YRQDLYKHQIDHTGEKPYNCK EGGKSFRWASGLSRIIVRVISG ETTFKCEEGGKGFFYNSQRYSI QRAHSGEKPYRCECGKGYKR RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLWHQRIHSGE PFKCEEGGKFTQNSQLYTHRI AQVHGVKDPAPASTGSVLAD TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPSYNSGGRGRI MKTV/TQGSQQPSLADPASHLE VGDHLTVSNETEPWRALLPDEI KEVKPPALSMSLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY		ŀ	l				FIHDSQLQEHQRIHTGEKPFKC
HRMVHTGEKRYKCEEGGKEI YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHVRVHSG ETTFKCEEGGKCFYTNSQRYSI QRAHSGEKPYRCEEGGKCFK RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRIHSGE PFKCEEGGKEFTQNSQLYTHRI 7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLNEEA AQVHGVKDPAPASTQSVLADI TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGRGRIR WKTVTQGSQQPSLADPASHLE VCDHLTYSNETEPVRALLPDEI KEVKPPALSMSLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY							DICCKSFRSRANLNRHSMVHM
YRQDLYKHQIDHTGEKPYNCK ECGKSFRWASGLSRHVRVHSG ETTKCEECGKGFYNSQRSY QRAHSGEKPYRCEECGKGYK RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLNHQRHINGEI PFKCEECGKRFTQNSQLYTHRI 7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLNEEA AQVHGVKDPAP/ASTQSVLAD TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNSGGRGRI MKTV/TQGSQQPSLADPASHLF VGDHLTYSNETEPVRALLPDEI KEVKPPALSMSNLIEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY		į.	1				REKPFRCDTCGKSFGLKSALNS
ECGKSPRWASGLSRIVRVHSC ETTFKCEECGKGFYTNSQRYSI QRAHSGEKPYRCEECGKGYK RLDLDFHQRVHRGEKPYNCKE CGKSFGWASCLLWHQRHINGE PFKCEECGKRFTQNSQLYTHRI  7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLNEEEA AQVHGVKDPAPASTGSVLADI TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGRGRI MKTV/TQGSQQPSLADPASHLE VCDHLTVSNETEPVRALLPDEI KEVKPPALSMSLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKKTGRSPQKEDRIPMADE YY		ľ	l				HRMVHTGEKRYKCEECGKRFI
7249 37617 A 7303 I 585 KRTAISPKDAFETROLNEER AQVHGVKDPAPASTQSVLAD TDSAGN**AQEHKAAL*PIQN TOSAGN**AQEHKAAL*PIQN TOSAGN**AQEHKAAL*PIQN TOSAGN**ARQEHKAAL*PIQN TOSAG							YRQDLYKHQIDHTGEKPYNCK
QRAHSGEKPYRCECGKÖYKR RLDLDFHQRVHRGEKPYNCKE CCKSFGWASCLLNHQRIHSGE PFKCEECGKRFTQNSQLYTHRI 7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLNEEEA AQVHGVKDPAP/ASTQSVLADU TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGRGRI MKTV/TQGSQQPSLADPASHLF VGDHLTVSNETEPVRALLPDEI KEVKPPALSMSLHEATMYU LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY							ECGKSFRWASGLSRHVRVHSG
RLD.DFHQRVHRGER.PYNCKE CGKSFGWASCLLNHQRIHSGEI PFKCEECGREFTQNSQLYTHEI 7249 37617 A 7303 I 585 KRTAISPRDAFETRODLNEEA AQVHGVKDPAPASTQSVLADI TDSAGN*ARGEPHKAAL*PIQN YQANLVNTFPYSNNSGRGRRI MKTV/TQGSQQ/SLADPASHLEI VCDHLT/SNETEPVRALLPDEI KEVEPPALSMSLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			l		1		ETTFKCEECGKGFYTNSQRYSH
CGKSFGWASCLLNHQRIHSGEI PFKCECGKRFTQNSQLYTHRI 7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLNEEEA AQVHGVKDPAPIASTQSVLADI TDSAGN'ARQEHKAAL*PIQN YQANLVNTFPYSNNSGGRGRI MKTV/TQGSQQPSLADPASHLE VGDHLTYSNETEPVRALLPDEI KEVKPPALSMSLHIEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			1				QRAHSGEKPYRCEECGKGYKR
7249 37617 A 7303 I 585 KRTAISPKDAFETRONSOLYTHRI 7249 37617 A 7303 I 585 KRTAISPKDAFETRONDINEEA AQVHGVKDPAPIASTOSVLADI TDSAGN*ARQEPHKAAL*PIQN YQANLVNTFPYSNNSGGRG/RI MKTV/TQGSQQPSLADPASHLE* VCDHLTVSNETEPVRALLPDEF KEVKPPALSMSLHEATMPVL LDHLRETRADKKRLRKALREF EQFFRKTGRSPQKEDRIPMADE YY			1				RLDLDFHQRVHRGEKPYNCKE
7249 37617 A 7303 I 585 KRTAISPKDAFETRQDLNEEEA AQVHGVKDPAPIASTQSVLADI TDSAGN*ARQEPIKAA.1**PIQO YQANLVNTFPYSNNSGGRG/RI MKTV/TQGSQQPSLADPASHLF VGDHLTYSNETEPYRALLPSIG KEVKPPALSMSNLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY	l		1				CGKSFGWASCLLNHQRIHSGEK
AQVHGVKDPAPIASTQSVLADI TDSAGN-ARQEHRKAAL*PIQN YQANLVNTFPYSNNSGGGGRI MKTVT/TQSQQPSLADPASHLE VGDHLTYSNETEPVRALLPDEI KEVKPPALSMSNLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			l				PFKCEECGKRFTQNSQLYTHRR
TDSAGN*ARGEPHKAÅL*PIQN YQANLVNTFPYSNNSGSRGRI MKTV/TQGSQQ/SLADPASHLE VGDHLITYSNETEPVRALLPDEI KEVEPPALISMSLIEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY	7249	37617	A	7303	I	585	KRTAISPKDAFETRQDLNEEEA
YQANLVNTFPYSNNSGGRG/RI MKTV/TQSQQPSLADPASHLE VGDHLTYSNETEPVRALLPDE KEVKPPALSMSNLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			1				AQVHGVKDPAP/ASTQSVLADG
MKTV/T/GSQQPSLADPASHLE VCIDHLTYSNETEPVALLPDEI KEVKPPALSMSNLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			1		l		TDSAGN*ARQEPHKAAL*PIQN
VGDHLTYSNETEPVRALLPDEF KEVKPPALSMSNLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			l		i		YQANLVNTFPYSNNSGGRG/RL
KEVKPPALSMSNLHEATMPVL LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY							MKTV/TQGSQQPSLADPASHLP
LDHLRETRADKKRLRKALREF EQFFKQTGRSPQKEDRIPMADE YY			1				VGDHLTYSNETEPVRALLPDEK
EQFFKQTGRSPQKEDRIPMADE YY							KEVKPPALSMSNLHEATMPVL
YY					1		LDHLRETRADKKRLRKALREFE
				1	1		EQFFKQTGRSPQKEDRIPMADE
7250   37618   A   7304   I     366			L				YY
	7250	37618	Α	7304	1	366	

SEQ ID			SEQ ID NO:		Nucleotide location of last	
NO:	of peptide	hođ	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	defection, (-possible nucleotide insertion)
	<u> </u>	L		L		
7251	37619	A	7305	1	1265	RYRPGIPGSTISSLVEEHAPPSW
			1			EPQHQNVEATVLVDSVLRPSM
						GNFKSRKPKSIFKAESGRSHGES
		1				QETEHVVSSQSECQVRAGTPAH
		1				ESPQNNAFKCQET\VRL\QPRID
		1				QRTATSPKDAFETR\QDLNEEE
		1				AAQVHGVKDPAPASTQSVLA\D
		ĺ	ŀ			GTDSADPSPVHKDGQNEADSA
					1	PEDLHSVGTSRLLL/YHITDGDN
		i				PLL\SPRLFPLSGQSQRFNLDPES
	İ	1				APSPPSTQQFMMPRSSSRCSCG
i						DGKEPQTITQLTKHIQSLKRKIR
l		1				KFEEKFEQEKKYRPSHGDKTSN
						PEVLKWMNDLAKGRKQLKEL
						KLKLSEEQGSAPKGPPRNLLCE
						QPTVPRENGKPEAAGPEPSSSG
						EETPDAALTCLKERREQLPPQE
						DSKVTKQDKNLIKPLYDRYRII
						KQILSTPSLIPTIVSQDTCMLLLC
7252	37620	Α	7306	797	1390	PRMGARPRAPAAQPPPAAAQR
l		1				PPARPATPTACGSSAHRAPSPA
			İ			RSRRSPCTPRAAPAAPGPKAAR
	1	1				QWAGTATRSSRPQRSARRSPRD
						SSRCWAISSRSKRAATACTPGA
i	Į.	1				KRRVATKARGALWSKPKSKA
			l	ľ		MRLWPWCLSGRLGS*KAQEVA
ĺ				i		QDPGSDEGRGRLVESGLQDEG
						WVPQGGEGGVAGQDASHRGSF
		_				RGALK
7253 7254	37621 37622	A	7307 7308	605	697 1263	
7255	37623	A	7309	257	1190	
7256	37624	A	7310	394	485	
7257	37625	A	7311	21	674	
7258	37626	Ā	7312	277	396	GLLPGWKI*CSRVFVTSAIHVE
1236	37020	l^	7312	2"	1550	VAELEANLPCTCKVHFPDPNKL
ĺ					1	HCFQLTVTPDEGYYQGGKFQF
						ETEVPDAYNMVPPKVKCLTKI
						WHPNITET
7259	37627	С	7313	74	316	WHENTIET
7260	37628	č	7314	211	390	
7261	37629	A	7315	1	2601	
7262	37630	Α	7316	1	1365	
7263	37631	Α	7317	358	760	SIPLLFRKSSLSRK*CSAASIFSG
						SSKFKRSVNKEFNPQTTSFNVL
						VGAQPVPSIECSLNKLRHISPVS
					į .	VIVGVPDSLVQAFHFGRHHVV
			l		1	RIRELQFQTEIFHPGSNPHLGLL
					1	LAENNEACLDQENALYMYKV
7264	37632	Α	7318	1	1728	
	37633	Α	7319	1	558	

SEQ ID	ISEO ID NO-	Mer	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide inscrtion)
				sequence		
7266	37634	A	7320	2	1884	PAGAGPGQEAGAGPGPGAVAY
,200	57051	ľ`	1.020	ļ .		ATGAEEGEMKPVAAGAAVPPG
		l				EGISAAPTVEPSSGEAEGGEAN
		l				LVDVSGGLETESSNG\KDTLEG
		l				AGDTSEVMDTQAGSVDEENGR
		l				QLGEVELQCGICTKWFTADTFO
		l				IDTSSCLPFMTNYSFHCNVCHH
		l				SGNTYFLRKQANLKEMCLSAL
		l				ANLTWOFRTQEEHPKTMFSKD
		ĺ				
	Į.	l				KDIIPFIDKYWECMTTRHRPGK
	ŀ	l				TTWPNNIVKTMSKERDVFLVK
		l				EHPDPGSKDPEEDYPKFGLLDQ
		l				DLSNIGPAYDNQKQSSAVSTSG
		l				NLNGGIAAGSSGKGRGAKRKQ
		l				QDGGTTGTTKKARSDPLFSAQR
		l				LPPHGYPLEHPFNKDGYRYILA
		ł				EPDPQAPDPEKLEIDCWAGKPIS
		l				GDLYRACLYERVLLALHDRAP
		ł				QLKISDDRLTVVGEKGYSMVR
		l				ASHGVRKGAWYFEITVDEMPP
		l				DTAARLGWSQPLGNLQAPLGY
		1				DKFSYSWRSKKGTKFHQSIGKH
		1				YSSGYGQGDVLGFYINLPEDTE
		1				TAKSLPDTYKDKALIKFKSYLY
						FEEKDFVDKAEKSLKQTPHSEII
	1	1				FYKNGVNQGVAYKDIFEGVYF
		l				PAISLYKSCTVSINFGPCFKYPP
		1				KDLTYRPMSDMGWGAVVEHT
		1				LADVLYHVETEVDGRRSPPWE
7267	37635	Α	7321	1	267	
7268	37636	Α	7322	60	888	RGAALARTRLSVRPVGPAGTRR
		l				SHALGPRPGARSSFRLRCELRR
					ŀ	CMCGNNMSTPLPAIVPAARKA
						TAAVIFLHGLGDTGHGWAEAF
						AGIRSSHIKYICPHAPVRPVTLN
						MNVAMPSWF\DIIGLSPDSOED
		l		i		ESGIKQAAENIKALIDQEVKNGI
				l		PSNRIILG\GFSOGGALSLYTALT
						TOOKLAGVTALSCWLPLRASFP
						QGPIGGANRDISILQCHGDCDPL
1						VPLMFGSLTVEKLKTLVNPAN
			l	l		
						VTFKTYEGMMHSSCQQEMMD
		<u> </u>				VKQFIDKLLPPID
7269	37637	A	7323	[1	1182	

SEO ID	TSEO ID NO	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
		1		sequence		
7270	37638	A	7324	li .	2469	MVDRARPTVLVTEVPLKSKHT
1/2/0	37030	^	/324	ľ	2409	AQMGLVLTANESOPLVHETAL
1		1				
		1				KNKKPQSWFPNPCVSYNRKPG
						LQD*GRAERPELGEQATEAALL
	1	1				KAPAESVRQEHRSTNT/PQTRS0
1		1				CPQYFPRAGCLPSRGHDVEPQF
		1				EAGDGPCRGIRNG*KLLSSFFG
i		1				QQVRT**R/CSELTPKQEFFKGS
	1	1				ESSNRTSGGLFGVVPGAAETGE
1		ı				VCVYTFKELEGQTSDEEGSRLE
1		1				NDFLEITDEDKKKSTKDRYDKY
ı		1				KEVGEHPPLSSSPVEHEGVLKG
1		1				QKSYRCDECGKAFNRSSHLIGH
1		1				QRIHTGEKPYECNECGKTFRQT
1		1				SQLIVHLRTHTGEKPYECSECG
-		1				KAYRHSSHLIQHQRLHNGEKPY
						KCNECAKAFTQSSRLTDHQRT
		1				HTGEKPYECNECGEAFIRSKSL
		1				ARHQVLHTGKKPYKCNECGRA
						FCSNRNLIDHQRIHTGEKPYECS
		1				ECGKAFSRSSGLISHHRVHTGE
						KPYSCIECGKAFNQNSQLIEHQ
						RMHRGKKVYKCKECGKAFGLS
						KCLIRHQRLHTGEKPYKCNECG
						KSFNQNSHLIIHQRIHTGEKPYE
	1	1			l	CNECGKVFSYSSSLMVHORTH
		1				TGEKPYKCNDCGKAFSDSSQLI
		1				VHQRVHTGEKPYECSECGKAF
1	1					
						SQRSTFNHHQRTHTGEKSSGLA
						CQEGNKEISKGPQKPPGYRLCP
ŀ		1				LQAVGGGEFGPTRVHISFSLSD
7271	37639	ļ.	7325	1	1596	LKQIKVFFPGGPLMLEKQKKKS
7272	37640	A	7326	2	3394	MAHAGGGSGGSGAGGPAGRG
1/2/2	37040	l^	7520	ľ	3394	LSGARWGRSGSAGHEKLPVHV
İ		1				
						EDALTYLDQVKIRFGSDPATYN
1						GFLEIMKEFKSQSIDTPGVIRRV
		1				SQLFHEHPDLIVGFNAFLPLGY
						RIDIPKNGKLNIQSPLTSQENSH
						NHGDGAEDFKQQVPYKEDKPQ
		1			1	VPLESDSVEFNNAISYVNKIKTR
						FLDHPEIYRSFLEILHTYQKEQL
1			1		1	NTRGRPFRGMSEEEVFTEVANL
						FRGQEDLLSEFGQFLPEAKRSLF
7273	37641	A	7327	1	738	TGNGPCEMHSVQ
7274	37642	A	7328	1	399	
7275	37643	A	7329	3	223	-
7276	37644	A	7330	1	1040	
7277	37645	A	7331	1	465	
7278	37646	A	7332	1	288	
	1	_				

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7279	37647	Α	7333	109	4770	
7280	37648	Λ	7334	109	4687	
7281	37649	A	7335	109	4860	
7282	37650	Α	7336	1	336	
7283	37651	Α	7337	1	441	
7284	37652	A	7338	305	446	
7285	37653	Α	7339	2	461	
7286	37654	Α	7340	59	620	FQKIGL**/FIDLKDGLFTIPLAE
						QDCEWFAFTIPVVNNLQPAKRF
					i	HCFTDGSNNGKASYSGSKNKV
						FQMSYTSAQKAELVAVIELIEN
						AQLRFHTDEQLMTLFTQLQTA
					1	VRSRMHPFYITHIRAHTPLPGPL
				1		TEGNQMADRLVANAISSARHF
	1					QQHLL/THSHPPGDRSRSCHRW
						RKKLEESGTSSHE
7287	37655	Α	7341	1	1410	
7288	37656	Α	7342	1	1740	MGQVWALVHSTLETFHTDEEE
						GEYNEVTEQVCLPAKAGSAAV
		ŀ				DLCCTKAVSLLPGESPQKVPTG
				l		AGGPLPAGMTGLLLGRSSLNIK
						AVQVQTGVTDSDYNGEIQIVTS
		ŀ				TSVPWKAKPGDHIAQLLIVPKK
		ł				F\EGLKEPLQVERQSSCQGLGY/
	l			1		PFLMAAIVKPPEPIPLKWLTDKP
		1				IWTEQWPLSKEKLEALEDLITQ
						QLKKGHIAPTFSPWNSPVFIIKK
	ł	ŀ				KSAEQDCEWFVFTILAVNNLQL
		ĺ				KPAKRFHWKVLPQGPNQQPIWI
						PSRYLKPYHKPDAKEEIPEGSQ
		1				GFPVAAMSRLTLRRTPTVTSNT
						HRTQPPTWGQIEKLPQMAEENL
						RKAGQPVTISNWILPRITKFKPI
					ļ	EGAENVFTDGSSNGKASYSGSK
	l					GPLTEGNQMADRLVAKVISNA
						RHFHNLTHVNASGLKRRYSIT
						WKEAKAIIQRCPTCQVMLSAAE
		l				QHLQKSAAKTEAEKLVWWRD
		1				PITKSREIGKIITWGRGYACVSP
	1	1	1			GPNQQPIWIPSKHLKPYHKPDA
	l	ĺ				GEKIPGESRGPPVAAMSRLTLR
						RMPTVMSNTHRTQPPTWGQIK
						KLSQMAEENLRKAGQPVTMNN
	1					LMIAVITTAFNKG
7289	37657	Α	7343	1	1239	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
<b>#0.00</b>	Tomac so	<del> </del>	7344		777	MPONSLEECALELGKKSLOEN
7290	37658	A	/344	1	I'''	
		1				VNNFPKTKLFQFLKLTNWILPK
		1				TKFKPIEGAENVFTDGSSNGKA
	1	1				SYFGLKGKVFQTPYTAAQKVE
		1				LVAVIEVLTAFDMPVSMISDST
						YVVHSTQLTENAQLRLHTDEQ
						LMTLFSQLQTAVR\CFAVMGIP
		1				ASTTT/DNAPGYT\$QALATFFS
		1				MWNIKRITGIPYNSQGQAIVER
1		1				MNLSLKQQLQKQTEGDREYGT
		1			l	PQMQLNLALLTLNFLSLPKGQ
	1	1	1			MLSAAEQHLQKPAVKTEAEQL
7291	37659	Α	7345	1	1307	
7292	37660	Α	7346	1	2040	
7293	37661	Α	7347	1	1898	MAGAPPPAWLPHCSSISDCCAR
l						NERGSVGVAPSKPARSAAVDL
		1				CCTKAVSLLPGEPPQKVPARVC
l		1				GPLPAGTVGLLLGRSSLSLKEV
ŀ		1				OIHTGVIDSDYKVEIOIVVSTSV
		ı				PWKAEPGERIAQLLVVPYVGT
		1				GKSEIKOTEGFGSTNKOGKAAN
		1		i		WVNOITDKHLTCEITIOGKKFK
						GLVDTGADVSIISLOHWPSMWI
		1				IOSTOFNIVGVDGSSNGKASYF
1		1				GSKCKVFOMPYTSAOKVELVA
		1				IIEVLTTFDMPINVISDSSYVVHS
l		1			1	TOLIENAOLOFHTDEOLMTLFT
		1				QLQTAVRSRMHPFYITHIRAR\H
l						TPLPGPLTEGNQMADCLVATA
		1				
		1				VSNARHFHNLTHVNASGLKCR
	Į.	1		1		YSNTWKAAKAIIQRRPTCQMV
				1		HSSSFTGGVNPQGLEPNSLWQ
						MDVTHVPSFGRLAYVHVCVDT
		1				FSHFVWATCQSGESSACVKHH
	1	1		İ		LLQGFVVMGIPASIKTDNVPGY
		1				TSQALATFFSMLNIKRITDIPYN
	1					SQDVEADANADVGVDVDADA
		1				DVDAEEEVFTDADADAEVDVD
		1				EDADAERLRCNADEDSDLDLD
		1			1	VDAEMDADVDTNLDVDAAVD
		1				VDVDADADVDADTDVDVDTG
		1	1			LNLEADLDLDVDADVDTDADV
		1	1			DRDADVEVAVDADATVNADV
1	1	1				DYVDVDTDSD
7294	37662	Α	7348	2	565	
7295	37663	Α	7349	1	996	
7296	37664	Α	7350	18	260	
7297	37665	Α	7351	1	594	
7298	37666	С	7352	232	603	
7299	37667	Α	7353	1	1236	
7300	37668	Α	7354	568	1370	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	locatinn of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7301	37669	A	7355	1	1800	
7302	37670	A	7356	1	498	
7303	37671	A	7357	1	3400	MDCSEKWRDPLDAVCVLPATE
,,,,,,	3,0,,	(`	,,,,,	ľ		EPVVOGSALYLVAHHDDYCV
		1				WYSLORTSPEKNERVROMRPV
			j			CDCQAHLLWNRPRFGEINDOD
						RTDRYVOALRTEIPLTLKGAKL
						OREEKEGDMPCRANILVTELFD
	1	1				TELIGEGALPSYEHAHRHLVET
						SLGEQVIVPPVDVESCPGAPSV
		1				CDIOLNOVSPADETVLSDVLPM
	ļ	1			ì	FSIDFSKQVSSSAACHSRRFEPL
		1				TSGRAQVVLSWWDIEMDPEGK
	1					IKCTMAPFWAHSDPEEMQ
7304	37672	A	7358	1	687	IKC IMAI I WALISDI EEMQ
7304	37673	A	7359	1	660	
7306	37674	A	7360	112	474	
7307	37675	A	7361	352	441	
7308	37676	B	7362	1	831	
7309	37677	A	7363	460	612	
7310	37678	A	7364	251	496	LFVSI/WQVFH*GRRGFLLVRN
/310	13/0/8	^	/304	231	490	DCVOIWCEMISHSGFDLHFSDG
		1				Q*/WMSISSC/DFLAA*MSSFEK
		1				CLFMSFAHFLMGLFVFFL
7311	37679	В	7365	1	729	CLEMSFARFLMGLEVEFL
7312	37680	A	7366	1	774	
7312	37680	В	7367	1	516	
7314	37682	-	7368	10	504	
		A C				
7315 7316	37683 37684	В	7369 7370	520	1656 1206	
7317	37685	A	7371	677	1126	AVTLTTKVCSFTPEASETTNPPG
/31/	3 /685	A	/3/1	0//	1126	GTNNSRRTALRAVALTAKVRS
	1	1			1	
		1				FTPRGSAASFLKSVRPRTHQFRT
				ĺ		Q*HVHQIEFSPGGLWESCPRAS
	1	1				SSTGDPGRPPERRGAAARKTVG
	1	1		l		VQGVGYSLPRKLCPLFSRTTYP
		_				HTSLRKDCLESDTTAE
7318	37686	A	7372	2	394	HLFIYLLVVLLWCPGWPQTAG
		1				LKGSSCLSLLSNWNYRPPL*AL
		1				LLGTQKLPRVWNFIMVRRIQDG
						VKPSVSIAEREMKSRKSAASLL
	1			ł	1	SQRDHEPTRRKKLRTHPNIRRN
	L	<u>L</u>				KLQTRHLKSCNTHCEGPWRHS
7319	37687	Α	7373	1	204	
7320	37688	Α	7374	1	879	
7321	37689	A	7375	139	4488	
7322	37690	Α	7376	1	933	
7323	37691	A	7377	335	582	VLQLLRQHVWSCSFLLVGSWS
		1	1	1		HWLQERSCRSSQ*VLQLIKAV
		1		1		WTQRTQEPSWLHLVDPAPGLQ
1	1	1	1	1		VELPASPTRYAHTPQPLGG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7324	37692	В	7378	1	3101	
7325	37693	A	7379	365	625	VAKIFSHVVGCLFTLMVVSFAV
						QKLFSLIRSHLSILAFVAIAFGVI
						DMKSLPTPMS*MVMPRFSSRVF
						MVLGLKFKSLIHLELIFV
7326	37694	Λ	7380	994	1167	NKGGHKQMEEHSMLMDRKNQ
	1					YRENGHTAQGNL*IQCHPHQAT
						NDFLHRIGKNKLASNM
7327	37695	С	7381	143	3529	
7328	37696	В	7382	54	1158	
7329	37697	Α	7383	1662	1919	LLNVFALAFLVLLIEMLGCQFW
	1					IFPAFSCRHLVL*ISLYTLL*MRF
						RDSGMWCLCSRWFQRTSLFLA
		ــــ				SFRYVPSSHSGAGCSVSM
7330	37698	Α	7384	63	1650	SPGHI*SSV*REIYSTKCPQEKA
						GKI*NSHPNITIKRTGEARANTF
						KS*QKARNN*DQSRTEGDRDT
		1				KNPSKNQ/CNPGAGFLKRSTKLI
	1	1				DR*QD**RRK*RRIK*T**KMIK
		1				GI/VTTDPTEIQTTIREFYKHFYA
		1				NRLKNLEEMDEFLETYTLPRLN
		1				QEEVESLNRPITGSEIEAIINSLP
	1					TKKSPGPDGFTAEIYQRTNDKN
1					1	HMIISIDEEKAFDKIQQPFMLEM
		1				LNKLGIYGMYIKIIRTIYDKSTA
l		1				NIILNVQKLEAFPLKTGTRQGCF
						LSPLLFNIVLEVLARAIRQEKEI
1		1				KGIRLRKEVFKMFLFADDMIVY
						LENPIISAPNLLKLISNFSKVSGY
						KINVQKSQAFLYTNNRQTESQI
						MSELPFTIATKRIKYLGIQLTRD
		1				VKDLFKENYKPLLNEIKEDTNK
		1				WKNIPCSWIGRINIVKMAILPKV
1						IYRFNAIPIKLPMTFFTELEKTTL
		1		1		KFIWNQKRALNAKTILSQKNK
		1		1		AGGIMLPDFKLPYKATWYWNQ
						NTEIDQWNKTEASEITPHIYNHL
		丄				VFDNPDKNKK
7331	37699	A	7385	392	493	
7332	37700 37701	A A	7386 7387	386	1223 553	NAME CICH IDODANT DECEMBER
1333	37701	l <sup>A</sup>	1381	200	333	KMIKGISPLIPQRYKLPSENTINT
	1	1	1	1	1	STQIN*KI*KKWIHSSTHTPSQD*
7334	37702	В	7388	285	1581	TRKKLNL
7334	37703	A	7389	1283	1473	
7336	37704	A	7390	755	1042	SSYATKKEPALPSQSEAKKTKL
, 330	157704	1	, 390	1,55	10-12	ETSCYLTSNYTTRLQ*PKQHGT
				1	1	GTKTEI*ANGTEQSPQK*YHTA
1		1		1	1	TTIWSLTNLTKTRNGERIPYLIN
	1	1	1		I	GVGKTG
7337	37705	c	7391	1	2334	0.00
,,,,,,	27703		1001	11	12001	L

SEQ ID		Met	SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7338	37706	A	7392	Tr.	1539	
7339	37707	В	7393	T	2361	
7340	37708	Α	7394	5071	5535	GTAFLWRRRGALRFRVSSFSVL
					1	FFPHLCGFIYFWSLMMVMYRC
	1	ı				VFGVDVLSVC*FSF*QTGPSAA
		1				GLLEYPAV*GVSVPLLGGASQL
						GC\$GVRGQGPT*GGSLPVLR\$P
		l				AACWENHCSLQSCQTGTFKSA
						EVTAVFLFVCALPPEVEPTEAG
7341	37709	Α	7395	1	459	
7342	37710	Α	7396	3	1063	
7343	37711	Α	7397	39	895	
7344	37712	Α	7398	2	277	
7345	37713	Α	7399	34	845	
7346	37714	Α	7400	1	3399	
7347	37715	Α	7401	1	3126	
7348	37716	Α	7402	1	387	
7349	37717	Α	7403	1	3578	RDLVVGCGGFVKSDVEINYSLI
		1			1	EIKLYTKHGTLKYQTDCAPNN
		ı				GYFMIPLYDKGDFILKIEPPLGW
						SFEPTTVELHVDGVSDICTKGG
					1	DINFVFTGFSVNGKVLSKGQPL
ļ		1			İ	GPAGVQVSLRNTGTEAKIQSTV
						TQPGGKFAFFKVLPGDYEILAT
						HPTWALKEASTTVSVTNSNAN
						AASPLIVAGYNVSGSVRSDGEP
						MKGVKFLLFSSLVTKEDVLGC
	1					NVSPVPGFQPQDESLVYLCYTV
		ļ.,				SREDGSFSFYSLPSG
7350	37718	A	7404	34	460	
7351	37719	A	7405	105	245	VSSEKVSLGVPCPAASAAASGD
						ASR*MATGRGGGGGGVAALPE
70.00	0.0000	l.	7406		1200	SAP
7352	37720	A_	7406	1	1289 5250	
7353 7354	37721	A	7407	462	887	
7354	37722	A	7408	714	109	DI BOI LEVERGECALITATIONS
/333	37723	A		1	109	PLRQLLCVKRGFC*HH*HEGCQ SRLLLRCLLCSTAI
7356	37724	Α	7410	1	1845	
7357	37725	Α	7411	192	1507	
7358	37726	Α	7412	2	688	
7359	37727	Α	7413	1	518	
7360	37728	Α	7414	1	276	

SEQ ID	SEQ ID NO:	TMar	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	'			sequence		
		<u> </u>				Law of Employs (B)
7361	37729	Α	7415	984	3112	MWQETFFRMENLQLIIILILGSP
				İ		SQLHFPVIRNNQGWTLYHQWP
						HFLNRFSSRLSNSSLLNQLKFTO
						ANCKKPLQKGQTAYQRKGSAF
		ł				LFCSTTCLSSFSHKPAPKKLCV
		ļ.				MCKKDITTMKGTI/VLAQVDSS
1		1				ESFQEFCS\TSCLISL/YEEQQNP
ŀ		ì				TKG\ALNKSRCTICGKLTEIRHE
						VSFKNMTHKLCSDHCFNRYRM
Į.	1	1				ANGLIMNCCEQCGEYLPSKGA
		1				GNNVLVIDGQQKRFCCQSCVSI
						YKQVGSHPSFLKEVRDHMQDS
		1				FLMQPEKYGKLTTCTGCRTQC
		1				RFFDMTQCIGPNGYMEPYCSTA
		1				CMNSHKTKYAKSQSLGIICHFC
		1				KRNSLPQYQATMPDGKLYNFC
1		1		1		NSSCVAKFOALSMOSSPNGOFY
		i				APSDIQLKCNYCKNSFCSKPEIL
1		1				EWENKVHQFCSKTCSDDYKKL
ł		1		1		HCIVTYCEYCOEEKTLHETVNF
		1				SGVKRPFCSEGCKLLYKQDFAR
į.		1				RLGLRCVTCNYCSQLCKGGAT
I		1				KELDGVVRDFCSEDCCKKFQD
		1				WYYKAARCDCCKSQGTLKERY
						QWRGEMKHFCDQHCLLRFYCQ
						QNEPNMTTQKGPENLHYDQGC
						QTSRTKMTGSAPPPSPTPNKEM
	1					KNKAVLCKPLTMTKATYCKPH
	1					MQTKSCQTDDTWRTEYVPVPI
						VPVYIPVPMHMYSQNIPVPTTV
						PVPVPVPVFLPAPLDSSEKIPAA
		_				EELKSKVSSDALDTELLTMTD
7362	37730	A	7416	88	1071	
7363 7364	37731 37732	A	7417 7418	2	2118	
				1		
7365	37733	A	7419	1	1677	
7366	37734	Α	7420	172	13329	
7367	37735	A_	7421	2	946	WITH A POLICE OF THE PART OF T
7368	37736	Α	7422	255	933	WIEAAPQAQEVQGDGLWLPCG
	1	1				AAGAGGLQSARSYGTVGEASV
						AEHPW/CAPGGCMAGCGSLAA
						AASPGLVPGHLP/QPTAAPSHPH
		1				RASLRVALLSGQWGLTCGQLL
1		1				ASAPLLQSWAWDTRLLMCRRL
1		1				SCSSEEGERIAQLLLLPYLKLGS
1						STVKRTGGFGNTNPAGKAVYW
1	1	1	1	1		VNQVSDKRPICTVAIQGKDFEG
1	1	1				LVDTEADVSIIAINQWPQHWPK
	1					QKASIGIVGVGAA
7369	37737	A	7423	718	2385	N
7370	37738	A	7424	1	180	
	1-7700	1::-	1		1	

SEQ ID	lero in vo.	IX4-4	SEQ ID NO:	Mindontida	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of péptide	hod	in USSN	location of first	codon fur last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7371	37739	A	7425	1	1713	
7372	37740	A	7426	1	774	
7373	37741	A	7427	2	158	
7374	37742	A	7428	1	174	
7375	37743	A	7429	252	1245	ELGECGCRQGSVSHCGRGSRPL
		1		l		LPRVRGKRHLPRARLARCQEAL
		1				SPWGFCRFRNHHQTGFSLAGA
1		1		l		NQRGPLAATLSGPGGEGQSAV
		1				ARLMGEKKNHPGAQYATRLSP
		1		l		RVGRFINAAGTTGFPTGKRAPT
					l	CWPGAD\IIPSCLALPRIETELM
1		1				GKFDEGKLPTDPHLMLGLAIET
		1				VAHDYDVIVIDSAPNLGIGTINV
						VCAADVLIVPTPAELFDYTSAL
		1			1	QFFDMLRDLLKNVDLKGFEPD
1						VRILLTKYSNSNGSQSPWMEEQ
				l		IRDAWGSMVLKNVVRETDEVG
	1			l		KGQIRMRTVFEQAIDQRSSTGA
						WRNALSIWEPVCNEIFDRLIKPR
7376	37744	Α	7430	1	1113	
7377	37745	В	7431	56	1234	
7378	37746	Α	7432	667	1048	LLLFRDLGIGTINVVCAADVLIV
						PTPAELFDYTSALQFFDMLRDL
		1				LKNVDLKGFEPDVRILLTKYSN
	1					SNGSQSPW\MEEQIRDAARFPV
						GKPVVPAALMNRPTRRGEAVC
		<u> </u>			1 400	VLGARVVFLFTSETGNS
7379	37747	A	7433	1	1428	
7380 7381	37748 37749	A	7434	1	756	SDRRYEWDRGPSLIIRPTIRVGP
/381	37/49	A	1433	l'	/36	WSQTNNQTDDTSGTVV/RRPFP
Ì		i				PVIGVVFHKGGVYKTSVSVHL
-				1		AQDLALKGLRVLLVEGNDPQG
1	i	i				TASMYHGWVPDLHIHAEDTLL
1						PFY\DPHLMLRLAIETVAHDYD
				ł		VIVIDSAPNLGIGTINVVCAADV
1						LIVPTPAELFDYTSALOFFDMLR
				l	1	DLLKNVDLKGFEPDVRILLTKY
				l		SNSNGSOSPWMEEQISDALRIS
					1	QRRNISSKFILQSACITLTTFIST
						CWAIIVTOSG
7382	37750	A	7436	1	1329	0.1.m. 1 200
7383	37751	A	7437	i	1185	
7384	37752	A	7438	1	1065	
7385	37753	В	7439	67	1033	
7386	37754	Α	7440	1	1192	
7387	37755	A	7441	1	1413	
7388	37756	A	7442	1	1176	
7389	37757	A	7443	1	1302	
7390	37758	В	7444	1169	3356	
7391	37759	Α	7445	14	3974	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /-possible nucleotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7392	37760	A	7446	677	1033	RATASSISTTRPCESTSNAPSCN
		1		1		SPIRSRSPLPHRPRASITLILVSM
	1	1	l	ĺ		MRMVRATISCAILVSRCQPAISP
	l		İ	l		PLCTAFFRPICAAGVPVFTLFTT
						TP*SLPLLLISAPSMPLKMELES
	25551	ļ. —	2442	1.550	1748	T
7393	37761	A	7447	1558	1/48	CSNASARFFAAVNPSGLGMILM
						*SRFIVFTKLSAIPLLSGLRTAVF
		ļ.			ror.	FGSSPNIRANWRVSLAR
7394	37762	A	7448	1	595	LKNSKPQVVMAAAGIFLIMCG
		1				VWLGFGGVLDPTKSSGYLIVDI
		1				YNEIICMLSNRIAGLGLSIMAVG
		1				GYARYMEGTPASRAMVSLLSR
		1				PLKLIRSPYIILSAT*VIGQIMP\Q
		1				FITSASGLGMLLMVPLFPTLVSL
						GVSRLSAVAVIATTMSIEWGIL
	1	1				ETNSIFAAQVAGMKIATFFCHA
		ļ				HNPVASRVILSVAISGTRAR
7395 7396	37763	A	7449 7450	32	978 316	
7396	37764 37765	C A	7451	1	2465	
7398	37766	A	7452	1	1416	MIILIDAEKAFDKIOOPFMLKTL
1396	37700	ı^	1432	l'	1410	SKLGTDGTYLKIIRAIYDKPTAN
1	l l	l				IILNGOKLEAFPLKTGTROGCPL
						SPLLFNIGLEDLARAIRQEKEIK
		l	l	l		GIOLGKEEVKLSLFADDMIVYL
	i i					ENPIVSAQNLLKLISNFSKVSGY
				İ		KINVOKSOAFLYTNNROTESOI
	1					MSELPFTIASKRIKYLGIQLTRD
		1				VKDLFKENYKPLLKEIKEDTNK
						WKNIPCSWVGRINIVKMAILP\R
		ı	i			DIDOW/NRTEPSEIMPHTYNYLI
		1				FDKPEKNKQWGKDSLFHKWC
						WENWLAVCRKLKLDPFLTPYT
ĺ		1				KINSRWIKDLNIRPKTIKTLEEN
			İ			LGITIQDIGVGKDFMSKAPKAM
						ATKAKIDKWDLIKLKSFCTAKE
		1	1	1		TTIRVNRQPTTWEKIFATYSSD
	1	l	1			KGLISGIYNELKQIYKKKTNNPI
	1	1		ĺ		KKWAKDMNRHFSKEDIHAAK
	1	l		1		KHMKKCSSSLAIREMDIKTTMR
		l		1		YHLTPVRMAIIKKSGNNRCWR
		l		1		
						GCGEIGTL

SEO ID	lero in No.	Mat	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	,,,,,	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1		l		sequence	' '	
		<u> </u>				
7399	37767	Α	7453	3	2272	RSTRQKVNKDTQELNSALHQA
		l	ŀ	İ		DLIDIYRTLHLKSTEYTFFSAPH
		l	ŀ	İ		HTYSKIDHILGSKALLSKCKRTI
		l				IITNYLSDHSAIKLELRIKNLTQ
		l		i		NRSTTWKLNNLLLNDYWVHN
		l		l		KMKAEIKMFFETNENKDTTYQ
		ł		l		NLWDTFKAVCRGKFIALNAHK
		l				RKQERSKIDTLTSQLKELEKQE
		l	İ			QTHSKASRRQEITKIRAELKEIE
		l	ŀ			TQKTLQKINESRSWFFERINKID
		l		l		RPLARLIKKKREKNLIDAIKND
		1				KGDITTDPTEIQTTIREYYKHLY
		l		ł		TNKLENLEEMDKFLDTYTLPRI
		l				NEEEVESLNRPITGAEIVAIINSL
		l	ŀ	l		PTKKSPGPDGFTAEFYQRYKEE
		l				LVPFLLKLFQSIEKEGILPNSCY
		1				EASIILIPKPGRDTTKKENFRPIS
		l	İ	l		LMNIDAKILNKILAKRIQQHIKK
		1				LIHHDQVGFIPGMQGWFNIRKS
1		1	ŀ			INVIQHINRAKDKNHMIISIDAE
1		1				KAFDKIQQPFMLKTLNKL/DIGF
		1		l		NYCKVHMEPKKSPHRQVNPKP
		l	ĺ	l		KEQSWRHHTT*LQTILQGYSNQ
1		ı				NSMVLVPKQRYRSMEQNRALR
1		1		l		NNAAYLQLSDL*QT*EKQAMG
		l		l		NGFPI**MVLGKLASHM*KAET
1		1		1		GSLPYTLYKNQFKMD*RLKR*1
i		1		l		*NHKNPRRKPRHYHSGHRHGQ
		1				GLHV*NTKSNGNKSQN*QMGS
		l		l		N*TKELLHSKRNYHQSEQATY
l		ı		l		KMGENFHNLLI*QRANIONLQ*
		1		i		TOTNLOEKNKOPHOKVÖKGHE
7400	37768	A	7454	1	3020	
7401	37769	A	7455	1	3046	MVKGSIOOEELTILNIYAPNTG
		1		ľ		ALRFIKQVLRDLQRDLDSHTIIM
		1				GDFHTPLSTLDRSTROKVNKDI
1		l				QELNSALHQEDLIDIYRTLHPKS
		1				TEYTFFSAPHHTYSKIDHIVGSK
		l				ALLSKCKRTEIITNCLSDHSAIK
		l				LELRIKNLTONRSTTWKLNNLL
						LNDYWVHNEMKAEIKMFFETN
		l	1	l		
		1	İ	l		ENKDTTYQNLWDTFKAVCRGK
1		l		I		FIALNAHKRKQERSKIDTLTSQL
		l		l		KELEKQEQTHSKASRRQEITKIF
	2000	l .	2126	107	1017	AELKEIETQ
7402	37770	В	7456	197	1917	
7403	3777I	В	7457	1	1954	

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7404	37772	Α	7458	1	1947	MNIDAKILNKILANRIQQHIKKI
						IHHDQVGFIPGRQGWFNICKSIN
						VIQHINRAKDKNHMIISIDAEKA
						FDKIQQLFMLKTLNKLGIDGTY
						FKIIRAIYDKPTANIILNGKKLEA
						FPLKTGTRQGCPLSPLLFNIVLE
						VLARAIRQEKEIKGIQLGKEEV
					l	KLSLFADDMIVYLENPIVSAQN
	i					LLKLISNFSKVSGYKINVQKSQ
						AFLYTNNRQTESQIMSELPFTIA
						SKRIKYLGIQLTRDVKDLFKEN
					1	YKPLLKEIKEDANKWKNIPCSW
	1	1				VGRINIVKMAILPKVIYRFNAIP.
						KLPMTFFTELEKTTLKFIWNQK
						RAHITKAILSQKNKARGITLPDF
	1	1				KLYYKATVTKTAWYWYQNRD
						IDQWNRTQPSEITPHIYNYLIFD
		İ				KPDKNKQWGKGSLFNKWCWE
						NWLAICRKLKLDPFLTPYTKIN
		1		}		SRWIKDLNVRPKTTKTLEENLG
				•		ITIQDIGMGMDFMSKTPKAMAT
		1				KDKIDKWDLIKLKSFCTAKETT
		1				IRVNRQPTKWEKIFTTYSSDKG
		1				LISRIYNELKQIYKKKTNNPIKK
		1				WAKDMNRHFSKEDIYAAKKH
			1			MKKCSPSLAIREMQIKTTMRYF
			1	ſ		LTPVRMAIIKKSGNNRCWRGC
				1	1	GEIGTLLHCWWINWMKKTWH
		ı	1	l		IYTMEYYASIKKNEFMSFAGA*
						MKLETII
7405	37773	A	7459	1	1713	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codnn for last amino acid	*-Stop codon, /-possible nucleotide
	sequenc <del>e</del>		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7406	37774	A	7460	281	2882	KPRLENYMKNAEASRADAINW
						KKGY/LVMEDKMNEMKREGKF
						REKRIKRNKQSLQEIWDYVKRP
		l				NLRLISVPESDRENGTKLENTL
		1				QDIIQENFPNLARQANIQIQEIQ
		1		1		RTPQRYSSRRATPRHIIVRFSKV
		l				EMKEKMLRAAREKEIQTNIREY
	ì					YKHRYANKLENLEEMDKFLNI
		l				YTLRRLNQEEVESLNRPIRGSEI
1		1				VAIINSLPTKKSPGPDGFTAEYY
		l				QRYKEELVPFLLKLFQSIEKEGI
		1				LPNSFYEASIILIPKPGRDTTKKE
						NFRTISLMNIDAKILNKILANRI
						QQHIKKLIHHDQVGFIPGMQG
		1				WFNIRKSINVIQHINRTKDKNH
	1					VIISIDAEKAFDKIQQLFLLKTL
	1			1		NKLGIDGTYLKIKRAIYDKPTA
	1					NIILNGQKLEAFPLKTGTRQGCF
		1				LSPLLFNIVLEVLARAIRQEKEI
		1				KGIQLGKEEVKLSLFADDMIVY
1		1		1		LENPIVSAQNLLKLISNFSKVSG
l		l		ł		YKINVQKSQAFLYTNNRQTETQ
						IMSELPFTIASKRIKYLGIQLTRD
						VKDLFKENYKPLLNEIKEDTKK
1				l		WKNIPCSWVGRINIMKMAILHK
						VIYRFNAIPIKLPMTFFTELEKTT
				1		LKFTWNQKRARIAKSILSQKNK
	1					AGGIMLPDFKLYYKATVTKTA
						WYWYQNRDIDQWNRTEPSEIT
		1		I	1	PHIYNYLIFDKPEKNKQWGKDS
	ŀ					LFNKWCWENWLAIWRKLKLD
		L_				PFFTPYTKINSRWIKDLNVRPKT
7407	37775	В	7461	1	2633	
7408	37776	Α	7462	3	1336	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nuelcotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino neid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7409	37777	A			2458	SWFFEKINKIDRPOARLIKKKRE KNOIDTINDKOGDITIDPTEIQIT IREYYKHLYANKLENLEEMDK FLDTYTLPRLNOEEVESVNRPIT GSEIEAITISKIPTKSSRGPDGFT AEFYORYKEELVPFLLKLFQPIE KKGILPNSFYEASIILIPKPGRDT TKKGNFRPISLMIDAKLINKIL ANQIQQHIKKLIHHDQVGFIPG QGWLEVALARJIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PTVSAQNLLKLISNFSKVSGYKI QVGKSQETYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK KNIPCSWIGRINIVKMALIPKI YTFNAIPKLPMTFFTELEKTIT KFIWKOKRSHIAKSILSOKNKA GDITLPDFKLHYKATVTKTAW YWYQNRDIDQWNTTEPSEIML HYYHLIFDKPDKNKQWGMDS LFNKWCWENWLAIGRKIKLDP FLTSYTKINSRWIKDIDNYRPKTI KTLEENLGNTIQDIGMGKDFMS KTPKAVATKAKIDK WDVIKLK KTNPIKKWWENSWIKDIDNYRPKTI KTLEENLGNTIQDIGMGKDFMS KTPKAVATKAKIDK WDVIKLK KTNPIKKWAKDMNHFSKED IVAAKTHMKKCSSSLAIREMOI KTNPIKKWAKDMNHFSKED IVAAKTHMKKCSSSLAIREMOI KTNPIKKWAKDMNHFSKED IVAAKTHMKKCSSSLAIREMOI KTMRYHLTPIRMVIIKKSCNN
		<u> </u>				ALKRVADLPAQRSSSAKGETAS
7410 7411	37778	A	7464	196	2101 792	GILSFAKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTLHCWLDCKLVQPL WKSVWRFLRDLELEIFPDPAIFL LGIYPNEYSKSCYKDTCTRMFI AALFTIAKTWEPPKCSNMIDWI K/KMWH/YYRDTMRPKNDEVQ SLVG/TWVNWETTFSVTIAVQK PTRLSH
7412	37780	Α	7466	3	610	
7413	37781	Α	7467	I	1986	

SEO ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
	37782	<del> </del>	7468	965	4421	TWKGTISTSRCKIMPKYRSTRC
7414	31182	A	/468	965	4421	
						KVNKDTQELNSALHQADLIDIY
						RTLHTKSTEYTFFSAPHHTYSKI
				1		DHILGSKALLSKCKRIEHTNYLS
1						DHSAIKLELRIKNLTQSRSTTW
						KLNNLLLNDYWVHNEMKTEIK
	1	1	l	1		MFFETNENKDTTYQNLWDAFK
						AVCRGKFIALNAYKRKEERSKI
						DTLTSQLKELEKQEQRHSKPSR
						RQEITKMRAELKEIETQKTLQKI
		1				NESSSWFFERINKIDRPLARLIK
						KKREKNQIDT
7415	37783	Α	7469	1	1674	MGQLQRNARDLQESVMSIRM
l .						MPMEYVFSRYPRLVRDLAGKL
l		1			1	GKQVELTLVGSSTELDKSLIERI
1						IDPLTHLVRNSLDHGIELPEKRL
		1		1		AAGKNSVGNLILSAEHQGGNIC
1		i				IEVTDDGAGLNRERILAKAASQ
1		1				GLTVSENMSDDEVAMLIFAPGF
		ł				STAEQVTDVSGRGVGMDVVKR
		1				NIQKMGGHVEIQSKQVTGTTIR
[		į.				LLPLTLAILDGMSSLLTHGIGQF
						ADVACAGPLLAAELDALGKAL
		1				KEPARPMVAIVGGSKVSTKLTV
		1				LDSLSKIADQLIVGGGIANTFIA
		į.				AQGHDVGKSLYEADLVDEAKR
		1				LLTTCNIPVPSDVRVATEFSETA
1		1				PATLKSVNDVKADEQILDIGDA
1		i i				SAQELAEILKNAKTILWNGPVG
1		1				VFEFPNFRKGTEIVANAIADSEA
		1				FSIAGGGDTLAAIDLFRIADKNS
		1				YISTGGGAFLEFVERLTTLTQLL
		1				HDQGYVTQAIGKWHMRETTEP
		1				QPQNVGFDDFRGFNSVSDMYT
		1				AWRDVHVNPEVALSPDRPAYI
		1				NOSPLSKDDVHALRGGDQQAI
		1				AD\ITPKYMADLDQRCTEYGAQ
		1				LLDKMAKSA
7416	37784	A	7470	1	3360	LLDKMAKOA
7417	37785	A	7471	2	543	
7418	37786	A	7472	1387	1805	QAIAFDVQPGRGDYAGNQRHH
1		Ľ		1		NQYNQHQAH*SWQRCGIGDGL
		1	1	1	1	ARFARHNATKPANKPGETGDR
		ı			1	FNHQKNHGGQQDPVLHQLIEV
		1			1	MLVGRGGDQAVGQATLGIDTN
		1		1	1	VGLHAKV/LTDCLSWSDASPDR
		ı			1	VAALCSWSSWVPQ
7419	37787	A	7473	4088	4228	SPPSA*VKALPGPKHHGGLKPV
1,419	3//8/	l <sup>A</sup>	14/3	14000	4220	HPIPGASLVLARRWSMFRRWG
		1				LIT
7420	27700	1	7474	332	538	EII
7420	37788	Α	/4/4	1332	1230	L

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide deletion, \*-possible nucleotide insertion)
742I	37789	Α	7475	1	1983	
7422	37790	Α	7476	856	964	
7423	37791	Α	7477	1	1563	
7424	37792	В	7478	I	1086	
7425	37793	Α	7479	372	886	
7426	37794	A	7480	2028	2368	RPPGNSLNVSRMGTRSSYSCRR HSPAFLSWGKGRCHLCNKAHL LAGA*HYSFLSGSAPY*N*VNG QI**R*TAHRSTPDAPTGH*NCC S*L*CHSY*QRA*PGYRHD*CR MCC
7427	37795	A	7481	146	402	LGFLLRLSEMPRKQGDYRTRI/C EIRGRVEQRVGYTIEQINHMRD VFDRRYEWDHGPRLIIRPTIRVG PWSQSDYQTDDTSGTVVPD
7428	37796	Α	7482	3	149	
7429	37797	A	7483	5	753	ARKYWAYAARHKCPA/CISFSA SHRLYRYWEEBMNPAPVEAMR TFQQFIDEGMYTSGDTHTLRDP HYYEDKAHKYLVFEANTGTEN GYQGESLFNKAYYGGTNFF RKESGKLQQSAKRDAELANG ALGIIELNNDYTLKKVMKPLITS NTYTDEIERANVFKMGKWYL FTDSRGSKMTIDGINSNDIYML GYYSNSLTGPYKPLNKTGLVLQ MGLDPNTNIGTDDTSGTVVQT NNQTADTSGTMVPD
7430	37798	С	7484	182	709	
7431	37799	В	7485	I	1488	
7432	37800	A	7486	2	1034	VLISQRGLIRRSKISLOTGSQIER AFLQAPVEER*SMACSK/YSSH9 DLTFTNFIRFTYNIF*NHASPGIP NLLLIPRGLEATITAVFGQOT YIRLEPFKINVLEQTIKHIEKLQC G/ECSQITQQAWEQSAHQQHIR H*SCRYPG*ARCQ*VHQARTL* DQRS*ADHEAYRKTAVRRCSQ TTQQA WEQSAHQQHIRH*SCR YGG*ARCQ*L'HIHSHEQQFQWW G/G/IRCGSVGSLPSSUCPLTQF QYGAEPDRKE*CQAPASK WALL LIKK*HRFPFQDRKAGECLLHEY EDLVPIRDITLRLFFGGRYLPRA KHVAPSEEPDFIRVGPWSQSDY QTDDTSGTVVPD
7433	37801	Α	7487	2	426	
7434	37802	A	7488	138	346	RWRLQNLSFCSSC/SRIWL*RGY VFCSWKPREQSSQSPLACSAAC LTLRTQSCLGTAGQTDDTSGT MVQY

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7435	37803	С	7489	Ţi .	1290	
7436	37804	Α	7490	48	439	HHHSGLDD/HRRKILNTAYRSR
		1		1		KLQASC*KSAERAWKTKASLT
		1				VNGWMKKIRCKTPMCRPTVR*
		1		l		SIRILIITTPLPRVPSRS*LKPPTS
		1				CT*CIFTQPTRC*KMTTCWRCS
		1				TSRKSSGHVCVSPGSVAVTI
7437	37805	A	7491	1126	1340	KARWMLQTRKRAVRRSNWRK
		1		ŀ		RNIWCAPAAICKRSTTLITSF*K
		1		į.		PVKMACPFICAMLRRSRLARRC
						AGALPN
7438	37806	Α	7492	12	960	
7439	37807	A	7493	1	1806	
7440	37808	В	7494	1	1318	
7441	37809	A	7495	1	1385	MLQIPKQQQNEKYQVPQFDQS
		ı		1		TIKNIESAKGLDVWDSWPLQN
		1		ì		ADGTVAEYNGYHVVFALAGSP
	1	1		ŀ		KDADDTSIYMFYQKVGDNSIDS
		1				WKNAGRVFKDSDKFDANDPIL
						KDQTQEWSGSATFTSDGKIRLF
		1				YTDYSGKHYGKQSLTTAQVNV
		i i				SKSDDTLKINGVEDHKTIFDGE
		ı				RKTYQNVQQFIDEGNYTSGDN
		l				HTLRDPHYQNTYIRLEPFKINVL
	1	1				EQITKHIEKLQCGGVVKQLSRR
	i					GNNQHISSTYDINRADTQVRRA
					l .	VNNYDIIVMSNSFNGQSEHQV
						WIDRKAGECLLHEYEDLVPIRD
						TLRLFPGGRYLPRAKHVAPSEP
						DPEQDEQKLSCCTYRKRYRVL
		1				VGELGDEQMAALSRLGNDYRP
						TSAYERGQRYASLLQNEFAGNI
						SALADAENISRKIITRCINTAKLP
	1	1		ı		KSVVALFSHPGELSARSGDALQ
		1				KAF*SASPDRADSSPG*EKRATT
	1	1			Į.	D/SRQFGGVDTAGNNLT*NIFRI
		1				SQRRNISSKFILQ*ACITLTTFIST
		1		1	1	CWAIIVTQSG/LMQPSAHHPAR
			I	1	l	QPEHDIAFGKCSSSVSVHLA/LG
			1	1		SGSEGATCFARGR*RPPGNSLN
					l	VSRMGTRSSYSCRRHSPAF\HRS
						TPDAPTGH*NCCS*L*CHSY*QR
	07010	<u>_</u>	7.00	ļ.——	200	A*PGYRHD*CRMCC
7442	37810	В	7496	1	3597	
7443	37811	A	7497	1	666	
7444	37812	Α	7498	J'	738	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ł	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7445	37813	A	7499	I	727	MKVLIVESEFLHODTWVGNAV
1.1.5	37013	ľ.		ľ		ERLADALSQQNVTVIKSTSFDD
						GFAILSSNEAIDCLMFSYOMEH
						PDEHQNVRQLIGKLHEROLNVP
		1				VFLLGDREKALAAMDRDLLEL
		1				VDEFAWILEDTADFYRRTAPVA
						RE*TRYPPGSCWPPLF/TAPLMK
		1				YS\DIHEY\SWAAPGHOGGVGF
1		1				TKTPAGRFYHDYYGENLFRTD
						MGIERTSTAVSLLDHSGAFGOS
1	i					EKYAARVFGADRSWSVVVGTS
1		1				GSNRTI
7446	37814	Α	7500	ï	744	GOILLI
7447	37815	Ā	7501	i	250	*
7448	37816	A	7502	1	850	
7449	37817	A	7503	1	1085	GNLAAGKTIQAQDRDAVGILSS
1777	3,01,	ľ.	,,,,,,	l'	1005	RTGESMENLQKNLLPKQRRRT
						RETFTMSGALDVLQIKEEDVLK
		1			ŀ	FLAAGTHLGGTNLDFQMEQYI
		l				YKRKSDGIYIINLKRTWEEL\LR
		l				OPRA\MVPIENPAD\VSVISSR\N
		l	Ì			TGQVCGTVRAV\LRFLAATGAT
		1				PIGG\RFTPGTF\TN\OIOASLPGS
		l				PRAFLWVT*PPGAEPPALSRSAS
		l				LC*PFLPLALVNPD/SPLRRYVII
		l				AIPCNNKGAH\SVGLMWW\ML
		l				AREV\LRMRGTISREHPW\EVM
		l				PDLYFYRDPEEIEKEEQAAAEK
		l				AVTKEEFQGEWTAPAPEF/TLA
		l				TOPEVADWSEGVQGAPLVP\IQ
		1				QFP\TEDWSAQPATE\DWS*A\P
		1				LAQATEWVGATTDWS
7450	37818	A	7504	1	1053	
745I	37819	A	7505	2	654	
7452	37820	Ā	7506	674	805	TLMOKSSIKYWOTESSSTSKSL
		ľ	l			STMIKWASSL*REIYSTKCPQEK
		I			1	AGKION*HPNITIKRTRKARANT
		l				FKS*OKARNN*NOSRTEGNRDT
		I	1		1	KNPSKN**/MPGAGFLKGSTKLI
		l				DR*OD**RKKERRIK*/IAIKNDK
		I				GDITTNPTEIQTTIREYYKHLYA
		l				NKLENLEEMHKFLDTYTLPRLN
		I	l	l		QEEVESLNRPITGAEIV\E*SIAY
		l			1	OPKKVODOMDSOANSTRGTRR
		1	l	l		NWYHSF*TIPINRKRGNP*TLM
		1		l		OKSSIKYWOTESSSTSKSLSTMI
		1				KWASSLGGKAGSIYANO
	L	L	L	L		I THOODOGIC TOOT TAIN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
7453	37821	A	7507	1	1577	MGDFNTPLSTLDRSMROK VNK
1433	37021	ı``	7.507	ľ	1377	DIQELNSALHOADLIDIYRNLHI
		1		l		ESTEYTFFSAPHHTYSKIDHILG
l						SKAPLSKYRRSEIKINGLSDHSA
		1				IKLELRIKKLTQNRSTTWKLNN LLLNDYWVHNEMKAEIKMFFE
		1				
		l		l		TNENKDTTYQNLWDTLKAVCR
						GKFIALNAHKRKQERSKIDTLT
						SQLKELEKQEQTHSKASRRQEI
			ŀ	l		SKIRGELKEIETQKTLQKINESR
1						GWFFEKINKIDRLLARLIKKKR
		1				EKNQIHAIKNDKGDMSTNHTEI
l	1	1	1			QTTIREYYKHLYANKLENLKEI
l		1				DKFLETYSLPRLNQEEVESLNR
1		1			1	PITGSEIEAIINSLPNKRSPGPDG
1		1				FTAKFYQRYKEELLISNFSKVS
1						GYKINVQKSQAFLYTNNRQTES
1		1				QIMSELPFTIASKRMKYLGIQPT
1	1					RDMKDLFKENYKPLLNEIKEDT
						NKWKNIPCSWVGRINIVKMAJL
		1				PKNWKKTTLKFIWNQKRARIA
1		1				KSILSQ/IEQSWRHHAT*LQTILQ
	ŀ	1				GYNNENSMVLVSKQRYRSMEQ
	27022	١.	7500		220	NRALRNNATYLQPSDL
7454	37822	Α	7508	58	330	FTENDDFQFHPCPYKGHELIIFY
l	į					GCIVFHGVYVPHFLNPVYHCW
1						TFGLVPSLCYCE*CRNKHTCAC
						VFIAA*FIVIWVYTQ*WDGWVK WYF
7455	37823	A	7509	1246	1522	DCLGNAGSFLVPYELGHYGHF
1433	37623	l^	1507	1240	1322	HNIDSSYQ*AW\MFFHLFVSFFI
						SLSSGL*FSLKRSFTSLVSWIPR
1						YFILFEAIVNGSSLMIWLSVCLL
7456	37824	A	7510	140	577	YSMYYMCHIFLIOSIIVGHLGW
1,150	5.02.	ľ.	1.5.10	1	J	FQVFAIVNNVTINIRVHVSL*QH
						DL*SFGY1PSNWMAGSNG1SSSR
						SLRNRHTVFHNG*TSLQSHQQC
						KSVPISPHPLOHLLFPDFLMIAIL
	l	1				TGVRWYLIVVLICISLMASDDE
		1		I		HFFMCFLAA
7457	37825	A	7511	399	677	NOREORHNIPESLGRIQSSV*RE
1,737	37023	l^	/511	J''	[""	IYSTKCPOEKAGKION*HPNITI
			İ	1		KRTRKARANTFKS*QKARNN*
l		1				NQSRTEGNRDTKNPSKNQ*IQE
						LVF
7458	37826	A	7512	1446	1855	IYKLPWAVWPFS*Y*FFLPMS/G
/430	3/820	l^	/312	1,440		GVFFHLFVSSFMSLSSGL*FSLK
						RSFTSLVSCIPRYFILSEAIVNGS
		1		I		SLMIWLSVCLLLVYKNACDFCT
	1	1				LILYPETLLKLSISLRRFWAETM
		1	l			
L			L		L	GFSRCTIMSSANRDNLISSFRN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7459	37827	Α	7513	I	2982	
7460	37828	Α	7514	5202	5430	
7461	37829	A	7515	2	454	
7462	37830	Α	7516	2	744	
7463	37830	A	7517	2	744 2422	MCPILREHRGSTEGKRRÖKR.P. LELTLKDEEVLAHRQEIEVAKE SPSKGNIHIFDYKGVEYHDQ DVTSNFLGAMWLISITFLSIGYC DMYPNTYCGKGVCLLTGIMGA GCTALVAVARKLELTKAEK HVHNFMMDTQLTKRHCPWAA TIQPKLSFLISLPGCDYRGESAR ARPLSIPPLQLGLGKDARYLRI CDRSLLCVCAAAGNAGLRRD SPHTLLHWSRSPYFFSEKPVPP QLLGGQPAAHSRRDJCGEAGV GRGGCFAALROVGSEWSGF SHTLLHWSRSPYFFSEKPVPP QLLGGQPAAHSRRDJCGEAGV GRGGCFAALROVGSEWSGF RHTJLBYGGGCFAALROVGSEWSGF BYPLTHHLGACTTAWSPCSFN SPDMETPLQFQRGFFPEQPPPP RSSHLHCQQQQQSDKPCPPFA SSHLHCQQQQQSDKCPCPPA SSHLHCQQQQSDKCPCPPA SSSLLLRTSSPGGGFRTRTSSPLSG SLLLRTSSPGGAFTRTSSPLSG SLLCCCCCCSSRRGSQLNVSELTI SSHASALRQQYAQQAQQSAS ASQYHQCHSLQPAASPTGSLGS LGSGPPLSHHHHPHPHAHHQH HQPQARRESNPFTELAMSSCRY NGGVMRRESNPFTELAMSSCRY NGGVMRRSNNFTSLGGGGGASSG SAAAAAAAVSSAPEVVSKP EHNISNILALVGTGGGGSTGG
7464	37832	A	7518	1	579	GGGGGGSGHGSSSGTKSSKKK NQNIGYKLGHRRALFEKRKRLS

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7465	27022	+	7519		1184	MSSANRSILEVPHLDILLOELPG
7465	37833	Α	/319	1	1184	VSKVVTVEVRGNWQRWLKVR
1		1				
		1		1		DLTKGVTYFFRVQARTITYGPE
		1		1		LQANITAGPAEGSPGSPRDVLV
		1			1	TKSASELTLQWTEGHSGDTPTT
l				l		GYVIEARPSVFGNGSFQVSKEE
1		ı				NQYFSEGLTSIEVPSQQVQQEG
		1			ŀ	AVAMALMVPDEGLWDMFVKD
	ļ.	1		l		IPRSATSYTLSLDKLRQGVTYEF
						RVVAVNEAGYGEPSNPSTAVS
		İ		l	ļ	AQVEAPFYEEWWFLLVMALSS
		1		i		LIVILL\VVFALVLHGQNKKYK
i				i		NCSTRQGISTMEESVTLDNGGF
					ŀ	AALELSSRHLNVKSTFSKKNGT
1		1				RSPPRPSPGGLHYSDEDICNKY
1	1	1				NGAVLTESVSLKEKSADASESE
ŀ		1				VSVGAYFRAVTISPYFCKDAGF
		1				AVRTIALGLAETAGSKADARK
7466	37834	Α	7520	1	1347	
7467	37835	Α	7521	512	1051	MAYCKSTPAVGLRVTV*SLSRL
	ì	1				SLICYTFCIGAPSHLSVGSLIIAT
ı		1				SFIVSNRPCRAPYVDTIYRLPSP
					l	LRLAGHRTLPLKPSFPRRSPPLL
						YYPSPRPPAHYPLSPSSEPNRRY
					l	TMALTAVPYPYTSPLQAFPFLH
1						SRIPQLQLFLLTNSFTSRTPVEP
						VQVLEILSQWKATTKWHYG
7468	37836	Α	7522	352	546	
7469	37837	Α	7523	1	360	
7470	37838	Α	7524	3	349	
7471	37839	Α	7525	1077	2142	SAVRYSVAITTADRRTAAGAIS
						YPTK*S*SEPIQEGQPEEQ/RAN
1						YPNGTYPTSLRHLERLWLRSAL
	i	1		l		SVKARF/YHQQYSLKKYRYKHI
1				ŀ		ADNVCQWLDEVFLRPKEMSDI
		1		1		HKLTFIEKRERLKNSVFKSLHD
l		1		l		VRTVEDPSGTQLEVVSNNPWD
		1				PKRQLLKWDGTKWTGWDIPD
	İ	l				YSAAPPEA VPSLNNPQTFSEQK
l		l				LDEALYHGAVLRVRPKAMTVA
		1		I		VIIAGLLPILWGTGAGSEVMSRI
					1	AAPMIGGMITAPLLSLFIIPAAY
		1			l	KLMWLHRHRWLKCKSARRPO
				I		YOSGYTDDRHSRSVKASPTAG
				I		LPSLTHEQQQKAVERIQELMAQ
		1		1		GMSSGQAIALVAEELRANHSGE
				1		RIVARFEDEDE
		Щ.	I	L	l	ia - Aia CDCDC

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7472	37840	A	7526	116	191	RLKFTETNLYTNIYVGSIHIHLN
						LEIIHMSLH**MDRTNINIRVOIC
		l				FCEFKSLVLLDKPGRQELIDDL
		l				NKRTDNFLTDSGISVSDWIDAA
		l		ĺ		TWEVFSSLRELELLGIKNIRLAS
		1				QDLHGVILSSETVAEDIWCRILD
		ł		ŀ		TVTRKGEHSRRIHSADDKSYLR
		1				PDLLEWFKQRVEDDQSRSGRKI
			ł			YVKRDLPHILTPFRAPMASVCA
						KRKGQVLHQQYSLKKYRYKHI
ŀ		1				ADNVCQWLDEVFLRPKEMSDI
		l				HKLTFIEKRERLKNSVFKSLHD
1		l		1		VSEFLGRVLLHATDPAAPRKPA
						YSLHAIRGKSRGRKNS
7473	37841	Α	7527	1	177	
7474	37842	Α	7528	I	399	
7475	37843	Α	7529	3	209	
7476	37844	Α	7530	I	288	
7477	37845	Α	7531	2	256	
7478	37846	Α	7532	414	1188	TSFLTTGGKKGS\KKKVVDPFS
		l				KKD/WL*YVKHPAMFNIRNIGK
		l				DVGSPRTQGTKIAS\DGLKG\RV
		l	ł	ŀ		FE\VSLADLQHDEVAFRKFKLIT
		l				\EDVQGKNCLTNFHGMDLT\RD
		l	ł			K\MCSMVKKW\QTMI\EAH\VD
		l	ŀ	-		VKTT\DG\YLLRLFCVGF\TKKR
				ŀ		NNQIGKPF*AQ\HHRVRQIGKK
						MMEIMTREVQTNDLKEVVNKL
		l		ŀ		IPDSIGKDIEKACQSIYPLHDVF
		l	ĺ			VRKVKMLKKPKFELGKLMELH
		<u> </u>				GEGSSSGKATGDETGAKVERA
7479	37847	A	7533	1	1140	
7480	37848	A	7534	131	410 861	
7481	37849	A	7535	I		MINISH ST SECTION OF STATE
7482	37850	Α	7536	1	406	MWEILELPROLLNGFAQNADS
	1					NMDNKVQAEVALDGNGELVG
	i			l		YYSKASAGDTQANRVWSGPPA
			ŀ			NSNRPAAEGPERNTININKKDIN
						TKTPSVGHRHQRPKVDKTTKT
		ĺ	l			R\KTRAEKLKILKTRVPLIFQRT
7492	27051	<u> </u>	7527	1266	1/20	AALRQR
7483	37851	Α	7537	1366	1629	TQSPVQTKPTPITTRGGGFLPTQ
1		1				PFPVILQRQFCPE*LVAFMGS*E DVP*GSFRVSAESSIL*RAP*GA
1						
7404	27052	-	7520	502	648	QSTCKPVNRNEKISKRIVH
7484	37852	A	7538	502	048	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletinn, \=possible nucleotide insertion)
				sequence		
7485	37853	A	7539	h	1169	PPLLIPRQTGSGVDLQQTPTDLQ
7405	37033	ľ	7557	ľ.	,	LRVLTVRRKTNKOKGHPHONSI
						CTSPSSKTKDFKPTKIKRDKEG
		1				HYIMVKGSIQQEELTILNIYTPN
1		1				TGAPRFIKQVLRDLQRDLDSHT
		1				IIVGDFNTPLSTLDSSKROKVDK
		1				DIQELNSALYQADLTDIYRTLH
1		1				PKSTEYTFFSAPHHTYSKIDHIV
ì		1				GSKALLSKCNRTEIITNCLSDHS
1		1				AIRLELRIKKLTENRSTTWKLN
		1	l			NLLLKDYWVHNEMKAEIKMFF
		i i				ETNENKDTTYQNLWDTGKAAC
		1				RGIFIAINAHKRNOKRSKMDTL
		1				TSQLKELEKQEQRHSKASRRLN
		1				QEEVESLNKPRTGSEIEAIINSLP
		1				TKKSPGADGFTAEFYQRYKEE/
		1				PGTIPSETIPINRKRGNTP*LIL*G
		1				OHHPDTKA
7486	37854	A	7540	1	404	MDEFLNTYTLPRLNQEEVESLN
	1	ı				RPITGSEIVAIINSLPRKKSPGPD
ì	1	ı				GFTAEFYQRYKEELVPFLLKLF
1		ı				QSIEKEGILPNSFYEASIILIPKPG
		ı				RDTTIKENFRPISLMNIDAKILN
		ı				KIILANRIQQHIKKLIHHDQVGFI
		1				PGMQGWFNIRKSINVIQHINRT
		1				KDKNHMIISTDAEKAFDKIQQP
		1				FMLKTLKKFGIDGTYLKIRIKYL
		1				GIQLTRDVKDLFKENYKPLLNE
						IKEDTKKWKNIPCSWVGRINIM
		1				KMAILPKVIYRFNAIPIKLPMTF
		1				LTELEKTTLKFIWNQKRARIAK
						SILSQKNKAGGITLPDFKLYYK
		1				ATVTKTAWYWYQKRDIHQWN
		1				TTEPSEITPHIYNHLIFDKPEKNK
		1				QWGKDSLFNKWCWENWLAIW
		1				RKLKLDPFLTPYTKINSRWIKD
		1				LNVRPKTIKTLEENLGITIQDIG
		1				MGKDFMSKTPKAMATKAKIDK
		1				WDLIKLKSFCTAKETTIRVNRQ
		1				PTKWEKIFTTYSSDKGLISRIYN
1		1				ELKQIYKKKSDNPIKKWVKDM
1						NRHFSKEDIYAAKKHMKKCSP
1		1				SLAIREMQIKTTMRYHLTPPSLL
1						IPRQTGSGVDLQQTPTDLQLKV
		1				LTVRRKTNKQKVHPHQNPICTS
		1	1			PSSKTKELEKQEQTHSKASRRQ
		1			l	EITKIRAELKEIETQKNLQKINES
		1				RSWFLEKVNKIDRLLARLIKKK
	1	1	1			REKDQIDAIKNDKGDITTDPTEI
	<u> </u>	1_			l	QATIREHYKHLYANKLENLEE

NO:   of peptide sequence   not   not   1.5SN   oods   not   1.5SN   oods   for pertide   of peptide   of peptide   oods   for pertide   oods   for pertide   oods   for pertide   oods   for pertide   of peptide	SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
7487   37855   A   7541   3   1284   SAADTOANRVWSYPTNSNRP   AAEGPDC*KEN*OKGHPHQNPI   CQSPSSKIPKVDKTTKMGKKON   RKTONSKNOSTSPPDGEHSSSPA   MEQRITNAEKYLKDIMELKTT   AQELHDECTSLSSPFDQLEERV   SVMEDOMNEMKREEKFREKRI   KRNEGSLERIPDYKRPNLENI   GVPESDRENGSKLENTLQDIQ   ENPPNLARHANIGOFIQEMPPQ   RYSSKRATPRVIIVRFTKVEMK   EKMIRAAROKSLVTHKGKLIR   LTAGKFIALIAHKGNGERSKIDT   LTSQLKELEKQEQTHSKPSRRQ   EITKIRAELKEIETGTTLQKINES   RSWFFEKINKIDRLLARLIKKKR   EKNQIDAIKNDKGDITTDPTEIQ   TTIRRYYKHHYANKLENLEKM   NKFLDTYTLPRLKQEEVESLINR   PIKALKLRQ   MLSSVGLLTHRIKKKSTDTIN   DESLNKEKDMTGNPHIFPRYQE   IWQVFVSSGNNYITTATOFTAV   PPLLIPRQTGSGVDLQQTPTDLQ   LRILTYGRKTNKQKGHPHQNPI   CTSPSSKTKERTTIREYYKHLYANKLENLEKM   CTSPSSKTKERTTIREYYKHLY   ANKLENLEEMDKFH*HIHPPKT   KPGRS*ISA*TNNRL*N*GNN*H*   LTNGKKSRTRWHSRILPEVQG   GADAQRAKHE*TPIHNCYEENSK   IPRNFTYKEHECPLQGELQTTS   QGNKRGYKQM/DRTFHAHG*E   ESIS*KWPYCPR*FIDSSPSSYQ   *LSSQNIGKNYFKVHMEPKKSP   YCQVNPKPKEGSWHHAT*LQ   TILQGYSNQNSMVLVPKQRYPR   MEQSPOK   MESSPO		of peptide		in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
7487   37855   A   7541   3   1284   SAADTOANRYWSYPTNSNRP   AAEGPDC*KEN*QKGHPHQNPI   CQSPSSKIKYDKTTKMGKKQN   RKTONSKNOSTSPPQEHSSSP   MEQRITNAEKYLKDLMELKTT   AQELHDECTSLSSPPQLEESSY   MEQRITNAEKYLKDLMELKTT   AQELHDECTSLSSPPQLEESSY   SVMEDQMNEMK REEKFREKR   KRNEQSLKEIN'DVYKRPNLPLI   GVPESDRENGNKLENTLQDIIQ   ENFPNLARHANIQIGFIQRMPQ   RYSSKAPTPRYINFETKVEMK   EKMLRAAROKSLVTHKGKLIR   LTAGKFIALIAHKGNQERSKIDT   LTSQLKELEKQEQTHSKPSRRQ   EITKIRAELKEIETQTTLQKINES   RSWFFEKNINIDIALKALKKKR   EKNOJDAIKNDKGDITTDPTEQ   TTIREYYKHHYANKLENLEKEM   NKFLDTYTLPRLKQEEVESLIN   PIKALKLRQ   MILSSYGLLLTHRKKKSTDTIN   DESLNKERDMTGNPHIFPRYQE   IWQVFVSSGNYITTATGPTAV   PPLLIPRQTGSGVDLQQTPTDLQ   LRLLTVGRKTNKCKGEHPHONPI   CTSPSSKTKEERTTIREYYKHLY   ANKLENLEEMDKFM*HHPPKT   KPGRS*ISA*TNKLN*GNNY*   LTNQKKSRTRWHSRILPEVQG   GADKQRAKHE*TPIHNCFKENK   IPRNPTYKEHECPLQGELQTTS   QGNRRGYKQMDRTFHAHG*E   ESIS*KWPYCPR*FIDSPSPSSYQ   *LSSQNIGKNYFKVHMEPKKSP   YCQVNPKPKEGSWRHHAT*LQ   TILLQGYSNQNSMVLVPKGRYKP   MEQSPOK   MILSSFHLDREKGELLWSLEWR   DPDGGSIRMEVGLGGWTQRLE   EEKKRNVCSHGNIEKDFPYYRIL   EFEKKNVCSHGNIEKDFPYYRIL   GGSCOTVLTMKERWPHCKSP   YCSSKHLLKTGFISEAVLCYGE   GGEGDTVLTMKERWPHCKSP   CTSSKHLLKTGFISEAVLCYGE   GGEGDTVLTMKERWPHCKSP   CTSSKHLLKTGFISEAVLCYGE   GGEGDTVLTMKERWPHCEVLU   QCNKGRLTHHTARYSSETKLPE   EEKSGNCGSHSAVLQPPLLIPR   GTGSGVDLQQTPTNLQLRVLT   VRRKTNKQKGHPHQKPICKMSP   SKTKDFKTKIKRGKHPHCKNSPS   SKTKDFKTKIKRGKHPHCKNSPS   SKTKDFKTKIKRGKHPHCKINSPS   SKTKDFKTKIKRGKHPHCKNSPS   SKTKDFKTKIKRGKHPHCKINSPS   SKTKDFKTKIKRGKHPHCKNERSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHCKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHQKPICKMSPS   SKTKDFKTKIKRGKGHPHCKPICKMSPS   SKTKDFKTKIKRGKGHPHCKPICKMSPS   SKTKDFKTKIKRGKGHPHCKPICKMSPS   SKTKDFKTKIKRGKDFATKINGTH   SKTETKLTH   SKTETKLTH   SKTETKLTH   SKTETKLTH		sequence	1	09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
AABGPDC* KEN*OKGHPHONPI CQSPSKIPKVDKTIKMGKKON RKTONSKNOSTSPPPQEHSSSPA MEQRITNAEKYLKDLMELKIT AQELHDECTSLSSPPQLERSY SVMEDQMNEMKREEKFREKRI KRNEQSLKEIWDYVKRPNLPLI GVPESDRENGRKLENTLQDIIQ ENPPNLARHANIQIGFIQRMPQ RYSSKATPRVIINFTKVEMK EKMLRAARDKSLVTHKGKLIR LTAGKFIALIAHKGNQERSKIDT LTSQLKELEKQEQTHSKPSRRQ EITKIRAELKEIETQTTLQKINES RSWFFEKINKIDRLARLIKKKR EKNOIDAIKNDKGDITTDPTEIQ TTIREYYKHHYANKLENLEKM NKFLDTYTLPRLKQEEVESLNR PIKALKLRQ  7488 37856 A 7542 I 1082 MLSSVGLLLTHRKKKSTDTIN DESLNKERDMTONPHIPPRYQE IWQVFVSSGNSYITTATOFTAV PPLLIPROTOSOVDLQOTPTDLQ LRLLTVGRKTNKQKGHPHQNPI CTSPSSKTKEIRTIREVYKHLY ANKLENLEEMDKF#HHIPPKT KPGRS*ISA*TNRLN*GNN** LTNGKKSRTRWIHSRILPEVQG GADKQRAKHE*TPIHNCFKENK IPRNFTYKEHEOPLQGELQTTS QONKRGYKQMDRTFHAHG*E ESIS* KWPYCPR*PIDSPSPSSYQ *LSSQNIGKNYFKVHMEPKKSP YCQVMPKPKEGSWHHAT*LQ TILQGYSNQNSMVLVPKQRYR MEQSPQK 7489 37857 A 7543 I 2012 MINSRHLINEVGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKRNCSHGNIEKERPPTYPIR EFEKSNCSHGNIEKERPPTYPIR LTGLQGKMDLKGVFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERRPHECTULI QCNKGRLTHHTARYSSETKLPE ERSGSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQRVLT VRRKTNKQKGHPHQKPICMSPS SKYKDFVFKIKROKEGEHJWNLY VRRKTNKQKGHPHQKPICMSPS SKYKDFVFKIKROKEGEHJWNLY VRRKTNKQKGHPHQKPICMSPS SKYKDFVFKIKROKEGEHJWNLY VRRKTNKQKGHPHQKPICMSPS			1		sequence		
AABGPDC* KEN*OKGHPHONPI CQSPSKIPKVDKTIKMGKKON RKTONSKNOSTSPPPQEHSSSPA MEQRITNAEKYLKDLMELKIT AQELHDECTSLSSPPQLERSY SVMEDQMNEMKREEKFREKRI KRNEQSLKEIWDYVKRPNLPLI GVPESDRENGRKLENTLQDIIQ ENPPNLARHANIQIGFIQRMPQ RYSSKATPRVIINFTKVEMK EKMLRAARDKSLVTHKGKLIR LTAGKFIALIAHKGNQERSKIDT LTSQLKELEKQEQTHSKPSRRQ EITKIRAELKEIETQTTLQKINES RSWFFEKINKIDRLARLIKKKR EKNOIDAIKNDKGDITTDPTEIQ TTIREYYKHHYANKLENLEKM NKFLDTYTLPRLKQEEVESLNR PIKALKLRQ  7488 37856 A 7542 I 1082 MLSSVGLLLTHRKKKSTDTIN DESLNKERDMTONPHIPPRYQE IWQVFVSSGNSYITTATOFTAV PPLLIPROTOSOVDLQOTPTDLQ LRLLTVGRKTNKQKGHPHQNPI CTSPSSKTKEIRTIREVYKHLY ANKLENLEEMDKF#HHIPPKT KPGRS*ISA*TNRLN*GNN** LTNGKKSRTRWIHSRILPEVQG GADKQRAKHE*TPIHNCFKENK IPRNFTYKEHEOPLQGELQTTS QONKRGYKQMDRTFHAHG*E ESIS* KWPYCPR*PIDSPSPSSYQ *LSSQNIGKNYFKVHMEPKKSP YCQVMPKPKEGSWHHAT*LQ TILQGYSNQNSMVLVPKQRYR MEQSPQK 7489 37857 A 7543 I 2012 MINSRHLINEVGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKRNCSHGNIEKERPPTYPIR EFEKSNCSHGNIEKERPPTYPIR LTGLQGKMDLKGVFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERRPHECTULI QCNKGRLTHHTARYSSETKLPE ERSGSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQRVLT VRRKTNKQKGHPHQKPICMSPS SKYKDFVFKIKROKEGEHJWNLY VRRKTNKQKGHPHQKPICMSPS SKYKDFVFKIKROKEGEHJWNLY VRRKTNKQKGHPHQKPICMSPS SKYKDFVFKIKROKEGEHJWNLY VRRKTNKQKGHPHQKPICMSPS	7497	27955	-	7541	13	1284	SAADTOANRVWSVPDTNISNED
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DESLNKERDMTONPHIFPRYQE IWQVFVSSGNNYITTATGPTAV PPLLIPRQTGSGVDLQQTPTDLQ LRLLTVGRKTNKQKGHPHQNPI CTSPSSKTKEIRTTIREYYKHLY ANKLENLEEMDKFM**HIHPPKT KPGRS*ISA*TNNRLI*N**GNN*** LTNQKKSRTRWIHSRLIPEVQG GADKQRAKHE*TPIHNCFKENK IPRNPTYKEHEGPLQGELQTTS QGNKRGYKQMDRTFHAHG*E ESIS*KWPYCP**FIDSPSPSSYQ *LSSQNGKNYFKYHMEPKKSP YCQVNPKPKEQSWRHHAT*LQ TILQGYSNQNSMVLVPKQRYRP MEQSPQK  7489 37857 A 7543 I 2012 MNLSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLLKTGTESAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPSAVLOPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKVLT VRRKTNKROKGHPTVRLTS			1				
IWQVFVSSGNNYITTATCPTAV	7488	37856	A	7542	I	1082	MLSSVGLLLTHRRKKKSTDTIN
PPLLIPROTGSOVDLOGTPTDLO LRLLTVGRKTNKQKGHPHQNPI CTSPSSKTKEIRTIREVYKHLY ANKLENLEEMDKFM*HHIPPKT KPGRS*ISA*TNKLN*GNN** LTNQKKSRTRWIHSRILPEVQG GADKQRAKHE*TPIHACPKENK IPRNPTYKEHEGPLQGELQTTS QGNKRGYKQMDRTFHAHG*E ESIS*KWPYCPR*FIDSPSSSYQ *LSSQNIGKNYFKVHMEPKKSP YCQVNPKPKEGSWRHHAT*LQ TILQGYSNQNSMVLVPKQRYR MEQSPQK TILGGYSNQNSMVLVPKQRYR MEQSPQK MINSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLETGFEAVLCYGE GGEGDTVLTMKERPPHEIVTLI QCNKGRLTHTARYSSETKLPE ERSGSSIGGSPSAVLQPPLLIPR QTGSGVDLQOTPTNLQLRVLT VRRKTNKQKGHPHQKPICKNSPS SKTKDFKFTKIRFOKEGHYMSPS	1		1				DESLNKERDMTGNPHIFPRYQE
LRLLTYGEKTHKOKGGIPHONPI   CTSPSSKTKEIRTTIREYYKHLY     ANKLENLEEMDKF#I+HIPPET    KPGR\$*ISA*TNNRL*N*GNN**     LTNOKKSRTRWINSRLIPEVOG     GADKQRAKHE*TPIHNCFKENK     IPRINFTYKEHEOPLOGELQITS     QGNKGYKGMDFTFHAHG*E     ESIS*KWPYCP**FIDS*PS*SYQ     LSSQNGKNYFKVHMEPKKSP     YCQVNPKPKEGWRHHAT*LQ     TILQGYSNQNSMVLVPKGYRP     MEQSPOK     TILQGYSNQNSMVLVEGRYRP     DPDGGSRMEVGLGGWTQRLE     EEKKGNVCSHGNLEKDFPYIPH     LFGLQQKKMDLKGVFKSCFKI     YCSSKHLLKTGTESAVLCYGE     GGGGDTVLTMKERWPHECIVLI     QCNKGRLTHTARYSSETKLPE     ERSGSSIGSPISAVLOPPLLIPR     QTGSGVDLQOTPTNLQLRVLT     VRRKTNKQKGHPHQKVLT     VRRKTNKQKGHPHQKVLT     VRRKTNKQKGHPHQKVLTSSE							IWQVFVSSGNNYITTATGPTAV
7489 37857 A 7543 I 2012 MINLSPHENEYSPEKLYSELSYN LFG GGEOTYLTMERWPHECKYGL GGEOTYLTMERWPHECKSEK I PRINTSPHENCES SKYLOG GGEOTYLTMERWPHECKS I PRINTSPHENCES SKYLOG STAR STAR STAR STAR STAR STAR STAR STAR			l				PPLLIPROTGSGVDLQQTPTDLQ
ANKLENLEEMDKFM+HIHPPKT KPGRS*ISA*TNNICH*N*GNN** LTNOKKSRTRWHSRILPEVQG GADKQRAKHE*TPIHNCFKENK IPRNPTYKEHEGPLQGELQTTS QGNKRGYKQMDRTFHAHG*E ESIS*KWPYCPR*PIDSSPSSYQ *LSSQNGKNYFKVHMEPKKSP YCQVNPKPKEQSWRHHAT*LQ TILQGYSNQNSMVLVPKQRYRP MEOSPOK  7489 37857 A 7543 I 2012 MNLSRHINEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLLKTGHSEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTHTARYSSETKLPE ERSGSSICGSPISAVLOPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKVLT VRRKTNKQKGHPHQKVLT VRRKTNKQKGHPHQKVLT VRRKTNKQKGHPHQKVLTSSSKTKDFEFFTIKROKEGHYJNVL VRRKTNKROKGHPHQKVLT			l				LRLLTVGRKTNKQKGHPHQNPI
RPGRS*IS.A*TNNRL*N*GONN* LTNQKKSRTRWHSRILPEVQG GADKQRAKHE*TPIHNCFKENK IPRNPTYKEHEGPLQGELQTTS QGNKGYKGMDFTFHAHG*E ESIS*KWPYCPR*FIDSPSSYQ *LSSQNIGKNYKKVHMEPKKSP YCQVNPKPKEGBYNYKVHMEPKKSP YCQVNPKPKEGSWHHAT*LQ TILQGYSNQNSMVLVPKQRYRP MEQSPQK  7489 37857 A 7543 I 2012 MNLSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTHTARYSSETKLPE ERSGSSIGGSPSAVLOPPLLIPR QTGSGVDLQOTPTNLQLERVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKFTKIKROKEGHYJMV			l	l			CTSPSSKTKEIRTTIREYYKHLY
LTNOKKSRTRWIHSRILPEVOG GADKORAKHE*TPIHNCFKENK IPRNPTYKEHEOPLOGELQTTS QGNOKRGYKOMDRTFHAHG*E ESIS*KWPYCPR*FIDSPSPSSYO *LSSQNIGKNYFKVHMEPKKSP YCQVNPKPKEGSWRHHAT*LQ TILQGYSNQNSMVLVPKQRYRP MEQSPOK  7489 37857 A 7543 I 2012 MINERHLINEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNUEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERFPPHEVILI QCNKGRLTHTARYSSETKLPE ERSGSSIGGSPSAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKYKDFKFTKIKROKEGHJWNSP			l			1	ANKLENLEEMDKF/H*HIHPPKT
GADKQRAKHE*TPIHNCFKENK IPRNPTYKEHEGPLQGELQTTS QGNKRGYKQMDRTFHAHG*E ESIS*KWPYCPR*FIDSYPSSYQ *LSSQMGKNYFKYMHEPKKSP YCQVNPKPKEQSWRHHAT*LQ TILQQYSNQNSMVLVPKQRYRP MEQSPQK  7489 37857 A 7543 I 2012 MNLSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLLKTGTESAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPSAVLOPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKVLT VRRKTNKQKGHPHQKVLT VRRKTNKQKGHPHQKVLT VRRKTNKQKGHPHCMSPS SKTKDFKFTKIKROKEGHYJMV			1			ŀ	KPGRS*ISA*TNNRL*N*GNN**
IPRNPTYKEHECPLQGELQTTS   QGNKRGYKQM/DRTFHAHG*E			l				LTNQKKSRTRWIHSRILPEVQG
OGNKRGYKQM/DRTFHAHG*E			1				GADKQRAKHE*TPIHNCFKENK
ESIS*KWPYCPR*FIDSPSPSSYQ *LSSQNGKNYFKVHMEPKKSP YCQVNPKPKEQSWRHHAT*LQ TILQGYSNQNSMYLVPKQRYRP MEQSPQK 7489 37857 A 7543 I 2012 MNLSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFRSCFKI YCSSKHLLKTGFISAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTHTARYSSETKLPE ERSGSSIGGSPSAVLOPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIKROKEGHYJMV			1				IPRNPTYKEHEGPLQGELQTTS
*LSSQNGKNYFKVHMEPKKSP YCQVNPKPKEQSWRHAT*LQ TILQGYSNQNSMYLVPKGRYRP MEQSPQK 7489 37857 A 7543 I 2012 MINLSRHLINEVKGELLWSLEWR DPDGGSIRMEVGLGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERFPRYHECIVLI QCNKGRLTHTARYSSETKLPE ERSGSSICGSPSAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKYTKDFKFTKIKRDKEGHYIMV	İ		1				QGNKRGYKQM/DRTFHAHG*E
7489 37857 A 7543 I 2012 MNLSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFRSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTHTARYSSETKLPE ERSGSSICGSPISAVLOPPLLIPR QTGSGVDLQOTPTNLQLRVLT VRKKTNKQKGHPHQKVLT VRKKTNKQKGHPHQKVLT VRKKTNKQKGHPHQKNT			l				ESIS*KWPYCPR*FIDSPSPSSYQ
7489 37857 A 7543 I 2012 MNLSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGWCSHGNLEKEFPFIJHH LFGLQQKKMDLKGVFRSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTHTARYSSETKLPE ERSGSSIGGSPSAVLOPPLLIPR QTGGGVDLQOTPTNLQLRVLT VRKTKNKQKGHPHQKPICMSPS SKTKDFKFTKIKROKEGHYIMVS			l		ĺ		*LSSQN\GKNYFKVHMEPKKSP
7489 37857 A 7543 I 2012 MNLSRIKINEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGYFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLIIPR QTGSGYDLQOTPTNLQLRWLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIRROKEGHYIMV			l				YCQVNPKPKEQSWRHHAT*LQ
7489 37857 A 7543 I 2012 MMLSRHLNEVKGELLWSLEWR DPDGGSRMEVGLGGWTQRLE EEKKGNVCSHGMLEKDFPYIPH LFGLQQKKMDLKGVFRSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPSAVLOPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKNCMSPS SKTKDFKPTKIRROKEGHYJMV			ı				TILQGYSNQNSMVLVPKQRYRP
DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKKGFYIPH LFGLQQKKMDLKKGFYSCFKI CSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIRROKEGHYJMSPS			ı				MEQSPQK
EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGYFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGYDLQOTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIRROKEGHYIMV	7489	37857	Α	7543	I	2012	MNLSRHLNEVKGELLWSLEWR
LFGLQOKKMDLKGVFRSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSIGSPISAVLQPPLLIPR QTGSGVDLQOTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIRKDKEGHYIMV			l		l		DPDGGSIRMEVGLGGWTQRLE
YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSETKLPE ERSGSSICGSPISAVLQPPLIIPR QTOSGYDLQQTPTNLQLRVLT VRRKTNKQKGIPHQKPICMSPS SKTKDFKPTKIROKEGHYIMV	İ		l		l		EEKKGNVCSHGNLEKDFPYIPH
GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPISAVLOPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIRROKEGHYIMV			1				LFGLQQKKMDLKGVFKSCFKI
QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGIPHQKPICMSPS SKTKDFKPTKIKRDKEGHYIMV						ļ.	YCSSKHLLKTGFISEAVLCYGE
ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQFPIGMSPS SKTKDFKPTKIKRDKEGHYIMV			1		l		GGEGDTVLTMKERWPHECIVLI
QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIRRDKEGHYIMV			1		1		QCNKGRLTPHTARYSSETKLPE
VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIKRDKEGHYIMV	1		1		l		ERSGSSICGSPISAVLQPPLLIPR
SKTKDFKPTKIKRDKEGHYIMV					1		QTGSGVDLQQTPTNLQLRVLT
	1				l		VRRKTNKQKGHPHQKPICMSPS
					1		SKTKDFKPTKIKRDKEGHYIMV
KGSIQQEELTILNIY							KGSIQQEELTILNIY

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7490	37858	Α	7544	402	675	QGYPGTELSSAPSGPNRHLQNF
		1				PPQINRIYILLSTTSHLFQN*PHS
	1	1				WK*STPQQM*KRRNYNKNO\L
		1				ELRIKKOTONRSTTWKLNNLLL.
		1				NDY
749I	37859	Α	7545	21	428	DKTSRGTIRQQHLLFTNIRCSAA
		l		ì		SAADTQANRVWSGPPANSDRP
		l				AAEGPDC*KEN*QTERTSTPKS
						HLYVTIIKDORNKIPKNPTYKG
			İ			CEGPLOGELOTTAQONKRRYK
						QMQEHSMLMGRKNQYHENGH
		1				TAQGNL
7492	37860	В	7546	1	1650	
7493	37861	A	7547	1	946	MAMPPLLIPROTGSGVDHQQTP
						TDPOLRILTVRRKTNTOKGHPH
		1				ONPNCTSPSSKTKELKEEVGTO
		1				RKEVKNLEKRLDEWLTRIANA
		1				EKSLKDLMOLKTMAGELOLDK
	ľ	1				TTLNFIWNOKRACIAKTILSKK
		1				NKAGGIRLPDFKLYYKATVTKT
		ı		i		AWYWHONRYIDOWNRTEASEI
		l		ŀ	l	MPHIYNHLIFDKPDKKKOWGN
						DSLF/K*MVLGKLASHMOKTEI
			1			GPLPYNFYKN*LKMD*RLKGK
		l				T*NHRNHRRKPKQYHSGHRHG
l		l				ORLHD*NTKSNGNKGON*OMG
		l				SN*TKELL/ROOKKLPSE*TRNL
		1			1	ONGRKFVOSIYLTKG
7494	37862	A	7548	189	380	OTERTSTONPICTSPSSKTKGR*
7424	57002	ľ``	7540	105	1	NHKDGEKTEQKNWKL*KAERL
1		ı				SSSKGMOLLSSNGTKLDGE
7495	37863	c	7549	1	2805	SSSKGMQEESSKGTKEDGE
7496	37864	A	7550	535	696	
7497	37865	A	7551	214	363	LLEGKLTNRKE*HOHOOKGHP
,,,,,	3,003		,551	217	100	HONPICTSPSSKTKVT*NHKDG
		1				EKT*OKS
7498	37866	A	7552	787	1056	GOKKKLMIIGINSRNHHGPO*P
, 490	7,000	ľ	. 332	1.0.	1	ALOKMPAS*VTEIMNNHFLFCF
						RKGKGRIKLVNSRVEHOAGSW
						GPWFQSLVAGQYFWTCSGPDG
	1		L			SPLP

SEQ ID	SEO ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
Ì		ľ		sequence		
# 400	00000	<del>                                     </del>	7553	<u> </u>	4560	MKHTLIPRIKNACLQMSSLAVP
7499	37867	Α	/553	1	4560	
				l		VNSLVCLGKILEYLDKWLVLD
l		į.				GILPFLQQIPSKESAVLMGILGIY
l						KCTFTHKLGITKEQLTGKVLPH
l		ŀ				LIPLSIENNLNQFNSFISIIKEML
l						NRLESEHKTKLEQLHIMQEQQK
ŀ						SLDIGNQMNVSEETKVTNIGNQ
		ŀ				QIDKVFSHIGADLLTGSDSENK
	ł				1	EDGALNVPPAGAKPTQQRPTD
						MSALNNLFGPQKPKVSMNQLS
1						QQKPNQWLNQFVPPQVSPATG
l						SSVMGTQMNMIGQ
7500	37868	С	7554	I	1359	
7501	37869	A	7555	272	915	YPGKQGLEWTSSKLQQTCC*GS
				ì		*LLEGKRTNRKDINTKNPSVRH
						HHQRPKMGEKTEQKNRKLKIR
						APLLLQRNTAPH/HAMEQSWM
1		1		1		ENDFDELREEGFRRSNYSELKE
						EVRTNAKEVKNFEKKLDEWIT
						RITNAEKSLKDLMELKTTA\EN
						YVTNAOAPVANATN*KKGYOR
		1				WKTK*MK*SEKRSLEKKE*KEK
1						KQSLQEIWDYVKRPNLCLIGVP
7502	37870	A	7556	196	494	HTDGVSVWMSFLFVSFPSNSQD
/302	3/6/0	^	7330	1190	434	POLOVOWSLLEVHSRPCLPGYO
				İ		OORIRLEPFKINV/T*ADHEAYR
ŀ		l				
						KTAVRRCSQTTQQAWEQSAHQ
7503	37871	В	7557	28	303	QHIRH*SCRYPG
7504	37872	A	7558	1216	1863	HPDITIKRTREARANTFKS*OKA
1304	37072		1550	1210		RNN*DERRTEGNRDTKNPSKKS
						VN/RRSWFFEKFNKIDRRLARLI
	1				1	KKKREKNQIDAIKNDKRDITTD
						PTEIOTTIREHYKHLYANKLEN
	ļ.					
						LEEMDKFLDTYTLPRLNQEEVE
						SLNRPITGSEIEAIINSLPTKKSP
						GPDGLTAKFYQRYKEE/PGTIPS
						ETIPINRKRGNPP*LIL*GLHHPD
		1_				TKAWQRHYKKREF
7505	37873	Α	7559	166	785	FRATSAADTQANRVWSGPPAN
I	1	1				SNRSAAEDPDC*KEN*PT\KGHP
I	1	1			1	HQNPICTSPSSKTKARQANIQIQ
	1	1		-		EIQRMPQRYSSRRATPRCIIVRF
l	1	1	1			TKVEMKEKMLRAAREKGQVT
	1	1			1	HKGNPIRLTADLLVKTLQARRE
I	1	1	1			WGPIFNILKEKNFOPRISYPAKL
			1			SFISEGEIKSFTDKQMLRDFGTT
				1		RPALKELLKEALNMERNNOYO
		1		i	1	PLQKHVRL
7506	37874	A	7560	I	1164	
,500	15/0/4		1,500	<u>ı </u>	1	<u> </u>

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7507	37875	A	7561	770	2670	RRARCSCAPSSTTTLGRTGPSLA RRRACPSSAGRSWRW*ARTTPR GGRPSESGTFTFEPASSPPRGSR RDPQEGGSWVRGWQLWTSTV GCSPHIFWCVDCETCDCEGYLK GHYVAGLRSFRLGCSERLGGG GEGKMSSGAESPELLTYEEVAR YQHQPGERPRLVVLIGSLGARL HELKQKVVAENPQHFGVAVPR APWDVKLQWAEDPGSECDKE DEEENENGART.EHGEFYENLY GTSLEAIQAVMAKNKVCLVDV EPEALKQLRTSEFKPYHFVKPAI QEKRKTPPMSPACEDTAAPFDE QQQEMAASAAFIDRHYGHLVD AVLVKEDLGAYSQLKVVLEK LSKDTHWPPLVIPROTGSGVDL QQTFTDLOLRVLTVRRKTKKQ KGHPHQNTPCTSPSSKTKVGER VSVIEDQMKEMKREKKFREKR KKRNEGSLGEHDVYKKFPLL LIGVPESDGENGTKLENTLQDI MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM PORTSTRAFTENDER PORTSTRAFTENDER PRINTER PRINTER MENDFRIARGANGLIGEDIM MENDFRIARGANGLIGEDIM PORTSTRAFTHHIIIRFTEVEM
7508	37876	A	7562	181	690	KEKMLRAAREKGWYTHKGKPI RLTADLLAETLQARREWEPIFNI LKGKNFQFRISYPAKLNFISEGE IKSFTDKQMLRDFVTTRPALQEL IKERALNERSNWYQPLQKHAK GHAIVTGDAVGMDDIPQEARQ YRHNQAYAYSIQGDGAEDDDE RIVRFHTRCLNGRVLL1*DK/IFQ RNDQAATFAAHQYPLFCSLHC* YPGTQGLEWTSSKHQQTCS*G6 **LLWFGDERLWPSWEEQKKLS LTTDPDTWL*GSPQAAQGPRCV PPPGAQPLSYVTASLCHC

SEO ID	SEO ID NO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7509	37877	Α	7563	2	2233	SSENILTVHEQANVESLKETKQ
İ						NCKDLDEDANGITDEGKEINEK
	İ					SSQLKNLSELQDTSLQHDDEEE
l				1		STVISVSEDMNSEGNVDFECDT
1					1	KLYTFLSSDESQQSENSENEED
1						TLCFVENSGQRESLSGDTGSLS
	İ			1		CDNALFVIDTTPGMSADKNFYL
						EEEDKASEVAIEEEKEEEEDEKS
1					ŀ	EEDSSDHDENEDEFSDEEDFLN
1						STKAKLGRLTPHMAGYSSETKL
1						PEERPGSNICCSPISAVLQPPLLI
1		1			ì	PRQTGSGVDLQQTPTDLQLRVL
1						TVIKKTNKQKGHPHQNPICTSP
1						SSKTKDRSTRQKVNKDIQELNS
1		1				ALHQADLIDIYRTLHPKSTEYTF
1		1				FAAPHCTYSKIDHIVGSKALLS
		1				KCKRTEIITNCLLDHSAIKLELRI
		1				KKFTQNCSTTWKLNNLLLNDY
1	1					WAHNEIKAEIKMFFETNENKDT
	l	1				TYQNFWDTFKAVCRGKFIALN
	i	1			l	AHKRKQERSKIDTLTSQLKELE
		1				KQEQTHSKASRRQEITKITAEL
		l				KEIETQKTLQKINESRSWFFEKI
		1				NKIETASKTNKKREKNPIDAIK
		ŀ		İ		NDKGDITTNPTEIQTTIREYYKH
	1	ŀ			l	LYANKLENLEEMNKFLDTNTIP
ľ		ŀ				RLNQEEVESLNRPITGSEIEAIIN
		l				SLPTKKSPGPHGFTARFYQEYK
		1				EE/PGTIPSETIPINRKRGNPP*LI
		1				L*GQHHPDTKAWQRHNKKREF
1		1				*TNIPDDHQCKNPQ*NTGKPNP
		1				AAHQEAYPP*SSGLHPWDARL
7510	37878	A	7564	3	377	DHNCATVLQPG*QSEIL*KEERE
		1				REREKKERKKERKKERK
		1				KEGKO*RKGGRKKERKEKEIK
		1				KERRKGKKEKKEEEKRRKERK
		1				KERERKKRRKEGRKKEYTRKA
		1				KRIHRPFEGNGSPLPAP
7511	37879	В	7565	1	834	
7512	37880	В	7566	1	915	
7513	37881	В	7567	1	666	
7514	37882	Α	7568	330	793	SCWLCPGPCCPAQPQNTAPFIPE
		1				A*TPAMAERGPATAAGQLEFT
		1				GGALQTLFAWVSAAAAAEQWI
		1				LVNRKCCCLIVPLEVLSQRSTW
		1			1	PCIGLVMPVLPGLLRDIVHSDSI
		1			1	ASHYGVLLALYALMQFLCAPV
		1				LGALSDRFGRRPGLLASLLGAT

	U1/U/SUG/	1	Iono mar	Territoria.	In	PC1/US01/08031
SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nuclcotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide
iio:	sequence	1100	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion
				sequence		
7515	37883	A	7569	991	1842	IOCHPHQATKNFLHRIGKNYI
						VHMEPKKGPHCQVNPKPKEG
	l					WRYVKQSKKIAVYAERSRCS
						GTEFAGTLILDFPSSRTAPSSR
						R/P/GRLTRPGTPLRQSFQRND
						AATFAVQQYSLFCSLCC*YPC
						QGLEWTSSKLQQ/YLQLRERS
	1					SPATEOSWMENDFDELREGF
	1					RSNYSKLKEEVQTHCKEAKN
		ı				EKRLDEWITRITNVEKSLNDL
		1				ELKNMAKELRDERTSFSSEFN
	1	1			1	LEERVSVIENOMNEMKREEK
		ł				
7516	37884	В	7570		2448	EKRVKRNEQSLQEIWDYVKI
7517	37885	В	7571	2379	4476	
7518	37886	A	7572	1	570	
7519	37887	A	7573	ı	1404	
7520	37888	A	7574	i i	474	
7521	37889	A	7575	746	1215	PNINRFLKHYREPVPKKRERN
321	37009	l^	1313	/0	1213	STLWPLCPSTLNKIYTIMSYL
		1				ATKEYPFFLLLLEQEC*AE*L
		1				LAVSOPLLSSTTNCLKN*MV
		1				NGSLIPWSPCKINLTP*/PAVV
		l				ONRRALDLLTAESGGTFLFLI
		1				KCCCYVNOSGITEKVKEIOC
7522	37890	A	7576	1	1178	MPESPTPLLGRDILAKAGAIII
1322	37030	l^	1310	["	1176	NIGEGTPVCCPLLKEGINPEV
		1				ATEGQYGRAKNAHPVQVKL
		1		1		DSASFPYQRQYPLRPEAQQG
	İ	l		j		KIVKDLKVOGLVKTCNSPCD
	Ì	1				
		l		1		ILGVQKPNGQWRLVQDLRIII
		1		1	i	AIVPLYPAVPNPYTLLSQIPER
	1	l			l	ELFTVLDLKDAFFCIPVHPES
		ı				LFAFEDPSIPMSQLTWTVLPQ
		l			İ	FRDSPHLFHHTLAQDLSQFS
		l				DTLVLCLPLRNQQECHQATQ
						LLNVLATCGYKVSKQKAQL
						QQVKYLGVKLSKGTRAL/QQ
	1	1			i	TDRT*LSTSNCSNLRHSRGPS
		1		I	1	SLD*SQPQLVY*WKFFCRKR
	1			I		KRGVCSGQ**WNT*KKSPHS
		1			ŀ	*CSAGGTNSPPSGTRIRRRKK
		Ļ		ļ		IRIYMLPLILSAPYDHLH
523	37891	A	7577	109	1338	
524	37892	C	7578 7579	279	346	LIBIALLIONOVEENAN ECC.
7525	37893 37894	A	7579	260	393	LLRLALLLQ*QKEEWVLFCCO VEVVILPMPVPNLPSIPARITK
7526	3/894	l <sup>A</sup>	1380	200	373	
	L	L	I	1		RMGTLLLRGLGTT*LYKSCS

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7527	37895	Α	7581	3	2677	TKETCFIRGPKTPVPVTDWEGS
		l				LPLVFNHCRDTSVIIHPRFKGVR
		l				PRRDACLGPSPLAASPAFLGKG
		l				QAELGPNSSSASAPPPYNLFIAS
		l				PPHTWSGLQFRSVTSPPPPAQQF
	l	l				TLKKVAGAKGIVKRLKTDTAR
		l			ì	SPWKTPRPSRTPSFRKAERTKG
		l				LLKIHLTKLSHQLKKDWTILLP
	1	l				LSLLRIQACPRNATRLATGQLG
		l				YPFISQSYVLVNGFQTVEDLCE
	ł	1				AADLRVSVADLRVSVTALKVA
		1				RLELFVPPGGLVVSLASAVKLQ
		1	ļ			TFAVLQLIKAKRWDWGTLEQG
		1				AALIGEARDAQEPTEGVGGSG
		l				MAGCRSRDLPRGKAAKARREI
		l				ERSAGLTIKKERCIRNGYSKEK
						MKLIVVSHGLHVNDLQHKLTL
						FTKETYTYLARDSEKQKQGYL
		1				AGLEGAHANRVNQQISDNLVV
		l		1		KTGALPPPYRTKGEKLYFYMSR
		1		i		QNCLFSVSGQLLQGFFPNGGQA
		l			•	APNPYALLSQIPEEAEWFTVLD
	İ	l				LKDDFFCIP/VHPDSQFFFAFEDF
	i	l				SNPTSQLTWTVLPQGFR\HLFG
		l				QALAQDLSQFSYLDTLVLCGVL
	1	1		l		KSPIIIVWELNQIDTIKNDKGDIT
	l	1				TDPTEIQTTIREYYKHLYTNKLE
	1					NLEEMDKFLNTYTLPRLNQEEV
	İ	l				ESLNRPITGAEIEAIINSLPTKKS
İ	i					PGPDGFTAEFYQRVADVKLREE
		1				KDENMLLVPLSDLLYQVHAPIP
		1				QLPEVLAANSPTCHLDPPTITES
7528	37896	Α	7582	1	459	MAVRYTDENVLRKGTREAGT
					1	MMRLRGTTECCADFAAWDVT
		1				HDALRATGGELPGAQVMLTTT
						ECGRHVDFCDRAVWLPRMWG
						YPLALPGEMRKLYTVRMAGRD
				l		ILAKAGAIIHLNIGEGTPVRCPL
ı	1					L/EGINPEVWKTEGOYROAKNA
		1		l		RPVOVKL

871

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				bequence		
7529	37897	Α	7583	3	910	YFSQPLSY\DWGALFFSHAFLIM
						LESPTTLLGRDILAKAGAIIHLNI
ł		1				GEGTPVCCPLLEEGINPEVWAT
						EGQYGRAK\NARPVQVKLKDS
						ASFPYQRQYPLRPEA/LTKGFQ
						KIVKDLKAQGLVKPCNSPCSTPI
ļ						LGVQKPNGQWRLVQDLRIIDE
1						AIVPLYPAVPNPYTLLSQIPEEA
ŀ						ELFTVLDLKDAFFCIPVHPESQF
ŀ						LFAFEDPSIPMSQLTWTVLPQG
l						FRDSPHLFHHTLAQDLSQFSYL
ĺ			ŀ			DTLVLCLPLRNQQECHQATQV
i						LLNVLATCGYKVSKQKAQLCS
						QQVKYLGVKLSKGTRAL
7530	37898	A	7584	158	1272	NPAARTPFFVIKKGGKRGRDIL
			İ			AKAGAIIHLNIG/GTPVCCPLLE
						EGINLEDWATEGQYGRAKNAR
						PVQVKLKDSASFPHQRQYPLRP
						EAQQGLQKIKDLKAQGLVKAC
						NSPYNNPTLGVQKPSGQWRLV
						QDLRIINEVTVPLYLAVPNPYIL
						LSQIPEEAEWFTDLDLKDAFFCI
						PVHPDSQFLFAFEDPSNPMSQL
İ						TWTVSPQGFRDSPHLFGQALA
						QDLSRFSYLGTLVLWPCISI/LCT
1						*TMEQLQHRNKHHFRFSRTSCF
1						QSGNNPYLKPHLCKI*QYCRHN
						QLPMHQCPHDHLH*TRFI/PIML
1		1		1		YLSPTTKEYSFFLLLSEQEC*VD
		l				*VLALAVPQPLLSSTTNYLKNS
						MVTWNGLPTPWSPCKINLTS

872

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first		*=Stop codon, /=possible nucleotide
	scquence	l	09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7531	37899	A	7585	li .	2083	MPLLQMIATPLOOSLISTEDEM
						DELTEVGFERWVITNFTEEPSP/
						LGFTPEHKGNVGHAGKGPLESS
		ŀ				SPDPFLCGQEKQEKGAGLLHRQ
						YPLRLEAKQGLKKIVKDLKAO
		ŀ		l		GLVTPCSSPCNTPTLAVQKPNG
				Į.		QWRLVQDLRIINEAVVPLYPAV
		ŀ				PNPYILLSQIPEEAEWFTVLDLK
	l					DAFFCIPVHPDSOFLFAFEDPSN
						PMSQLTWTVLPQGFRDSLHLFQ
						OALAODLSOFSYLDTLVLOYM
						DDLLLVTHSETLCHQATQALFN
		1				FLATCGYMVSKPKAQLCSQQ/F
				1		YLGLKLSKGTRALSEEHIQPILA
					1	YPHPKTLKOLRGFLGVIGFCRK
				1		WIPRYGEIARSLNTLIKETQKAN
						THLVRWTTEVEVAFOALTOAP
		İ				VLSLPTGODFCSYVTEKTGIAL
				1		GVLTQIRGMSLQPVAHLTKEID
				1	l	VVAKG*PHCLRVVVAVAVLVS
İ				ì	1	EAVKIIOGRDLTVWTSHDVNGI
I						LTAKGOLWLSDNCLLKCOALL
						LEGPVLRLCTCATLNPATFLPD
						NEEKIKHNCQQVISQTYATRGD
						LLEVPLTDPDLNLYTDGSSFVE
						KGLRKVGYAVVSDNGILESNPI
						TPGTSAQLAELIALTWALELGE
						EKRANI/YTDSKYAYLVLHAHA
						AIWKEREFLTSERTPIKHQEAIR
						KLLLAVQKPREVAVLHCRGHH
						KGKEREIQENCQAYIEAKRAAR
7532	37900	Α	7586	80	678	LCCNMPAAQHRERASNESRHG
ĺ						GCCPP/PWLLSS/APPHDAFTTPC
		l				EAVLSAPSALPSSAATSLLSLLT
						PQQMFCSKTAGPKPFSSNPHPR
						LKAPTSSC/PL*PQAAPSGNAHC
		l	1	l		Y*GHRRGRTVPEDPGCLSPRAR
		l	1	l		PHRTSGTSSPPSLQPSRTIPPASS
						APKQGDAGSPPYQAVPEKNKP
						GATPRTCAESPKRLPRPGPKSFL
			1			

SEQ ID	SEQ ID NO:	Dist	SEO ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u></u>				
7533	37901	Α	7587	3	804	GLLQATALQPAQQI*IFL*KKEE
						EEEGGGGEGEEKKKKKKTEEE
						EEEEERKK\EEEEGEEEGEEE
						EEEEKEERTGAGDSSEDEGFDE
l		l				PSPGDSRQKTEGNAANIISGCD
	l	1				QRYEESEMDLGTRGIVSGHRYI
1		l			i	FTFRVSPLEAIGELLFPFSVAPA
1				l		QGGLGFRRVDQLALPMGAQSL
		l				ERPFCVDGGSRPPLNYAVSSVE
		l		l		DLLNGNNFKCPTTLRTIEITVGN
l				i		LIISPRQKQLNANIGKNFNAAEN
		1				HENAKTTTRSSTVGADTHLTA
7534	37902	A	7588	3	191	SSHPVFSPRWVLSPHPQSQCYT*
						GSGAQNLTASPPFCVCRGDRGN
		l				HLRKDTKVEVKRKTCWL
7535	37903	Α	7589	1	1899	HVGASDPDAGPGWGGLTSRPR
						LVTPRSAPRGRAFQGATVGLAP
						VEGMCRAESSGGVSTDHSELPI
				i		GAAATMAHEIGHSLGLSHDPD
		l				GCCVEAAAESGGCVMAAAT/G
		İ		ł	İ	VRGWGVGAAAGRLVLGTSSA
				l		AFLWSSLSFLFCKMGIMIIVSAS
						GWFMRLKGKKLROSGFSTV*R
					İ	LFSE*PGEVTPTPGGAPSGRDST
		1		ŀ		LGPGLLTIGASSSPVPLVV*LCA
		1				GYFPSLGSARLAAVAKPRGGD
						QRSAGVGGLSLHAQCPPRAGR
1		1				HPFPRVFSACSRROLRAFFRKG
1		1				GGACLSNAPDPGLPVPPALCGN
		l				GFVEAGEECYCVS\GQECRDLC
		1				CFAHNCSLRPGAQCAHGDCCV
		1				RCLLKPAGALCROAMGDCDLP
1		1				EFCTGTSSHCPPDVYLLDGSPC
		l				ARGSGYCWDGACPTLEQQCQQ
		1				LWGPGSHPAPEACFQVVNSAG
		1				DAHGNCGQDSEGHFLPCAGRD
						ALCGKLQCQGGKPSLLAPHMV
	l	1	l			PVDSTVHLDGQEVTCRGALAL
	l	1	1	1		PSAOLDLLGLGLVEPGTOCGPR
	1	1				MVCNSNHNCHCAPGWAPPFCD
	1	l				KPGFGGSMDSGPVQAENHDTF
	İ	1	l	l		LLAMLLSVLLPLLPGAGLAWC
1		1		l		CYRLPGAHLQRCSWGCRQGPC
	ĺ		İ			VQWPQRWPTQGPPPGRRSPHG
	l	1	1			VGPHSHWTALAPGP
7536	37904	A	7590	2	280	TOTAGAWIALATOF
7537	37904	A	7591	1	1266	
1331	2,303	l^	1,271	Ľ	1200	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
7538	37906	A	7592	1	458	LQQSQIFEIHSQKTIVKKCLDLF
/336	37900	^	1332	1	136	FELAEEKENYKNFFEAFSKNL\K
						LGIHEDSTNRRRLSELLRYHTS
		1				
					1	QSGDEMTSLSEYVSRMKETQK SIYYITGSPCWCLVFFSLSCPCV
		1				EGSKLRVSSPIPSLLLTAGLDVV
		l.—	8500		0.00	YCGLFYFLHFVLKLKYAK
7539	37907	A	7593	1	862	TOTAL VIEW OF THE STATE OF THE
7540	37908	Α	7594	3	437	IPEF/LNF/IRGVVTLGLPLNISRE
			İ	l		MLQQSKILKVIRKNIV*EC/LFEL
		1				LSELAEDKENYKKFYEAFSKNL
		l l			1	KLGIHEDSTNRRRLSELLRYHT
						SQSGDEMTSLSEYVSRMKETQ
	l	1				KSIYYITGESKEQVANSAFVER
						VPLSHLAPPAGV
7541	37909	В	7595	106	1966	
7542	37910	Α	7596	453	719	ARGSKHTGLIAQWAHEQSGHG
						GRAGGYAWAQQHGLPLTKAD
		1				LP\AMATAECPICQQQRPTLSPR
		1	1		ŀ	YGTIPW/WAWDAPGGRGCWRL
		1				QKAGE
7543	37911	Α	7597	3	837	PECVIGIDILSSWQNPHIGSLTG
						RVRAIMVGKAKWKPLELPLPR
						KIVNOKOYHILGGTVEISATIKD
						LKDTEAVTPTTSPFNSPIWPVO
		ŀ				KTDGSWRMTVDYCKLNOVVT
						PIAAAVPDV/VSLLEOINTSPGT
				l	•	WFEWSPK\KALOOVOAAVOAA
1						LPFGPYDPADPMVLEVSVADR
				l		DAIWSLWNAAIGESORRPLGF
						WSKALLSSADNYSPFERQLLAS
						YWALVETERLTVGHQVTLRPE
		l				LPIMNWVLSDPSSHKVSGAOO
		l				RSIIKLKWYIHDWVRAGPEGT
7544	37912	Α	7598	h	399	ROMEER WITHD WITH GITE CO.
7545	37912	A	7599	126	392	ARGSKHTGLIAOWAHEOSGHG
1343	37713	l^	1327	120	372	GRAGGYAWAQQHGLPLTKAD
						LP\AMATA ECPICQQQRPTLSPR
			l	1	1	YGTIPW/WAWDAPGGRGCWRL
			l	1	1	QKAGE
7546	27014	١.	7600		1622	QKAGE
7546	37914	A		1	1677 465	
7547	37915	С	7601	37		
7548	37916	В	7602	1805	2542	

SEQ ID	SEQ ID NO:		SEQ ID NO:		Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7549	37917	IA	7603	13	865	VIPTTSQFNFPIWPVQKTDGSW
,,,,	3,,,,,		7005	1	000	RMTVDYCKLNQEENFNNOVDE
						MTHSVDTTQPLSPATHVITQWA
		l				HEQSGHGGRDGGYTRVQQHGL
		1			i	PLTKADLATAGKVFQKAV*AL
						N*HSIYGTLSLIARIHRSRNQGV
						EVEVAPLTISPSDPPAKFLLPVP
		1		1		PTLRSAGLEFLVPEEGMLPSGD
						TTVPLNWKLRLPPGHFGLLFPL
		l				HQQANKGRLSPHSRERGTSVFA
						SSNSQPVTALNNEPAGPNKRDI
						GKAKGLKFHHPGPHRQERDML
					İ	E/SML*PWGYPVGKQWNHLIK KOGRH
7550	27010	١.	7004	-	067	VTASLSPVVATSPPOPMLPSDFF
7550	37918	Α	7604	3	857	, , , , , , , , , , , , , , , , , , , ,
					ŀ	PLSEEINPMLPEATVIASPKEIAR
				1		QDNVDSPQEPPPTPQFSSRPITR
						LKSQWAPRGPECVIGIDILSSW
		1				QNPHIGSLTGRVREGYMVGKA
						KWKPLELPLPRKIVNQKQYCIP
		1				GEIAEISTTIRDLKDTGVVIPTTS
		ŀ				PFNSSIWPVQKTDGSWRMTVD
		1				YCKLDQVVTPIAAAVPDMVSL
						VKQINTSPGTWQHITHLDVLLW
						RIYQVTQKAASFEWGPEQEKA
						LQQVQAAVQA\LCHLGHMTQQ
7551	37919	A	7605	1	608	IQWCLRRNGEMCDYILIYGL MAPGMVPIPPPGKYHSPKKLIY
/551	3/919	A	/603	1'	008	1
		1			ľ	STPPKPGTYGISDSLSQYPTSAK
		ł				AEPVPTHKNPRRESPIPHSSPSSF TDG/PSPNSPGDARPHPQNKTSO
		1				RGRPAPRORVPTTITTPAPPARS
						PNSAHSPAFRDLPFRAEKGTAA
						ARVPREPHSPAPPKNKGSLQPP
						AGELLORGARTTLPRILGTAPG
						,
7552	37920	A	7606	179	544	PHLPGCSAPPGAP*RPAAPIGL HTRLHSHPQLRGFPSWLFHSVS
1552	3/920	l <sup>A</sup>	/606	179	1344	
				l		RSPASGHLEFPSFARSSGSGSTS
						PLSFGAMTTEKQALGGRAAFPP
						KYK*AQGRAACFVLTSQQQPS
						WQ*GVTVTATGSPMHRGTFWH
7662	27021	١.	7.07	00	(52	SCTGTPGSGDR
7553	37921	Α	7607	90	653	VPGERPRGQSGPQVLPYGPTWC
		1	l	I		SSNTPEPQSLRAPQ*LQVPVPLQ
		1		I		SRGQR*QPQPMP/VRSQPKAP*V
		1				QMPPTPSSAKGPHLDGVRVPA
		l				ANPE*PTAGPTRAAILRATPAPS
						LPMPGTNRPSPRGNSLQDSAPA
		1		I		SDAGWPPTEAVTCP\PWSRENP
		1		l		PQRNL*AHRPQGPRPVPGTERR
	1	l				NGRGGAGCRQL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codun fur last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \mpossible nucleotide insertion)
7554	37922	A	7608	H	804	
7555	37923	A	7609	28	682	TTCEMSDLEDDETPOLSAHG/T
,		1				LAALQEFYAEQKQQIEPGEDDK
		1				YNIGIIEENWOLS\OFWYSOETA
					1	LQLAQEAIAAVGEGGRIACVGS
		1				P*CLPET/HESCAEKTFSIYIFFY
					ŀ	DKRFAME*KE\LIFYDYNNPLD
		l				LPERIAAHSFDIVI\ADPFPYLSG\
						ECLRKTSETVQV\LTRGKILL\CT
						GAHHGRTGSRTPLE*RCARLFP
						RHTRNFGKWSFRLVYVNL
7556	37924	A	7610	1	611	МАРКАКМЕАРАРРЕАЕАКУКА
						LKAKKVVLKGVHSH/KKKKKI
						RTSPTFR*/PLRLRRQPKYPWES
		1				VPRRTSTOISSGERPLENKOPRY
		ļ				PRESSPPPGEQAPKYPPEERSPG
		l				ETRLDHLCLSIKFP\LTH*VLPM
		l				KKIEDNNTL\VPLVNVKANKH\
		l				QIKQAVKKLYDI\DVAKVNTL\I
						RPDGEKNGICSDLAP\DYDALG
		l				CLPTKFGII
7557	37925	Α	7611	1	1035	DKDSLCDSCKTSCSYNCSKPRS
		l				SWODODISSGTGLHSRLTLANT
		1				GKESKTVQASLDQQLGRLLSVS
				1		LRLGVEPSLOSSGNLLVSLLLSR
		l				FITYKVTIVEWVKTYALGLDLK
ł						KSERPGFESELHSHNSCECAVS
		l				HLKPVHLRVSPMGHSEYYLVT
		1				TADYSEANGSQSAGDEFFQTQS
						FPSRQQALFRPKIQITIREYYKH
		l				LYANKLENLEEMDKFLNTCTL
		1				QRLNQEEVESLNRPITGSEIEAII
						NSLPTKKRPGPDGFTAKFNQRY
		l				KEELVIYKKFQIPCIVPELNSTIS
		i				ANSTNADTCTPKYVTFNSKGT
		1				AQNADSDSAGLE/CEPDVLHI**
		1				SLRLGVEPSLQSSGNLLVSLLLS
						RFITYKVTIVEWVKTYALGLDL
	1					KKSERPGFESELHSHNSCECAV
		ł				SHLKPVHLRVSPMGHSEYYLV
		1				TTADYSEANGSQSAGDEFFQTQ
		1	1			SFPSRQQALFRPKIQITIREYYK
		l	1			HLYANKLENLEEMDKFLNTCT
		1	I			LQRLNQEEVESLNRPITGSEIEAI
	i					INSLPTKKRPGPDGFTAKFNQR
		1	l	I		YKEELVIYKKFQIPCIVPELNSTI
		1	i			SANSTNADTCTPKYVTFNSKGT
	1			I		AQNADSDSAGLEWSLMFCISD
	l		l			KVSGDDDADAVDS
						AQNADSDSAGLEWSLMFCIS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:		Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7558	37926	A	7612	3	573	KEETFSAWYVDGRVLVVIVTF
						GIILPLCLLKNLGYLG\YTSGFSL
					\	SCMVFFLIVVIYKKFQIPCIVPEL
			ļ.			NSTISANSTNADTCTPKYVTFN
						SKTVYALPTIAFAFVCHPSVLPI
						YSELKDP\SQKKMQMVSNISFF
						AMFVMYFLTAIFGYLTFYDN\V
						QSDLLHKYQSKDDILILTVRLA
						VIVAVILTVPVL
7559	37927	Α	7613	1	831	MSELEDRLFENTQSEESKGKRI
						KKNEVCLQDLKYSLKRANLRD
						TGLKEEVIYKKFQIPCIVPELNS
1						TISANSTNADTCTPKYVTFNSK
						KKMQMVSNISFFAMFVMYFLT
						AIFGYLTFYDNVQSDLLHKYQS
						KDDILILTVRLAVIVAVILTVPV
		1				LFFTVRSSLFELGLRKQRFNLW
		١.				PSIPVVTCILLVVINLVGDLHTP
		1				P*RIFFGVVGSYILLNMLIFILP/S
		1				IFFILKITDQDGDKGTQRIWAAL
		1				FLGLGVLFSLVSIPLVIYDWACS
						SSSDEGH
7560	37928	Α	7614	1	1118	FNCEIFYSF/SYGDEEISKTFALN
		1				ERRGEIKIIRKLDFEKIVSYQVDI
		1				KASDGAGLSGKCTVIIQVVDIN
		1				DNAPELTMASFTSPIRENSPETV
		1				AALFSIQDRDS\FALRSLDYEAL
		1				QEFEFRVGASDPGF\PALSSE\AL
		1				VRVL\VLDANDSSLFVLFPLQN
		1				GSAPCTEL\IPGRAAEPGYLVTK
	1	1				QLLKATEPGLFGVWAHNGEVR
		ı				TARLLSERDATKHRLVVLVKD
		1				NGEPPRSATATLHVLLVDGFSQ
		1				PYLPLPEAAPAQAQAEADLLTV YLVVALASVSSLFLLSVLLFVA
		1				VRLCRRSRAASVGRCSVPEGPF
		1				PGHLVDVSDTRTLSORYKYEVF
		1		Į.		LTRGSGTNEFKFLKSVIP/QASG
		1				RCE*WEEKSNFVNGFGFN
7561	37929	A	7615	1	764	TRPGAHGASLTDLANLSEGVSL
7501	31929	<u> </u> ^	7013	1	704	AERGSFGAMDDPFKNKALLFS
		1				NNTQELHPDPFQTEDPFKSDPF
		1				KGADPFKGDPFQNDPFAEQQTT
		1	1	1		STDPFGGDPFKESDPFRGSATD
		1		İ		DFFKKQTKNDPFTSDPFTKNPS
		1	l			LPSKLDPFESSDPFSSSSVSSKGS
		1	1		l	DPFGTLDPFGSGSFNSAEGFAD
		1				FSQMS/KGKSTPVSQLGSADFPE
		1			I	APDPFOPLGADSGDPFOSKKGF
					1	GDPFSGKDPFVPSSAAKPSKAS
						ASGFADFTSVS
	L		L		l	1.1001.101 1010

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		0.7.5.40,217	sequence	or pepade sequence	
7562	37930	IA.	7616	<u> </u>	817	MGFCHVGQASLKLLASDPFGT
						LDPFGSGSFNSAEGFADFSQMS
		ŀ				KTDPQVRSELLK\GTAARLVTR
				i		LDPLVSGPH\TR*PELTVALVPD
		ŀ				SCRASPDAGSVVGAHL*GLGTT
		t				GAADGGTP\NSNRSFVLGVIIVV
						WSMCOLYLVPPPPSGPFTSSLG
		ŀ				GAGFSDDPFKSKODTPALPPKK
1		Į				PAPPRPKPPS/GHRLPVPDGGGP
		1				GPPCSP/DPE*QQMPWDPVWGA
		ŀ				RGSPRPSCPGPRKCRMCVVPRV
		1				IQHPSLLLPSLVGRRSQPQIWRS
		l				HPMPAAPPS
7563	37931	A	7617	3	1039	GSLMFQQVPMVEIDGMKLVQT
						RAILNYIASKYNLYGKDIKERA
		į į				LYAMTHDDE\AELRTPAAACKL
		1				*SECQFRTRVDAVRTMMIP/AFT
		1				QVLKSHRQDYLVGNKLSWADI
		1				HLVELFYYVEELDSSLISSFPLL
		ł				KVKLLASSVKPVPLPSALRWPA
	İ	1				HAVAQNIVTSWLTGGRFIELKT
		1				VQILDRLELEKPCIDAEDECFNT
		ł				EWSTEFTLLKAWDEYLKAWFA
		1				LHLLEAMFQPSDSGKSFIFNMS
		1				VGYNLEGQPLNPKNYPSQGVP
		i i				RVLKSHRQDYLVGNKLSWADI
	1	1				HLVELFYYVEELDSSLISSFPLL
		1				KPHTHVDNTKKGSHPHMCAYT
						DYVNNPNDRMPQREITFVS
7564	37932	A	7618	2	698	NQKTVTMAGKPKLHYFNGRGR
		1				MEPIRWLLAAAGVEFEEKFIGS
		1				AEDLGKLRNDGSLMFQQVPMV
		1				EIDGMKLVQTRAILNYIASKYN
		1	1			LYGKDIKERALIDMYTEGMAD
		1				LNEMILLLPLCPAEEKDAKIALI
		1				KEKIKSRYFP\AFEKVLQSHGQD
		ŀ				YLVGNKLSRADISL\VELLYYV
		İ				EELDSSLIS\NFP\LLKALKTQNP
		1				ATLPHG*RSFLQP\GSPRKPPAD
7555	27022	Ļ.	7610	102	936	AKALEEARKIFRF
7565	37933	Α	7619	102	825	RNLQETAIMAEKPKLHYFNAR
					1	GRME\PPRWLLAAAGVEFEEKF
				1	1	IKSAEDLDKLRNDGYLMFQQV
	1				l	PMVEIDGMKLVQTKAILNLHLP
			1	1		ANYNLLMGKDIKGREP*FDYVF
				1		*EGFSQILGLN*SSFLPVC\PPE\E
			1			KDAQALPLIQEKTKNRYFPAFE
	1			1		KVLKSHG\QDYLVGPTSLSRGW TFIWWELLYYVEGAWTPRLISS
			1			FPLLKALKTRISNLPTVKKFLOP
			1			,
				L	l	GSPRKPPMDEKSLEEARKIFRF

SEQ 1D	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		İ		sequence		
7566	37934	A	7620	2	1256	CHCGPP/VKVEAYGSOVLKGVL
/500	37934	<u>۱</u> ^	7020	-	1230	AQVQLTVGPVGPRTHPVVIFPV
	1					PECIIGIDMLSSRONPHTGSLTG
			l			RVWTIMVRKAKWKPLELPLPR
	l					KIVNOKOYHIPEGIVEISATIKD
			l	ĺ		LKDAGVVIPTTSPFNSPIWPVQK
	1	l				TDGSWRMTVGYCKLNQVVTPI
			Ì	l		AAAVPDVVSLLEQINTPPGTWY
	1					AAIDLANDFFPIPVHKAHQKQF
	l .		ĺ			AFRWQGRQYTFTVLPQGRWEI
	1		l			NMTKIQGPST\$VKFLGVQWCG
	1		i	l		ACQDIPSKVKDKLLHLVPPTTK
	i .		ļ			K/EAQCLSGFRREHIPHL\PIYRV
						SRKAANFEWSPEQEKALQQVQ
	1					AAVQAAWPLGPYDPADPMVLE
	1					VSVADRDADWSCWQASI/GHK
	1					VGHAQQHSIIKWKWYIRDWAR
	l					ADPEGTTKGQGQRRWWQLAE
		l				RQDSRDREAAIGERQETAVGKT
	l	l				ARDGEAVCD
7567	37935	Α	7621	1	518	MTVDYCKLNQVVIPIAAAVSD
	į.	1	ļ.			VVSLLEQINTSPGTWYAAIDLA
	i i					NAFFSIPVHKAOOKOFAFSWOG
	l					OOYTETVLPOWYINSPALCHNL
						IRRDLDCFSLPLDITLVHYIDDI
l		1	l			MLIGSTIKWVVHSS/DSIIKWKW
l		1	l	l		YVHDWARAGPEGTTNGLAG*S
				l		GTCKKHEWKTGDKGIRGRG
7568	37936	Α	7622	1	696	
7569	37937	В	7623	1	1014	
7570	37938	В	7624	1	837	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
7571	37939	A	7625		2592	MVRKAK WKPLQLPLPRKINNO, KOHRIPGGTVEISAITKOLKDA GVVIPTTSPFNSPIWSVQKTDGC WRAMTVDYCKLTQVMTPIAAV VPDVVSLLKQUNTYPGTCKIFLG VQWCGACRDJPSKVXDKLLHIL APPTTKKEAOHLVGLFGFWRE EIIIPIILGVLLQPMYQVTTRKAASF EWGLEQEKALQQVQAAVQAA LPFGGYDSDDFTVLEMSVADBV AVWSL WQAPIGESQWRPLGL SKALPFSADNYSPFERRLLACY WALMETEGLTMGHQVTMQPE LPIMNWVLSDPSRHKVGHAQQ LPIMNWVLSDPSRHKVGHAQQ LPIMNWVLSDPSRHKVGHAQQ LPIMNWVLSDPSRHKVGHAQQ LPIMNWVLSDPSRHKVGHAQQ LPIMNWVLSDPSRHKVGHAQA LAGLSGISLKDSGGKSSQWT **LNKEVAQMPMGTTRKWTAA ALQSLSGISLKDSGGKSSQWT **LNKEVAQMPMGTTRKWTAA ALQSLSGISLKDSGGKSSQWT **LNKEVAQMPMGTTRKWTAA ALQSLSGISLKDSGGKSSQWT **LNKEVAQMPMGTTRKWTAA ALQSLGISLKDSGGKSSQWT **LTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
7572	37940	A	7626	20	238	CHVEGVDHVSDPAQRRECDRH
7573	37941	A	7627	3	229	
7574	37942	A	7628	1086	1369	ETGMLPLRLLKPFLSDFAGPLH TSIMPTRRFCSKSPT*HTLATAL SQGLS*GT*NEASLTKEKVGKN RCRYSPSYPPSGIREGKAQLCFY THWK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino zeid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7575	37943	A	7629	sequence	1805	MSGRSRGKKSSRAKNRGKGRA KARVRPAPDDAPRDPDPSOYOS LGEDTQAAQVQAGAGWGGLE AAASAQLLRLGFEAACRLPLDC GLALRARAAGDHGQAAARPCP GKAASLSERLAADSVFVGTAG TVGRPKNAPRVGNRRGPAGKK APETCSTAGRGPQVIAGGROKK GAAGENTSVSAGEEKKEERDA SGPPATGSBOTTLENVQLL ENMRAQADRAYLRLSRKFGQLR LQHLERRNHLIQNIPGVSQQAF HIVLLASFLNSQEKEVLSYLN SLEVEELGLARLGYKIKFYPDR WHYDLNSLKFVGSGQV SRSTPIQWLPGHDLQSLSQGNP ENNRSFGWFSNHSEISSKIVE HINELWSPYDNYSULFSVGARF KGKEKEGRQGGKGVPMETTOP GPLSFVWAVSPSWLPGOGQ QELPVDRGPLPVHETHTYPPQL SRNPTGQTTDGRAGLPVTPCDK KALPCAQCFYSHLLYCMGQ RQKEKINPEVSSITNVAPKDME KVHAGALDKPMCGRGKESQ GATHHATPSAISPAPPLGSST TLDIDGLAHFLEHSQINPSLLSR VULOROHLRHAVATNG GATHHAVATNG
7576	37944	С	7630	66	206	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *-Stop codon,/-possible nucleotide deletion, \-possible nucleotide insertion)
7577	37945	A	7631	3	1643	VQASQAEADQQOTCLKQLQSS- QLSRL*KQAIELREAVEQHKVK. NNDLREKNWKAMEALA TVAEQ ACKEKLHSWTQAKEESYERNQ LCLIEAQTIMEALLALLPIELSVL. AQQNWYTEWLQDLKEKGPTI.LL KHPPAPAEPSFGTWAFQV*GEA EUTQSTICRAEPDQYRSILGGD GRALLRDLQKSVEEEEQVWWR. AKVGAAEELGQKSRVTVKHLE EIVEKLKGELESSDQWREHTI. HLEAELEKHMAAASAECQNYA LLEVAGGLRESSDQWREHTI. HLEAELEKHMAAASAECQNYA KLKSHVEDGDIJAGPANSSYEA KLKSHVEDGDIJAGPANSSYEA APOPSRDPRSA*RTOLELDQKPI. PWRMRQTTSRQKLHGPSFENA APPRSFFRNRREAFTA*RDLEK RGSLTSDLGRAPRFRLQELSE RRTOEOLGKGRTTRVKKLQEQ LEKAEDGSSSKECTSVLSFLFG KKKLLFQLYQNALTHSFTIKPT NLHSVYPGPPNFVLRSKAHERT
7578	37946	A	7632	3	247	Service Quintility of Indian
7579	37947	A	7633	3	389	GQEFSPKVY/FVNQTMGN/SCG PIGLFNAVANNQDKLGFEY\GP LLNQFLF*NR*KCPFKDRAKCF ER\NEAIRAAH\DAVDKEG\QCR VDDQGEFPFLFCLQNVDGPPSM NLDG\RMPFPRGPMAPSFRRTP

SEQ ID	SEQ ID NO:					Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	İ	
7580	37948	A	7634	1506	3135	RGLGGGLAEQELQPWSPERSPV
						HNN/RM/QEKSLKDLMELKTM
				l		AQELRDECTSLSSRFDQLEEKV
				l .		SVMEDEINEMKQEEKVREKRIK
1						RNEQSLQEIWDYVKRPNLHLIG
ł						VPESDRENGTKLENTLQDIIQEN
				i		FPNLARQANIQIQEIQRMPQRYS
1				i .	1	SRRATPRHIIVRFTKVEMKEKM
1		1		1	ł	LRAAREKEIQTTIREYYKHLYT
		l				NKLENLEEMDKFLDTYSLPRLN
		1				QEEVESLKRPITGSEIGAIINSLP
		1				TKKSPGPDGFTAEFYQRYKKEL
		l				VPFLLKLFQSTEKERILPNSFYE
		l				ASIILIPKPGRDTTKKENFRPISL
		1			1	MNINAKILNKILANQIQQHIEKL
		l				IHHDQVGFIPGMQGWFNIRKSI
		l				NVIQHINRTNEKNHMIISIDAEK
		1				AFDKIQQPFMLKTLNKLGIDGT
		l				YLKIVRAIYDKLTANIILNGQKL
		l	ĺ			EAFPLKTGTRQGCPLSPLLFNIV
		l			1	LEVLARAIRQEKEIKGIQLGKEQ
1		i				VKLSLFADDMIVYLENPIVSAQ
1		l				NLLKLISNFSKVSGYKINVQKS
		<u> </u>				QAFLYTNNRQTESQIMSELPFTI
7581	37949	В	7635	I	594 744	
7582	37950	A	7636	434	744	TLACLARLGKFSWIISCRVFSNL
	1	l				VPFSPSLSGTPIRRRFGLENRVT
	,	l				ATRILRESDRLKKRRTTRLYPTP
		l				GSEGPTPTESR*LLAQQSEIKLQ GGSEAGGGAPA
7583	37951	<del> </del>	7637	1	1077	GGSEAGGGAPA
7584	37952	A	7638	i	348	
7585	37953	A	7639	1	831	
7586	37954	A	7640	275	457	LIAYOPK*AODYMDSQLNSTRG
1.500	1000	ľ.,		I	l	TKKSC*GRL*GSGVIHIGSMPVP
		l				TRTAGPLPFFAGPCR
7587	37955	A	7641	341	504	ILRESDRLKKRRTTRLYPTPGSO
1,00,	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	ľ				GPTPRESR*LLAQQSEIKLQGGN
		l				EAGGGAPA
7588	37956	В	7642	1	627	17717
7589	37957	A	7643	121	375	DGQQLIALHRLALRELQQAVH
		1		1		AGLPQQAKILFDGGSEIGKIH*L
		l				RCAHCPLSSRETCRASCINESAT
		1				RGERPFAYWAPGWFFFHQ
7590	37958	Α	7644	3	479	
759I	37959	Α	7645	382	642	
7592	37960	Α	7646	273	1464	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last eodon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7593	37961	A	7647	76	1763	IRGITRFLPFIYQKIHIFSKEQLPD LHSHRSDLNLEAHMYASQWFL ILFTAKFPLCMYPHIDLLLCEG LNIIFHYALALLKTSKEDLLQA DFEGALKFFVQLPKRYRAEEN ARRLMEQACNIKVGVYTGTEL QYDFSLDSLWSWDSSCCGK ASWQDDGRNLHYGSL*RPCFQ PAAR*RLPH*SGGHQQAQVYG TNIKKLKYEKEYQTMRESQL QQEDPMDRYKFVYL*VTPAVA FILGIFIRS*EKERGKRWLSTF KNETKRKNGKVLF*ILGMSYPQ RLLAGELFQD*HKDVSNLPLSV ENVKNTNSLGRKNKNHK'REN RRLQEASMRLEQENDDLAHEL VTSKIALRNDLDQAEDKADVL MKELLITKGRU*VETEEEKRKOE EETAQLKEVFRKQLEKAEYEIK KITAIIAEYKQICSQLSTRLEKQ QASSKEELEVVKGKMMACK CSDIFSKEGALKLAATGREDQG IETCHURDEN GALKEVFRKQLEKAEYEIK KTTAIIAEYKQICSQLSTRLEKQ QASSKEELEVVKGKMMACK CSDIFSKEGALKLAATGREDQG IETCHURDEN GALKEVFRKQLEKAEYEIK KTTAIIAEYKQICSQLSTRLEKQ QASSKEELEVVKGKMMACK CSDIFSKEGALKLAATGREDQG IETCHURDEN GALKEVFRKQLEKAEYEIK KTTAIIAEYKQICSQLSTRLEKQ QASSKEELEVVKGKMMACK CSDIFSKEGALKLAATGREDQG IETCHURDEN GALKOVERSTEN GALKATGREDQG IETCHURDEN GALKOVERSTEN GALKATGREDQG IETCHURDEN GALKOVERSTEN GALKATGREDQG IETCHURDEN GALKOVERSTEN GALKOVERSTEN GALKATGREDQG IETCHURDEN GALKOVERSTEN GALKOVE
7594	37962	В	7648	1	618	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7595	37963	A	7649		2375	MAGAPPPASLPPCSLISDCCAIN QRDSVGVRPSKPGAGYNLVVR RFLSLLEKRSIPVGVTRFSRCRP SPLSLTRKGNSLTPCASRIINMIH FQAFWLCLGLLFISINAEFMDD DVETEDFEBNSEEIDWNESE EIKVKTPQPIGEVYFAETPDSGR LAGWVLSKAKKDDMDEEISIY DGRWEIEELKENQVPGDRGLV LKSRAKKHAISAVLAKPFIFAD KPLIVQVE VNPQDGIDCGGAY KLLADTDDLILENFYDKTSYJIM FGPDKCGEDYKLHFYDKTSYJIM FGPDKCGEDYKLHFYPKKTSYJIM FGPDKCGEDYKLHFYPKKTSYJIM FGPDKCGEDYKLLEDVYPPJKPKEI EDPNDKKPEEWDERAKIPDPSA VKPEDCALGLELWSMTSDIYFD FIICSSEK EVADIWAADGWRW KIMIANANKKHKDTEYKKTDI FIPTKGYLEGKEKSAALEK PMDLEEEKKQNDGEMLEKEE SEPEEKSEEEIEIIFGGESSNGSN KGGSEDGALAEQFREGPGVPGP IPPKRPSRSPIPEPRAAKRJPTOG LRGESYTMSASGTARGPSPKER LGLTTKTGEKEVAQGFCREPGL RRPPNAQARDRSSRAPATHREE
						RDTVHRNLVLDTKRHPALILVE YKERTSSPATEQSCMENDFDEL REEGFRRSVITNFSELKEDVQT
7596	37964	Α	7650	914	2786	
7597	37965	В	7651	1	2369	
7598	37966	А	7652	333	752	MSYVSRYGCGGRKNVATVSKG WAGSLAWPGGFPRKVKGGGS WRPSGGVDVAAPVRARLALLL SGPIASESPLTTNPHSHSARRPR TYUGHAPALRVTN/PESFSYWG TRGPSATMACDGLTRTGHSSPS RARSPPLLCARSL
7599	37967	A	7653	1	177	RPLPSRPHAAPPGHHTISSGPCF HRKFSPKAGDSNTPRTRSRPGV SCALPPDVRGSWLS*KWNQIW YHTLPQPQENTPKSQENEPKSK POPTOR*TRGPWPSSRCKVRSG THRRPGLFLS*KQ/PSSIGHSR ALSAFTPAEMSTLPPPPTSKSPL AARAAPPGNG*SPKAGDSNTPR TESRPRVSCALPPDVRGSWLS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	lucation of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7600	37968	A	7654	1	1430	MQDTCSEIISPADFPTFSSSLKIR
/000	37300	1	705	l'	1	FSTDSPSQIFKKHCIQKIVLILLP
				1		KNSYTRRLLVSNQMYLESFEH
		1				QCRKTHILCKRTAGSGPFCSCP1
	1	1		i		GOPRHNSSASKCPASERGLCLK
	1					PKSKREKREPGPVAPAPLHAAP
						SSPGLGAPQLR*PGRTRSFGRD
	1					HVGSPGPPRAGPRLFAPRPVLS
	i					RCSANPSGSPHTQSPKQSSTGQI
ļ	1					SGRADQVCGCWIRKRGVPGAA
	1	1		ŀ		RGSPGCARTCHSRGHPHAAPFP
	1					OCNSLAPSAPAGLWRTONAGP
		1				SG/HAQPSCPPPVPL*PPHPHP*G
	l	1		İ		LSFSSCSRSWVPNTPP/EPREGE
					ļ	GQVPGRRAASAPGASFSAPGT/I
		1				RAPOPLPHPFPVAOSPPAAVAA
		1				SSESCKREAARRSPGASALHLPF
1		1				KSARPROAPCPTLTDGGHIFPAS
		1		1		AARP*HKGHQTAEGKNPGRAD
	ł					TSTSPFATFPFISGGEEKSRSPVL
				i		PERTROREEAPGPPSSPLRGLW
		1				LTFWFVFL
7601	37969	A	7655	1	609	LIFWITE
7602	37970	A	7656	3	649	AKD/ELHIVEOGHDIRGRSIKIT/
7002	3,5,0	l^`	7050	ľ	0.00	LATLKMS/VQPTFS/LGGFEIQPT
1					ł	VV*GLKCVSGPCHISGOHLVA/
						VEEDAESEDEEEENVKLLSISER
		1				RSAPGVVSMVPQKKVK\LAAD
l					ŀ	EDDDDDDEEDDDEDDDDDDD
1	i	1				DEEAEEKAPVKKSIRDTPAKNA
ł						QKSNQNGK\DSNPYSHPRSQG\
	ı	1				QDPFRKQEKT\PKTPKGP\SSVE
1						DIKAKMOASIGKKRIEPVLGTY
7603	37971	A	7657	1	1013	PWCDSVLRGCSLEQRSFISVRLL
				1		SYLSACRHPMEDSMDMDMSPL
1	1			l		RPQNYLFGCELKADKDYHFKV
	i					DNDENEHQLSLRTVSLGAGAK
				ł		DELHIVEAEAMNYEGSPIKVTL
		1				ATLKMSVQPT\VSLGG\FEITPPV
1						V\LRLKCGSGPVHISGQHLVAV\
						EEDAESEDEEEDVK\LLSISGK
						RSAP\GGG\SKVPQKKSKTCML
1		1	1			MKDDDD\DDEED\DDEDD\DDD
		1	1			DF\DDEE\AEEKAPSERNLYRDT
		1	1			PS/AKNAQKSNQNGK\D\SKPSS
1	1	1	1			TPR\SKGTRIPSKKQEKTPKTPK\
			1			GPSSVEDIKAKMQASIEK\GGSL
						PKVETKFINYVKN\CSRMT\DOE
		1				AI\QDLW\QW\RKSL
		L	L	J	L	ULIKADEM IK M IKKOE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN -	location of first	codon for last amino acid	
1	sequence	1	09/540,217	eodon for peptide	of peptide sequenee	deletion, \=possible nucleotide insertion)
ĺ				sequence		
7604	37972	A	7658	9	271	GRVCKALWHSDWHTARVLCIN
						STTTITASCNP/RHTARRSLTTPT
ĺ		1				*MCRLENWTKNLLFNGPVPVL
ĺ		1				VMSLLFIASVFMLHIWGKYTRS
7605	37973	С	7659	189	500	
7606	37974	Α	7660	5	291	ATPSPPSPPG/VPT*RPELLGPRR
ĺ		1				ERLLGPEGS/PGGGALPGVPPSR
ĺ		1				FVRTASSTLFLPPSPRPAFPPSSIF
ĺ		1				LVPSPPRHCARSRETWPRTLRIG
		L .				SAP
7607	37975	Α	7661	1	431	LALQFSFLQNRQGLNLLIAEKG
ĺ	i	ı				RLCIFLNEECCFYLNQSGLVYD
ĺ		1				NIKKLKDRVQKLANQANNYAE
ĺ		1				PPWALS\NWMSWVLPILSPLIPV
1		1				FLLLLFGPCVFCLVSQFIQNRIQ
		1		1		AIANNSI*QMLLLTTPQYQPLPQ
1		1		1		NLSSVESLPL
7608	37976	В	7662	41	1547	
7609	37977	В	7663	74	298	
7610	37978	Α	7664	3	647	ELWTRGPRKRQNGSSKPLWLL
		1				YGESGAQKSVVEVTKPRLLWP
1		1				QWIQHRARRPCLQQAPCSSRPH
ı						APAS\LPPSSSPTARDTKHRAQV
ı		1				KTTDSGARRRDGRVLGVLEVS
ĺ						RSIADGQYKRCG\VTSVPD\IRR
ĺ		1				C\QLTPQ*PGSILLACDGLF\KVF
ĺ		1				TPEEAVNFIL\SCLEDEKIQTREG
		l				KSAADVR\YEAA\CNMLANKA
						VAAGARPDNVTV\MVVR\IGH
7611	37979	В	7665	1	1302	
7612	37980	Α	7666	3	1268	SCARVAAWGGKLRRGLAVSRQ
ĺ		l				AVRSPGPLAAAVAGAALAGAG
ı		ļ				AAWHHSRVSVAARDGSFTVSA
		1				QKNVEHGIIYIGKPSLRKQRFM
l		1			İ	QFSSLEHEGEYYMTPRD\FLFSV
1		1			ŀ	MFEQMERK\IQSRS*QKRFIEDT
						LSGIPTAGCGSSFFQRPWAIKGL
		1				I\SYNRVIFFFALQSSLNPIPGFH
ı						VAFKMLDTDGNEMIEKK/ENFL
l						SCRRS*VNKMT*LTVKTNETWI
	1					SGSNK*KNLKL/DTTLQMRFFG
1						KRGPRKLHYKEFRRF\WENLQT
		1	1	1		EIQGN/VEFLQFSKGLSFMRKRR
		1		1		TLQSGYFFSTNTENKDIYWKNV
		1				REKLSAGESISLDEVKAFCHCT
				1		RQIGTLCY/SAMQMFTLAHRPV
1		1				RLAEFKRAVKVATGQELSNNIL
	1	1		1		DTVFKIFDLDGDECLSHEEFLG
1	1			1		VLKNRMHRGLVGTTTSEYTRIL
	1	1	1	1		EVCEERKH
						VAFKMLDTOONEMIEKK/ENI SCRRS*VNKMT*LTVKTNETV SGSNK*KNLKL/DTTLQMRFF KROPRKLHYKEFRRFWENLC ELQGN/VEFLOFSKGLSFMRKF TLQSGYFFSTNTENKDIYWKN FEKLSAGESISLDEVKAFCHC RQIGTLCY/SAMQMFTLAHR RLAEFKRAVKVATGGELSNN DTYFKIFDLODGECLSHEEFLG

SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide inscrtion)
				sequence		
7613	37981	A	7667	2	342	ONRGPGRT*DFLPNS/VGEKILS
		l				FCNCSLGSIGALGPACCRVLSEL
						SEEQVFHVNYLDVEELSLSRLC
						QCLVELSFQLATAYHGSATTRE
		1				AARGEAACRAHLMFWCLCIWO
					ł	FCRL
7614	37982	A	7668	1	1166	VGCVLGRVEAAVTVAPAGTEE
						GMSEEEQGSGTTTGCGLPSIEQ
						MLAANPGKTPISLLQEYGTRIG
İ						KTPVYDLLKAEGQAHQPNFTF
		1				RVTVGDTSCTGQGPSKKAAKH
				l		KAAEVALKHLKGGSMLEPALE
				l	1	DSSSFSPLDSSLPEDIPVFTAAA
ľ		1				AATPVPSVVLTRSPAMELOPPV
		1				SPOOSECNPVGALOELVVOKG
l						WRLPEYTVTOESGPAHRKEFT
						MTCRVERFIEIGSGTSKKLAKR
						NAAAKMLLRVHTVPLDARDG
						NEVEPDDDHFSIGVGFRL\DVL
	ĺ					ONRGPGCTWDSLRNSVGEKILS
i						LRSCSLGSLGALGPACCRVLSE
						LSEEQAFHVSYLDIEELSLSGLC
		1			•	OCLVELSTOPATVCHGSATTRE
						AARGEAARRALQYLKIMAGSK
7615	37983	Α	7669	2	328	
7616	37984	Α	7670	181	1271	LEASLDQH*ASVHSFRSHIHVIS
						RTHRK\SQRDPSELDAEHAQKV
		1				LEMEHTQQMKLKERQKFFEEA
		l				FQQDMEQQYLSTGYLQIAERR
	1				1	GEWGLGLLVWGLTGCAGCHD
		l		l		SSWGLVRWYKCYSFKFVDEPC
						LQFERNCKPIGSMSSMEVNVD
l						MLEQMDLMDISDQEALDVFLN
		1		1		SGGEENTVLSPALGRVDKLALA
		1				EPGQYRCHSPPKLQQWCGSVM
		ı		1		NSSQRFDMLHSGNFEIHLSLLL
			l	1		VVKDWRLQGGADSPAGLTGNS
	1	1				SLFVRQAFRGVPAMGKAMGSS
		1				QVLQAPGPESSTCQNEITLQVP
						NPSELRAKPPSSSSTCTDSATRD
	1					ISEGGESPVVQSDEEEVQVDTA
1		1	l	l		LATSHTDREATPDGGEDSDS
L					L	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence ( X=Unknown, *=Stop codon, /=possible nucleotide detetion, \=possible nucleotide insertion)
7617	37985	A	7671	60	965	QRGVGGVGPRGRQRQQPEA* GEETMAAAMLETLERLLSVQ DPFTSGLAKT.DSUSRGAKVKSK PRTVPFLPKYSAGLELLSRYED TWAALHRRAKDCASAGELVDS EVYMLSAHWEKKTSLVELOB QLQQLPALIADLESBMTANLTHL EASFEEVENNLLHLEDLCGQCE LRRCKHMQSQQLENYKKNKR KELETFKAELDAFHAQKVLEM EHTQQMKLEKERQKFFEEAFQQ DMEQYLSTGYLQIAERREPIGS MSSMEVNVDMLEQMDLMDIS DGEALDGLPELWRRREHCAVP
7618	37986	A	7672	ī	124	
7619	37987	A	7673	3416	3920	CCLIKNDIKEKLHYSDCRLNVG QPCILPRNAFEFDLLIFYLGNLH FYISEIGLLGYCTFFFFFEMES SLTQAGVQ*CNLGPLQPLPPGL E*F/SCLSLPSSWDYRHVPPHWL IFVFLVEMGFCYVGQAGLEFLT SGDPPTSASQSARITGVSHHAQ PGYCILLGFC
7620	37988	A	7674	1	387	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7621	37989	Α	7675	1	1827	MKKVGGRVFWAKERASAEAL
						RHELAGLLKKCKGSAADADQG
						GLGQGCRRHSKRWEGFTRGAS
				ŀ		RAARLGNEEQDAASAGPGPNG
					ŀ	CGHLGAEEPSAAASGMDQCVT
						VERELEKVLHKFSGYGQLCER
				ŀ		GLEELIDYTGGLKHEILQSHETC
1						LSVVLLSLPMVMAGSGNLKVL
						QLCRFLHMKTGGEMNYGFHLA
						HHM\ALGTSIFGEEGRYSL\STS
					i	NSSIAALLCALYPHFPGFTALD
						NRYHLQ\ALR\HLYVL\AAEPRA
					l	FLVPVGCGTQTRPCY\ALLGSLP
						YKGTQWY\EQTKE\DLMAPTLL
						PELHLLKQIKVKGPRYWELLID
		1				LSKGTQHLKSILSK\DGVLYVK
		1				LRAGQLSYKEDPMGWQSLLAQ
						TVANRNSEARAFKPETISAFTSD
		1				PALLSFAEYF\CKPTVNMGQKQ
						E\ILDLFS\SVLYECVYPRETP\E
						ML\PAYIAMDQLIRRLGEREMS
						ETSELW\QIKLVLEFFSSRSHQE
	1	ı				RLQNPPLKRGALLMELGNSPPF
		1	t .			CKCT\INNTL\DTW\LQVRGDIC
						VNAYLTGQPL\EESQL\DMLACF
		1				LVFHFVPSSTALPTL*D*KGSTS
						FA\ELLFKFKASLKMPSAELCLR
						LAPLPSLEIPQPNGDVTVSGGEP
7622	37990	В	7676	374	515	
7623	37991	A	7677	102	1237	HSHRAACPDTNRLVPGASR*HY
		l				LHRCRSRHSSS/NIGKNI/HSLRA
		l				GAVNNQSRPQSHSSGEFSLLHD
		l				HEAWSSSGSSPIQYLKRQTRSSP
		l		i		VLQHKISETLESRHHKIKTGSPG
		l				SEVVTLQQFLEESNKLTSVQIKS
		l				SSQENLLDEVMKS\LSVSSDFLG
						KDKPVSCGLARSVSGKTPGDFY
						DRRTTKPEFLRPGPRKTEDTYFI
						SSAGKPTPGTQGKIKLVKESSLS
		l				RQSKDSNPYATLPRASSVISTAE
		l				GTTRRTSIHDFLTKDSRLPISVD
						SPPAAADSNTTAASSEYHLHQ
		1				WSSHILDIPTHTIGSCAQNDLAI
	l					DMPEPLYAQARNSRTGRSHFL
	I			l		NQTFATIRMPSDAFGMLAKDK
	L			L		HRTIYCGPFISAILIPEYRIS

SEQ ID			SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7624	37992	A	7678	1256	11971	HNCALHADSTMRGKAPLFRPT
/624	3/992	l <sup>A</sup>	/0/8	1236	19/1	
		1				YKLMEQLLLRIFRWISQKCQNV
		1				EVTSICWF/CTCTYSGWVEAYP
		1			i	TRTEKPYKKGKNDPSCTKGQC
		1				NPLELVITNPLNPHWKKGERVT
		1				LGIDRARLDPRVNILVRGGEVY
		1				ERSPEPVFQTFYDELNVPVPEIP
		1				GKTRNLFLQLAECVAQPLNVTS
		1				CYVCGGTVTGYQWPWKAREL
		ı				VPVDPVPDEFLAQKNYPDNFW
		<u> </u>		ļ		VLKPSITGQYCIAREGKKFTHP
7625	37993	A	7679	1	1710	
7626	37994	Α	7680	1	561	
7627	37995	В	7681	1	642	
7628	37996	A	7682	2	611	A CLOCKLY BY BY BY BY BY BY BY BY BY BY BY BY BY
7629	37997	A	7683	1	1718	MLSIQSTHAEKELENFFQNTED
		1				WYFHTSHHLSSLRFFSARESNC
		1				SMKLYEEAYMERYRDFLPATM
		1				WSAHTEVDVPGQATWIKQKSE
1						KDPVHLQKGKNGPSCTKGQCN
		1				PLELVITNPLDPCWKKEERVTL
		1			i	GIDGAGLDPQVHILVRGEVYKH
		1			l	SPEPVFQTFCDELNVPVPEIPGK
		1				TRNLFLQLAWHVAQCLNVTSC
		l		1		YVCGRTIIGDQWPQEAQELVPT
		1		l		DPVPDEFLAQKNHPDNFWVLK
		1			1	A\SIIGQYCIAREGKEFTHPIG*L
		1				SCRRQKLYNGTTKTIT/W/RGSS
		1			ŀ	NHTERNPFSKFPKLQTVWTHLG
		1				VP\RAWEQPPLGFLLGYVRAWS
		1			ľ	LLTGLLDHWAGSCCLLGTI\KPS
		1		l		FFPTAP*KQGKLLGFPVYASRE
		1		I		KRIIAIENWKDDEWPPPERIIQY
		1				YGPVTWAQDGLWGYQTPIYVL
		1			i	NRIIRLQAALEIITDKISRALTIL
		1				AWQETQMRNAISQNRLALDYL
		1				LAAEGGVYGKFNLTNCCLHVD
					1	DQGQVVEDIVRDRTKLAHVPV
1		1		1		QVWHEFDPGAMFGKWFPALG
				1		GFKTLIIGVLIVIGTCLLLPCLLP
7620	27008	<del> .</del> -	7604		100	VLLQMIKSFIATLVHQNASAQV
7630	37998	Α	7684	3	406	TLISFIYPAQNPELLNKLSQRKT
		1	1	I		TVLAMDQVPRVTIAQGYDALS
			1	1		SMANIAG/YLIVGGGVAGLASA
1		1				GAAKSMGAIVRGFDTRAAALE
1		1		1		QFKSLGAEPLEVDLKESGEGQG
1		1	1	1		GYAKEMSKEFIEAEMKLFAQQ
		١			000	CKEVDI
7631	37999	A	7685	1	236	
7632	38000	A	7686	11.5	978	
7633	38001	С	7687	415	453	l

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7634	38002	A	7688	3	408	
7635	38003	В	7689	1	2137	
7636	38004	A	7690	112	3688	GNWGARKLGTHINMANLLKTV
						ATGCSCPLLNNLGSCKGLRVK
		1			l	KDFLRTFYTHQELWCKAPVKP
	1					GIPYKQLTVGVPKEIFQNEKRV
						ALSPAGVQNLVKQGFNVVVES
	1					GAGEASKFSDDHYRVAGAQIQ
	1	l				GAKEVLASDLVVKVRAPMVNP
				i .	ļ.	TLGVHEADLLKTSGTLISFIYPA
	1	l		l	l	QNPELLNKLSQRKTTVLAMDQ
						VPRVTIAQGYDALSSMANIAGY
	1	1				KAVVLAANHFGRFFTGQITAA
						GKVPPAKILIVGGGVAGLAS
7637	38005	Α	7691	2	288	EFPATIQSNRARGAKPGRRVDR
		1				GPQARCFDVGGCPRSAPSNGLR
	1	1				NSEPSP*GR/CGRSPVSPALSSSR
	1	1				DVNLPCMLSSGTDSGACSEVLV
						GTLYRPL
7638	38006	Α	7692	54	522	RFHMSSLSASPPPRRLWTQMNT
	į.					QCLVFSASHLPRCQEMLFQGTV
	i					*EKPHSPRCFSPAKKPRPAGAPA
						ASHKCR/CTP*PGPPSEPTV/PSD
		ł				KAPLVGNAESQRVASPSGPPAP
	i i					CSPV\GWPGTYKAIPASGTVAP
						TPLSAGTTDMTRLCPLSLEFLL
		_				ND
7639	38007	Α	7693	3	57	RAGAGRSERAVAEES*GGLSGS
	1					CGRHNPGQSRLQRRPSQDVELE
		1				DCCRGC*SGSLWLRTLRPKRPA
						PFGGFSVPASSAASIPTGSAVVQ
						PGPLPGPTGKSPPVFAGSGPSSN
						PQPAFS\NMRTRDGSKPGSA/SF
	1	1		l	1	APLTPPLEPPAGLRAPSSGVSPL
	1	1	1	I		LPATIQSNRARARSPGDA*AAP
				l		PRPGVLTSAVPLPRRVT/CLRNS
				l		RAFAPAVRTNAVTP*PGGVSGP
	L	_				SQRRAEAA
7640	38008	A	7694	3	237	
7641	38009	A	7695	114	186	_

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
7642	38010	IA	7696	173	904	
7042	30010	I^	7090	1'3	204	NILSSTSGLETLILAAVEPSNSGD
	į.	1		1		RFTLS*ELLAVILSIGGVGLVNL
		1		ŀ	1	AGSEKPAGRDTVGSIWSLAGA
		1			1	MLYAVYIVMIKRKVDREDKLD
		1		1		IPMF\FGFAGLFNLLLLWPGFFL
		1				LHYTGFEDFEFPNKVVLMCIIIN
					ŀ	GLIGTVLSE\FLWLWGCFLTSSL
						IGTLALSLTIPLSIIADMCMOKV
		1				OFSWLFFAGAIPVFFSFFIVTLL
		1			1	CHYNNWDPVMVGIRRIFAFICR
		1				KHRIORVPEDSEOCESLISMHSV
		1				SOEDGAS
7643	38011	A	7697	1	308	SQEEGAS
7644	38012	A	7698	3	397	
7645	38013	В	7699	1	963	
7646	38014	A	7700	3	1433	KIRVTSKALELGKAQGQTGTD
						GSGRGWGRPNSGGKEGHFYYN
		1		1	1	ISE*VGGGASRSGAGPRRWRRG
		1		1		PRMLQITNASLGLRFRRQLLYW
	1	1		1		FL*GPSTLRGVESGSGGLEVLW
	1	1				GSRDPAGRMKVSNVSCOASVS
					1	RMHAAFGGTFK*APAPTPAHPF
ĺ		İ				RAPOLICLAOVWAATGRRVAR
		1				VGMLSL*EGPGELVAGESGCA
						AVMQHLRAGPFRALLFTSNLD
		1				MDFRVSCLGWCMTSDFLTRPL
		ı				SLLSLQEEERMVYVAFSEFFFD
		1			i e	SAMESYFRAGALQLLLVGDKV
	l	1				CHGLFVGWAREGL*QSSLPHC
	l	1		1		AGGGRDRATCTPVRPRRGAAIK
	l				1	PSGTTISVTASVTIALVPPDQPE
		1				VQLSSMTMVRVPEWGLLAGG
		1				QGKMGCGLLSR*AGALPCTSVI
		1				GGQSHLSTGMGWAGFVRS*PS
	ł					PSPRKA/RGVRMEEER\GVNWA
		1	1			GPD*ATNHAVSGGRMGKEGGP
	1					SPLSIAPQCHRPADVRASTAPTP
7647	38015	Α	7701	2	391	MALRGKALRTTSDLRRFRIYSN
						HSATWKSLA/L*IPLQAPLK\TM
				i		LPELG*MPQCSNERT\WRG\VQ
						DPHYPEGIKLCAMKVVTNPCGI
ì						PSPIGA*SPTFAKGLREVIEKNR
		1				P\ADVRAS\TAPTPSHSSCLSP
7648	38016	A	7702	1	189	
7649	38017	Α	7703	202	455	KCDILPTALDSIHH/SSHRVHLA
	1	1	l	1	l	HSPHSLQ**HPHPLAQPSQQDRP
1	1		1	1		SVPL**MSLADPESHLSESHSHF
		L				HL*PACRV*AYDLLPL
7650	38018	Α	7704	313	378	

	SEQ ID NO:		SEQ ID NO:			Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletiun, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	of peptide sequence	determin, (~possible nucleotide invertion)
7651	38019	Α	7705	126	1246	PNGLRPPCPSPASETPGNAPVCD
		l		:		PGSSSQGAQGKLNAWWAPGM
		l				A/ASRSLHSLHPVR/RACALPAQ
		l				SLLGPLRSFRCHLSDPVFRTGAP
						PGQGSWQYKVLVHAQERELTQ
						LREKLREGRDASRSLNEHLQAL
						LTPDEPDKSQGQDLQEQLAEGC
						RLAQHLVQKLSPENDNDDDED
						VQVELAEKVQKSSAPREMQKA
			l			EEKEVPEDSQEECAITYSNSHGP
		l				YDSNQPHRKTKITFEEDKVDST
		l				LIGSSSHVEWEDAV/HHYSRK*
						K***GRGRKRASVSQKPEETPS\
		1				PRPEPPRGSGEAERSVGSWDA
						SSRSLRRLHPLREPVPTLPSRFR
		1				GRCGASAAIFGSCVPHGGSTRA
						GMMGSKEVGKGGDPGEETSPV
		<u> </u>				ALFS
7652	38020	A	7706	3	5665	LLEKLRQRIHDKAVALERAIDE
		i				KFSALEEKEKELRQLRLAVRER
						DHDLERLRDVLSSNEATMQSM ESLLRAKGLEVEQLSTTCQNLQ
ĺ			ŀ			WLKEEMETKFSRWOKEOESIIO
ŀ						QLQTSLHDRNKEVEDLSATLLC
ļ	ļ	l				KLGPGOSEIAEELCORLORKER
		l				MLQDLLSDRNKQVLEHEMEIQ
		l				GLLQSVSTREQESQAAAEKLVQ
		1				ALMERNSELOALROYLGGRDS
						LMSQAPISNQQAEVTPTGRLGK
						QTDQGSMQIPSRDDST
7653	38021	В	7707	1	1098	
7654	38022	Α	7708	193	5850	HCQRNTTGEHCEKCLDGYMIK
		l				S*DSLFGDVWN*LPIFASNFSFA
						EL*K*GFVRDYHK*TFVCS/CLL
			ŀ			NP*GPEFVGKKIKRKKNHDAK
		l				YLNV*YS/CFRCAPGYYGNPLLI
		l				GSTCKKCDCSGNSDPNLIFEDC
		1				DEVTGQCRNCLRNTPGKYCHIL
						SIKKCISRLLFLFPTVCNCGGGP
		{				CELH*EQNFWFKNYFNSRHPLP
			ŀ			QTDVSWCSAKTACL*HAFDL*F
			l			*RNVSPPGCDKCVWDLTDALR
l	ŀ	1				LAALSIEEGKSG

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence ( X-Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
7 <b>6</b> 55	38023	Α	7709	I	713	TPCFESPN/ETGTYFSTKAGYVL
		ŀ				LN/ESSN/IGIEFEIAFKVRPRSSS
						GTLVHGHSVNGEYLNVHMKN
						GQVIVKVNNGIRDISTSV\TPKQ
		l				SLCDGRWHRIT\VIRDSNVVQL
		Į.				DVDSEVN\HVVGPLGIQKPIDH
						REPVL\VGGVPRILY*HPRFCPP
		1				QNPFTG\CIR\HFVIDGPPQWSFQ
		l l				VKAAPGQAGARKASNSLSQQP
		l			ŀ	GHGQKHSCPKYKVPLRALEKE
						HKASPGGTVTLSFGVGSFSSS
7656	38024	A	7710	3	322	DGVSHCRPGWSAVA*SQLTAT
		l			ŀ	STSWVQMIACFTLPSSWDYRCT
		l			1	PPCLTNFCVCIFSRDRVWAMLA
		l				GW\LKNS*PQAIRPPQPPKVLGI
		<u> </u>				TGHEPRAPGQKILTFHILT
7657	38025	Α	7711	2	480	YSPPECPFCGKIEEHSEDMETH
		l				VKTKHANLLDIPLEDCDQPLYD
		1				CPMCGLICTNYHILQEHVDLHL
		1			ŀ	EEN\TFSKAWIESSVLVIYNWLT
		1				SFSKKKTERGD/PEESRQEIEEF
	1	1		ŀ		QKLQRQYGLDNSGGYKQQQLR
		1			ŀ	NMEIEVNRGRMPPSEFHRRKA
		<u> </u>				DMMESLA
7658	38026	A	7712	187	468	MINISTER OF THE PROPERTY OF TH
7659	38027	Α	7713	I	1110	MHCIETGVERRILGLLLFRGSLA
		1				SVIRPGEVLDAAHALVCQRGPK
		1				GKPSGAQCGSCWPLGRPKALT QLVPASFVCLACAFGAERLGDS
		1				ALRSSDLTHHLLVNTMLSCNIC
		1	ļ		i	GETVTSEPDMKAHLIVHMESEII
						CPFCKLSGVNYDEMCFHIETAH
						FEONTLERNFERINTVOYGTSD
		l				NKKDNTLOCGMEVNSSILSGC
		1	ľ	l		ASNHPKNSAQNLTKDSTLKHE
		l				GFYSENLTESRKFLKSREKOSSL
		1				TEIKGSVYETTYSPPECPFCGKI
		l				EEHSEDMETHVKTKHANLLDIP
		1		1		LEGMDRVQCSGDLQLAHQLQQ
		1				EEDRKRRSEESRQEIEEFQKLQR
		l				QYGLDNSGGYKQ\NNYEIWR*
		l				K*IGEECLHLNFIGEKLI
7660	38028	A	7714	2	303	K IOLECENEN IOEKEI
7661	38029	A	7715	97	233	RTVTCYHRNSRACHPOOITSCP
, 301	30025	ľ	1,,,12	ľ'	233	*HRALPCLPLWSPKCPSRWPWF
		l		l		G
			1	ı	1	
7662	38030	Δ	7716	229	359	MKWVYCSVTGMGKGOHRMP\
7662	38030	Α	7716	229	359	MKWVYCSVTGMGKGQHRMP\ SKG*GWVQRYNRDGIPSPRVLE

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	Ì	l	ŀ	sequence		
7663	38031	A	7717	1	1185	MSTIDDPRLOGRRMCLMLRGT
7003	38031	1^	l''''		1103	PEQKALVIGGEACMWGEYVDN
		1			\	TNLVPRLWLCPPSTQDLANEGI
		1				REMTILHRHIPDRGKGVMRSCS
		l				FRTPRPFTLACGPEKSLMDPOS
		1				OSNSEGASSSLVVKLADTDRER
		l				
		l				ALRRMQQMAGHLGAFHPAPLP
			Ì			LGACGAYTTAILQHQAALLAA
		l				AQGPGLGPVAAVAAQMQHVA
		l				AFSLVAAPLLPAAAANSPPGSG
		1				PGTLPGLPAPIGVNGFGPLTPQT
		1	l			NGQP\APTRSTITGSPLi/SGWSQ
	l	1				SRPILRIMKYAEQRIPTLNEYCV
		1				VCDEQHVFQNGSMLKIQPDTII
	ł	1				QVWREDIPVNYMKELELVTKA
ŀ	I	l				GFRALLSAPWYLNRISYGPDW
	1	1				KDFYIVEPLSFEGTPEQKALVIG
	l .	l				GEACMWGEYVDNTNLVPRLW
		<u> </u>				AHRIQL
7664	38032	В	7718	I	1196	
7665	38033	В	7719	184	1689	
7666	38034	Α	7720	228	407	
7667	38035	A	7721	1	725	MQRGALSPVLMLSAAPEPPPRP
ĺ		ł				PPGLSPPGSGPGSGSRHGSARPG
						PTPEPSGSLGAALDSSLRAAVA
		ł				FKAEGQRCYREKKFREAIGKY
		l				HRALLQLKAA/LGGPP*RPARP
		1				RPPGPTSSPGPARLSEEQRRLVE
						STEVECYDSSPA\CLLQSELVNY
		l			l	ERVREYCLKVLEKQQGNFRPP
	l	l				YRAG\IAFYPLGDYARALRFLQ
		1				EAPSREPPDTNVLRYI\QLTQLK
		1				MNRCSLOREDSGAGSOTRDVI
7668	38036	A	7722	1	262	NGKEPGRYTFEDAOEHIYKLM
						KSDSYPRFIRTSAYQELLOAKK
	1	1	l		l	KGRNIPIFPCHKNCTPTLRASTN
					1	LL*KEGKSLTSKRLTSLAQSY
7669	38037	Ι_Δ	7723	1	1392	55 125112111111111111111111111111111111
7669	38037	A	7723	1	1392	DE REUKSLISKKEISEAC

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		l
		<u> </u>				<u> </u>
7670	38038	A	7724	1	1544	MAQGNNYGQTSNGVADESPN
1						MLVYRKMEDVIARMQDEKNGI
l						PIRTVKSFLSKIPSVFSGSDIVQ
l						WLIKNLTIEDPVEALHLGTLMA
					l	AHGYFFPISDHVLTLKDDGTFY
						RFQTPYFWPSNCWEPENTDYA
						VYLCKRTMQNK\ARL\ELADYE
		1				AESWA/RGLQRAFAPKW\EFIF
		1				M\QAGAQAKVDKKRDKIERKIL
						DSQERAFWDVHRPVPGCVNTT
						EVDIKKSSRMRNPHKTRKSVY
						GLQNDIRSHSPTHTPTPETKPPT
		ı				EDELQQQIKYWQIQLDRHRLK
		1			1	MSKVADSLLSYTEQYLEYDPFL
		i				LPPDPSNPW\LSDDTTFWELE\A
ļ	1					SKEPSQQRVKRWGFWAWDEGI
		l				GKTQLGRRNSFLKIF*EFRISGS
İ		l				GNFKVLGWASGRTLKKRPF\KE
İ		1				VPSRVQEIWQEFLAPGAPSAINL
		1				DSKSYDKTTQNVKEPGRYTFE
		ł				DAQEHIYKLMKSDSYPRFIRSS
	i	1				AYQELLQAKKKGKSLTSKRLTS
		1				LAQSYLNGSSCSMNADWSHCT
	ľ	1				HFVAQCCDLEQRTLEQDVA
7671	38039	С	7725	81	439	
7672	38040	Α	7726	531	686	GWQWLHRPPGATQHCGGNLP
		1				AEESLPARATN*ARPAAHTRGG
		1				RGQDLPPGG
7673	38041	Α	7727	93	428	LHCQVHLSLIDLPLLI\SFLLLLF
		1				*D*VSLLLPRLECSGAISSHCSL
		1				H/LGPGSRDSPASAS*VAGITGT
		1				CHHVQLIFVFLLETGFHRVSQD
		1				GLDLL/NLVIRLPRPPKVLGLQA
7674	38042	В	7728	99	425	
7675	38043	Α	7729	35	861	
7676	38044	В	7730	141	586	
7677	38045	Α	7731	116	926	AEIVAQEVSEEGGKSRKGPQFG
		ı				KSQYQELIRRSECGLNRGEGESI
		ı				KANMQQVIYIFPITLAEVVLRP
		1				HSYPSKKTGLTLLAAASIAYISR
		1		1		*EWLYFETGTWVYPVFAKLSLL
		1				GLAAFFSLSYVFIASIYLLGEKL
		1				NHWKW\VSVRNSTLILYIRMAK
		1				SHTQSPTSLAHMPFCSIKIEMAE
		1			1	VPSSAQSMNWCEKLLVFPPR*C
		1				CFLRPRDSVSPPVFAWFILMHF
1		1			1	NTRLFQEAFPGQPQILQRWRLE
		1				SVGICFQWPDWKSPAKHQLVK

SEO ID	Tero in No.	Mat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence ( X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	
1.0.	sequence	""	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	Jacque nec			sequence	,	
	i			1	1	l
7678	38046	IA	7732	32	394	GKAVLPIMRETLGDFHYQIHCC
		1.		1		PDLPGTDLGHPGSPDLGEVKFL
	1					SQT*EVTSLQVSGKVWR*WTAI
1	1					CTHTSQSLSISLL\FCLRSASATS
1	1					LTLSHCVNVVKGLLDFKKRRG
1	1			1		HSIGGAPEOR
7.770	22047	+-	7722	<del> </del>	765	HSIGGAPEQA
7679	38047	A	7733	1		
7680	38048	A	7734	3	1295	QARVSQELKKAAKRTVSISEGP
		1				DTLGDGMRERRETLALAPEPEP
1	1				1	LEKEACEKWKRPFRSASATSLT
				I		LSHCVDVVKALLDFKKRRGHS
						GGAPEQRYQIIPVCVAARLPTR
						AQDVLDAHLSEVQCCSF\GPNS
						SLLATGGADRLIHLWNVVGSR
	1					LEANQTLEGAGGSITSVDFDPF
			l	1		G/SNQVLAATYNQAAQLWKVG
						EAOSKETLSGHKDKVTAAKFK
		1		1		LTRHQAVT\GSRDRTVKEWDL
						GRAYFSR\TIQCSFSYCNDVVCG
i	į.					DHIIISGHNDOKIRFWDSRGPHC
1		1		į.		
		1				TQVIPVQGRVTSLSLSHDQLHL
1						LSCSRDNTLKVIDLRVSN\TARG
		1				FRADGFKCGSDWTKAVFSP\DR
1		1				SYALATLPVMGPF*IWECGTPG
		1		l	į .	KNWKKQELTGTPIALPVQTPW
		1			ŀ	PWCLLPGSPHGETWTQGRKGC
						AFGSRAHDLPALGWRLLPEA
7681	38049	Α	7735	123	463	DVEVGLISQLQDCELGGCIPLK
		1				VFPAVFRLPLSLHTFLPLPLSRT
		1				LASGGDGATSASCCRCPGAVSI
	İ					S*L*OTVASP*VLVFVHSRKE\T
						GKTARAIRDMCLEKDTLGLFLR
7682	38050	A	7736	1	489	
7683	38051	A	7737	1	423	
7684	38052	В	7738	i	900	
7685	38053	A	7739	<del></del>	1824	
7686	38054	B	7740	400	969	
		A	7741	3	4781	EISATOIIVCTPEK WDIITRKGGE
7687	38055	I <sup>A</sup>	//41	3	4/81	
						RTYTQLVRLIILDEIHLLHDDRG
	1	1				PVLEALVARARRNIEMTQEDVR
	1	1				LIGLSATLPNYEDVATFLRVDP
		1		1		AKVLFYFDNSFRPVPLEQTYVG
1	1	1				ITEKKAIKRFQIMNEIVYEKIME
		1	1			HAGK\NQVLVFVHSRKETGKT
	1	ı				ARAIRDMCLEKDTLGLFLREGS
1	1	1	1			ASTEVLRTEAEQCKNL*LKDLL
1	1	1	i			PYGFAIHHAGMTRVDRTLVED
1		1				LFA\DKHIQVLVSTATLAWGVN
						LP*H\TALFK
7600	20057	-	7740	-	610	LI INIALEK
7688	38056	A	7742	2	518	L.,